

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 02:17:22 ; Search time 934 Seconds
(without alignments)
1440.553 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggagaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New.*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2745	100.0	2745	6	US-10-647-956A-5
C 2	44.6	1.6	3352	6	US-10-750-185-46142
3	42.4	1.5	2025	6	US-10-750-185-36257
4	41	1.5	152335	7	US-11-121-086-73
C 5	40	1.5	199321	7	US-11-121-086-10
6	39.8	1.4	40000	6	US-10-995-561-13509
7	39.4	1.4	1423	6	US-10-750-185-56105
C 8	39	1.4	151828	7	US-11-117-187-197
9	38.2	1.4	1306	6	US-10-750-185-25909
C 10	38	1.4	82596	7	US-11-117-187-207
11	38	1.4	1082144	7	US-11-117-187-211
C 12	37.8	1.4	1624	6	US-10-750-185-29572
13	37.6	1.4	1908	6	US-10-750-185-59339
C 14	37.6	1.4	50959	7	US-11-117-187-210
15	37.6	1.4	72600	7	US-11-117-187-206
C 16	37.4	1.4	4417	6	US-10-821-234-350
17	37.2	1.4	53323	6	US-10-995-561-13345
C 18	37.2	1.4	398287	6	US-10-995-561-13396
19	36.6	1.3	1513	6	US-10-750-185-26295
C 20	36.4	1.3	1720	6	US-10-750-185-25513
21	36.4	1.3	193084	7	US-11-121-086-82
C 22	36.4	1.3	207908	7	US-11-112-908-21
23	36.2	1.3	146656	7	US-11-121-086-68

24	36.2	1.3	150437	7	US-11-112-908-44	Sequence 44, Appl
25	36.2	1.3	150491	7	US-11-112-908-46	Sequence 46, Appl
C 26	36	1.3	600	6	US-10-750-185-363	Sequence 363, App
27	35.8	1.3	633	6	US-10-793-626-2863	Sequence 2863, Ap
28	35.8	1.3	633	6	US-10-793-626-3319	Sequence 3319, Ap
29	35.8	1.3	3030	6	US-10-793-626-4246	Sequence 4246, Ap
30	35.8	1.3	3734	6	US-10-793-626-4103	Sequence 4103, Ap
C 31	35.6	1.3	3032	7	US-11-000-463-659	Sequence 659, App
C 32	35.6	1.3	3405	7	US-11-000-463-187	Sequence 187, App
33	35.6	1.3	3535	6	US-10-750-185-48788	Sequence 48788, A
34	35.4	1.3	600	6	US-10-750-185-368	Sequence 368, App
C 35	35.4	1.3	600	6	US-10-750-185-3634	Sequence 3634, Ap
C 36	35.2	1.3	482	7	US-11-123-896-301	Sequence 301, App
37	35.2	1.3	1523	6	US-10-750-185-36494	Sequence 36494, A
C 38	35.2	1.3	1540	6	US-10-485-517-39	Sequence 39, Appl
C 39	35.2	1.3	1565	6	US-10-750-185-46922	Sequence 46922, A
40	35	1.3	399	6	US-10-467-657-8213	Sequence 8213, Ap
41	35	1.3	1659	6	US-10-750-185-53431	Sequence 53431, A
C 42	35	1.3	4399	6	US-10-750-185-44371	Sequence 44371, A
C 43	35	1.3	170837	7	US-11-121-086-97	Sequence 97, Appl
C 44	35	1.3	199130	6	US-10-995-561-13233	Sequence 13233, A
C 45	35	1.3	241805	6	US-10-995-561-13215	Sequence 13215, A

ALIGNMENTS

RESULT 1

US-10-647-956A-5

; Sequence 5, Application US/10647956A

; Publication No. US20050251878A1

; GENERAL INFORMATION:

; APPLICANT: firench-Constant, Richard

; APPLICANT: Bowen, David

; APPLICANT: Rocheleau, Thomas

; APPLICANT: Waterfield, Nicholas

; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS

; FILE REFERENCE: 61645

; CURRENT APPLICATION NUMBER: US/10/647,956A

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514

; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: US 60/191806

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 2745

; TYPE: DNA

; ORGANISM: Photorhabdus luminescens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2745)

US-10-647-956A-5

Query Match 100.0%; Score 2745; DB 6; Length 2745;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGCAGTTACAAATTCGCAATTCGCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60
Db	1	ATGAGCAGTTACAAATTCGCAATTCGCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60
Qy	61	AGGAATTAATGCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Db	61	AGGAATTAATGCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy	121	GAATTAATACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAGAACCGATCCT	180
Db	121	GAATTAATACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAGAACCGATCCT	180
Qy	181	CGTAAATAAATAAACAGACGCGCCCAAAATTCATTCGTGTCCTTTTAACTCTTGGCGGTCAA	240

Db 181 CGTAAAAATAAAACCAGAGCGGCCCAAATTTTCATTCGTGTCCTTTAAATCTTTGCCGGTCAA 240
Qy 241 GTTTTACGTGAAGAAAGTGTGATCCGGTCCGACTATTACCCCTCAATGATATTGAAGT 300
Db 241 GTTTTACGTGAAGAAAGTGTGATCCGGTCCGACTATTACCCCTCAATGATATTGAAGT 300
Qy 301 CGCCCGGTGTGTATCATCAATGCAACCGGTGTCCGCCNAACCAATCGTTATGAAGATAAC 360
Db 301 CGCCCGGTGTGTATCATCAATGCAACCGGTGTCCGCCNAACCAATCGTTATGAAGATAAC 360
Qy 361 ACCCTTCCCGTCTGCTGCTGCTATCACCGAAACAAGTACAGGAGGAGAGAAACGACC 420
Db 361 ACCCTTCCCGTCTGCTGCTGCTATCACCGAAACAAGTACAGGAGGAGAGAAACGACC 420
Qy 421 GAACGTCTTATCTGGGCGGGAATACGCCGCAAGAAAAAGATTACAACCTCGCCGGTCTAG 480
Db 421 GAACGTCTTATCTGGGCGGGAATACGCCGCAAGAAAAAGATTACAACCTCGCCGGTCTAG 480
Qy 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC 540
Db 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC 540
Qy 541 GTCGTGCTATCACAAATCTCAACAACCTGCTTACCATAACCAAGGATGCCGACTGCACAGGT 600
Db 541 GTCGTGCTATCACAAATCTCAACAACCTGCTTACCATAACCAAGGATGCCGACTGCACAGGT 600
Qy 601 GAAGACAGAGCCTCTGGCAACAAAACTGAGTAGTAGTGTCTATATACCCCAAGTAAAC 660
Db 601 GAAGACAGAGCCTCTGGCAACAAAACTGAGTAGTAGTGTCTATATACCCCAAGTAAAC 660
Qy 661 ACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCACGGCGTG 720
Db 661 ACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCACGGCGTG 720
Qy 721 GCCTATGATGCGCGGCGAGCTAAAAGGGAGTTGGTTAAACACTCAAAAGGTCAGCGCGAA 780
Db 721 GCCTATGATGCGCGGCGAGCTAAAAGGGAGTTGGTTAAACACTCAAAAGGTCAGCGCGAA 780
Qy 781 CAGGTGATTCAAAATCGCTAACTACTCCGCGCGCGGGGCAAAAAATTCAGTGAAGAGCAC 840
Db 781 CAGGTGATTCAAAATCGCTAACTACTCCGCGCGCGGGGCAAAAAATTCAGTGAAGAGCAC 840
Qy 841 GGTAAACGGGATGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGCTTATCGGCATT 900
Db 841 GGTAAACGGGATGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGCTTATCGGCATT 900
Qy 901 ACCATCGCCGTCCATCAGACGCCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Db 901 ACCATCGCCGTCCATCAGACGCCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Qy 961 GTAGGCAATGCTAATTAATCCGTAAATGATCGGGAAGCCACTCGCTTTTGGCGCAATCAG 1020
Db 961 GTAGGCAATGCTAATTAATCCGTAAATGATCGGGAAGCCACTCGCTTTTGGCGCAATCAG 1020
Qy 1021 AAAGTAGCCCGGAGAAATAGCTATACCTTACCATTCCTGTATACGCTTATCAGCGCCACC 1080
Db 1021 AAAGTAGCCCGGAGAAATAGCTATACCTTACCATTCCTGTATACGCTTATCAGCGCCACC 1080
Qy 1081 GGGCGGAAATGGCCAATATCGGTGAGCAAAACCAACCTTCCCTCGCCTACCT 1140
Db 1081 GGGCGGAAATGGCCAATATCGGTGAGCAAAACCAACCTTCCCTCGCCTACCT 1140
Qy 1141 TCTGACAAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAT 1200
Db 1141 TCTGACAAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAT 1200
Qy 1201 CTGACGAAATTCGSCACAGCTCGCCAGCTACCCAGAACACTACCGTGGCTATCAC 1260
Db 1201 CTGACGAAATTCGSCACAGCTCGCCAGCTACCCAGAACACTACCGTGGCTATCAC 1260
Qy 1261 CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTAGCTTAAACCGATCCAAATCAAGTG 1320
Db 1261 CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTAGCTTAAACCGATCCAAATCAAGTG 1320

Qy 1321 GATACGTTGTTTCATGCGCGTGTGCACAAACCCAGTTTATTATCCCGGACAGACACTTATC 1380
Db 1321 GATACGTTGTTTCATGCGCGTGTGCACAAACCCAGTTTATTATCCCGGACAGACACTTATC 1380
Qy 1381 TGGACACACGAGGAGGTAAAGCAGGTAAATAATTTGGCCCGGAAATAGTGGTACCGC 1440
Db 1381 TGGACACACGAGGAGGTAAAGCAGGTAAATAATTTGGCCCGGAAATAGTGGTACCGC 1440
Qy 1441 TAGCAGACGAAACCGCATGAGACAACTGAAAAGTGAAGTGAACAGCAACCCAGAAATACG 1500
Db 1441 TAGCAGACGAAACCGCATGAGACAACTGAAAAGTGAAGTGAACAGCAACCCAGAAATACG 1500
Qy 1501 CAGCAACACCGGTAAATCTATTTTGGCGGACTCGAGCTAGCACAACCCAGAGCAACGCC 1560
Db 1501 CAGCAACACCGGTAAATCTATTTTGGCGGACTCGAGCTAGCACAACCCAGAGCAACGCC 1560
Qy 1561 ACAACACGGAAGGTATACACGTTATCACATCTCGGTGAAGCCGCTCGCGCACAGGTACGG 1620
Db 1561 ACAACACGGAAGGTATACACGTTATCACATCTCGGTGAAGCCGCTCGCGCACAGGTACGG 1620
Qy 1621 GTGTTGCACTGGGAGAGCGGTAAAGCCAGAAAGATGTCAAATAATCAACTACGTACAGC 1680
Db 1621 GTGTTGCACTGGGAGAGCGGTAAAGCCAGAAAGATGTCAAATAATCAACTACGTACAGC 1680
Qy 1681 TAGCATAACTCGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATATTCAGC 1740
Db 1681 TAGCATAACTCGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATATTCAGC 1740
Qy 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGACGCTGTGGGCAGCAAAACAGCAACAGAA 1800
Db 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGACGCTGTGGGCAGCAAAACAGCAACAGAA 1800
Qy 1801 GCACGCTAATAAACGATTCGCTATTCCGGCAAAAGAGATGCCACCCGGGTTGTATTAT 1860
Db 1801 GCACGCTAATAAACGATTCGCTATTCCGGCAAAAGAGATGCCACCCGGGTTGTATTAT 1860
Qy 1861 TAGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGGACCCGGCAGGA 1920
Db 1861 TAGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGGACCCGGCAGGA 1920
Qy 1921 ACCATTGATGGGTGATCTATACCGAAATGGTAAGAAATAATCTCTGTAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGGTGATCTATACCGAAATGGTAAGAAATAATCTCTGTAGTTTACAAGAT 1980
Qy 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Qy 2041 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCANAATGGAAACGAAAGAGC 2100
Db 2041 TTAATAATTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCANAATGGAAACGAAAGAGC 2100
Qy 2101 AGTTATACAAAAATAAATCAATTTGAAAGTGGTTCTGTCGTCGATCCGATCCGTCGGGT 2160
Db 2101 AGTTATACAAAAATAAATCAATTTGAAAGTGGTTCTGTCGTCGATCCGATCCGTCGGGT 2160
Qy 2161 TATTTGCTAAGCCAGGAAGTTACTAAAGAGTATAGAAAAAGTCAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCAGGAAGTTACTAAAGAGTATAGAAAAAGTCAAATCATATATAGC 2220
Qy 2221 CGACTTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Db 2221 CGACTTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Qy 2341 CATAAATATAGAAAGTAAATCACCTGATTTTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400
Db 2341 CATAAATATAGAAAGTAAATCACCTGATTTTTTATTCAGAAACCGATTTCTTTGGGTTAATG 2400

QY 2401 GATAAAGTGAAAAAATGATTATTCGGGTGAAAGAAAAATTTATGCGCAATGGAGTT 2460
DB 2401 GATAAAGTGAAAAAATGATTATTCGGGTGAAAGAAAAATTTATGCGCAATGGAGTT 2460
QY 2461 AAGGTTTATCATGATTAAATAAATAAACAATCAGAAATACATGTCACATTCATTCGCGC 2520
DB 2461 AAGGTTTATCATGATTAAATAAATAAACAATCAGAAATACATGTCACATTCATTCGCGC 2520
QY 2521 CATCCCTATACGCAATAGTAATGAAGAAAGAGCGCTGTTCAGAAACAGAACCCGCT 2580
DB 2521 CATCCCTATACGCAATAGTAATGAAGAAAGAGCGCTGTTCAGAAACAGAACCCGCT 2580
QY 2581 ATTGCAATAGATAGAAATATTAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAAGCA 2640
DB 2581 ATTGCAATAGATAGAAATATTAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAAGCA 2640
QY 2641 ATTAAAAATCATTTGAAGGACATATAATTTATAGGATATCAACAGAGGCTATTATATT 2700
DB 2641 ATTAAAAATCATTTGAAGGACATATAATTTATAGGATATCAACAGAGGCTATTATATT 2700
QY 2701 CGCTCTGCGGCTATCGCTGAGATTTAGGAATCGGAGAACTTCA 2745
DB 2701 CGCTCTGCGGCTATCGCTGAGATTTAGGAATCGGAGAACTTCA 2745

RESULT 2
US-10-750-185-46142/c
; Sequence 46142, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46142
; LENGTH: 3352
; TYPE: DNA
; ORGANISM: Bovine 19866881360268
US-10-750-185-46142

Query Match 1.6%; Score 44.6; DB 6; Length 3352;
Best Local Similarity 49.2%; Pred. No. 0.12;
Matches 146; Conservative 0; Mismatches 149; Indels 2; Gaps 1;
QY 2201 AAAGTCAAATCATATATAGCCGACTTGAAGAAAAAGCTCCCTTTTCAGAAAAATCAAAA 2260
DB 3323 ATGTCAATATATCAATAAATAAAGTGAAGAAAAAGCTCAATAAATAATTTCTAATA 3264
QY 2261 CGAATCTTTTATGATCTGAATATCCGGTTATATGCGCAAGAACCATCAAGATACGA 2320
DB 3263 TAAATCAAAGAAAGCAGATGAATGAACAAACAAAGCAAGAAATTCATAATATGAAAA 3204
QY 2321 TATCAGAAATGCGGAAGACATAAATATAGAGTATACCCCTGATTTTATTCAGAA 2380
DB 3203 AAAAATACTATAAAGATAAGTAAAAAATCATTTTATTTAAAGACTTATATTTGCAAA 3144
QY 2381 CCATTTCTTTGCTTAATGATAAAGTCAAAAAATGATTATTCGGTGAAGAAAAA 2440
DB 3143 CCCTCACA--GATTATTAAGACAAAGAGCAATGAATAAAGAGATGTTATCATTA 3086
QY 2441 TTTATGCGGCAATGGAGGTTAAGGTTTATCATGATTTTAAAAAATAAACATCAGAA 2497

DB 3085 CAGATGAGGTATAGTATATTAAGGATACTTCATGTTAATAATAGAGAAAAACCAGAT 3029
RESULT 3
US-10-750-185-36257
; Sequence 36257, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36257
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Bovine 19866881087862
US-10-750-185-36257
Query Match 1.5%; Score 42.4; DB 6; Length 2025;
Best Local Similarity 57.6%; Pred. No. 0.34;
Matches 76; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2506 AACTATGCAATGCGCCATCCCTATACGCAATTCAGTAATGAAGAAAGAGCGCTGTTGCAA 2565
DB 45 AATAATCCATTTGTCAAACTTTGTACACACCACCAATTAAGAAAAAGAACTATTTAAGA 104
QY 2566 GAAACAGAACCGCTATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTGCAAAATTC 2625
DB 105 GCAACTGTAATCAAAATTTACAAATTAAGAGAGATCACAATTTCAAGGCTTTATACAGATTA 164
QY 2626 CTGACAAATGAAA 2637
DB 165 AATAAAACTAAA 176
RESULT 4
US-11-121-086-73
; Sequence 73, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, TIM S.
; APPLICANT: POULSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 152335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-73
Query Match 1.5%; Score 41; DB 7; Length 152335;
Best Local Similarity 46.4%; Pred. No. 7.7;
Matches 134; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 2194 ATAGAAAAAAGTCAATCATATATATACCGCACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAA 2253

```
Db 58783 ATACATATACATCTATATGTATATAGATATATAGATATATATGTATATAGATATATGTAGAT 58842
Qy 2254 TCAAAAACGAATCTTTCTTTAGGATCTGAATATCCGGTTATATGCGAAGCAACATACAA 2313
Db 58843 ATATATCCATATATTTATATAGATATATACATATGTATATAGATATATTTATATATGTAT 58902
Qy 2314 GATACGATATCAGAAATATGCGAAGACATATAAATAGAAAGTATACCCCTGATTTTAT 2373
Db 58903 ATACCTATATACGTATATAGATATATACATATATACATATATGTATATATAGATATATAT 58962
Qy 2374 TCAGAAACCGATTTCTTTGCGTTAATGATGATAAAGTGAAAAAATGATTATTCGGTGAA 2433
Db 58963 ACATATATACATATGTATACATAGATGTATACATATGTATATATGTATATACATCTATGTAT 59022
Qy 2434 AGAAAAATTTATGCGCAATGAGGTTAAGTTTATCATGATTTAAAAA 2482
Db 59023 ACATAGATGTATACATCTATGTATATACATAGATGTATATACATAGATATATA 59071

RESULT 5
US-11-121-086-10/c
; Sequence 10, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 10
; LENGTH: 199321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-10

Query Match 1.5%; Score 40; DB 7; Length 199321;
Best Local Similarity 50.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 2481 AAATAACAATCAGAATTACATGTCACTATGCAATGGCCCATCCCTATACGCAATTGAG 2540
Db 51397 AAAAAAACCTGGAGAATTAGGTTTCTGTTCTGCTTTGCCCACTAATTATGTGACCTTGA 51338
Qy 2541 TAATGAAGAAGAGCGCTGTTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAGAATA 2600
Db 51337 TAATGCTTAATTGATTGAATATCCCTAACATAGAGGTTAGTTTACATGAATC 51278
Qy 2601 TAATTTCAAAGGTTTGGCAAAATTCCTGACAATGAAAGCAATTAAAAAATCATTTGAAAGG 2660
Db 51277 CAAGTGTCTGTGCTTTAAAGTCTGTAAGTCTAGCAATTGAAACTACAGTACAG 51218
Qy 2661 ACATAAAATTA 2672
Db 51217 AAAAAAAAAAAAA 51206

RESULT 6
US-10-995-561-13509
; Sequence 13509, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
```

```
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13509
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7;
US-10-995-561-13509

Query Match 1.4%; Score 39.8; DB 6; Length 40000;
Best Local Similarity 48.2%; Pred. No. 7.9;
Matches 144; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

Qy 2144 ATTCCGATCGTTCGGGTATTTGCTAAGCCACGAGAGTTACTTAAAGGTATGAAAAA 2203
Db 14127 ATTTAAATACTTCTGTCAATTAGGACAGTTTGAGAAAAAGAGATAACAAAAATCAAAAGCAA 14186
Qy 2204 GTCAATCATATATAGCCGACTTGAAGAAAAACAGTCCCTTTTCAGAAAAATCAAAACGA 2263
Db 14187 AACTCAAACTTTGTACTGAAAAATCTAATAAAACACTGACTTAATTATAGAAAAACCTAAGA 14246
Qy 2264 ATCTTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATACGATAT 2323
Db 14247 AACTCATATCAATTAATAAAATTT---TAATATGAGAGAACCATATATGACACCTTTCT 14303
Qy 2324 CAGAAATATGCCAAGAGCATATAATAGAAAGTAAATCACCCTGATTTTATTCAGAAACCG 2383
Db 14304 GCCAATATATTTGAAAAACAGATAAATAGGATTTATTGTTAGAAATTTGTCAGAGAAATG 14363
Qy 2384 ATTTCTTTGGTTAATGATAAAGTGAAAAAATGATTTATTCGGTGAAAGAAAAATTT 2442
Db 14364 AAATACTTGGTTGATGAATAACAGTTACAGAAATTCGATTGCAATTTAAAAAATAAATTT 14422

RESULT 7
US-10-750-185-56105
; Sequence 56105, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56105
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56105

Query Match 1.4%; Score 39.4; DB 6; Length 1423;
Best Local Similarity 52.1%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 2325 AGAATATGCCGAGAGCATATAATAGAAAGTAAATCACCCTGATTTTATTCAGAAACCGA 2384
Db 1043 AAACTTTCCCTAGAGCCTCCATATCACTGCCAACCTTGACTTTAGCTTACAGACCCA 1102
Qy 2385 TTTCTTTGCGTTAATGATAAAGTGAAAAAATGATTTATTCGGTGAAAGAAAAATTTA 2444
```


Db 1103 TTTCAGACTTCTCATCTTTAGAACTGTAAAGAAATAAAATTTGGTTCAAGTCAACACGTT 1162
 Qy 2445 TCGGCAATGGAGGTTAAAGTTTATCATGATTTTAAAAAATAAACAAATCA 2493
 Db 1163 TGTGGCAATTTGTTACAGCAGCAATAGGGAACCTGATACATATGCACACA 1211

RESULT 8
 US-11-117-187-197/c
 ; Sequence 197, Application US/11117187
 ; Publication No. US20050266560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PREUSS, DAPHNE
 ; APPLICANT: COPENHAVER, GREGORY
 ; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
 ; FILE REFERENCE: ARCD:309US
 ; CURRENT APPLICATION NUMBER: US/11/117,187
 ; CURRENT FILING DATE: 2005-04-28
 ; PRIOR APPLICATION NUMBER: US/09/531,120
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/125,219
 ; PRIOR FILING DATE: 1999-03-18
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 197
 ; LENGTH: 151828
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-11-117-187-197

Query Match 1.4%; Score 39; DB 7; Length 151828;
 Best Local Similarity 44.1%; Pred. No. 26;
 Matches 162; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
 Qy 2282 AATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAC 2341
 Db 49305 AAAATATATAATAAATAGTTTGTGTCATATCATAAACCAATTTTAAATAATAGTATACCTAAT 49246
 Qy 2342 ATAAATATAGAAGTAATCACCCGTGATTTTATTCAGAAACCGATTTCTTTGGCGTTAATGG 2401
 Db 49245 TAAAAATTTAATAGTTTATCATGTTTAAACATATAAAAAATATCATGTACATAT 49186
 Qy 2402 ATAAAGTGAATAAATATATTCGGTGAAGAAATAATTTATCGGCAATGGAGTTA 2461
 Db 49185 AAAAAAGACATTTATATATATGTCCATCAAAAAGATAGTTTAAATAGAAAAGATTCT 49126
 Qy 2462 AGTTTATCATGATTTAAAAAATAAACATCAGAAATACATGTCAACTATGCAATGGCCCC 2521
 Db 49125 TGTCTACAAAAATTTACATATCTTATATTCACAAATCTTTTTTTTCTATATAAAGAT 49066
 Qy 2522 ATCCCTATACGCAATGAGTAATGAAGAAAGAGCGCTGTGCAAGAAACAGAACCCGCTA 2581
 Db 49065 AAATAAGTTGTCATATATATTTTTCATCTTATTTCTTCCACCATATAAATAAATATTT 49006
 Qy 2582 TTGCAATAGATAGAGATAATAATTTCAAAGGTTGTGGCAAAATTCCTGCAATGAAGCAAA 2641
 Db 49005 TTGTTCAAAATATTAATAAACTCTTGTAAACCATCATCCAAAGAAAGGACATAAGCGTCAT 48946
 Qy 2642 TTAATAA 2648
 Db 48945 TTTAACA 48939

RESULT 9
 US-10-750-185-25909
 ; Sequence 25909, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25909
 ; LENGTH: 1306
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880625794
 US-10-750-185-25909
 Query Match 1.4%; Score 38.2; DB 6; Length 1306;
 Best Local Similarity 55.7%; Pred. No. 3.4;
 Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 Qy 1953 AAGAAATAATCCTGTGAGTTTACAAGATGAAATGGATTAGCGCCAGAAAAAGGGAATA 2012
 Db 546 ATGGTATGTTCTGTGGCTCTTTACAAGAAGATCACTCTCTCTCCCTATTGTGGAGCTA 605
 Qy 2013 TACCAAGAGGTAAATTTCTTTTGATGAATTAATAATTCAAATTTGGCAGCCAAAGTTTACA 2072
 Db 606 TAGAATTGAATGCAATTTCTCTTTTGAATGTAATAATAGAATTTGTACTGTAAATATGCATA 665
 Qy 2073 TGTGTCAAAAT 2083
 Db 666 TCTGGTGAAT 676
 RESULT 10
 US-11-117-187-207/c
 ; Sequence 207, Application US/11117187
 ; Publication No. US20050266560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PREUSS, DAPHNE
 ; APPLICANT: COPENHAVER, GREGORY
 ; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
 ; FILE REFERENCE: ARCD:309US
 ; CURRENT APPLICATION NUMBER: US/11/117,187
 ; CURRENT FILING DATE: 2005-04-28
 ; PRIOR APPLICATION NUMBER: US/09/531,120
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/125,219
 ; PRIOR FILING DATE: 1999-03-18
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 207
 ; LENGTH: 82596
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-11-117-187-207
 Query Match 1.4%; Score 38; DB 7; Length 82596;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 95; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
 Qy 2231 AAAACAGCTCCCTTTTCAGAAAAATCAAAACGAATCTTTCTTTAGGATCTGAAATATCCG 2290
 Db 70938 AGAGTAGATGTTTTTAAATTTAGATCATGAATGAATATATCTTATTACTAGAGAAATCT 70879
 Qy 2291 GTTATATGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGACGATATAATA 2350
 Db 70878 CACGCAACTTTTGAATTAATAATAATCAATCAACATTTTGTGGCTAAGCATACATATC 70819
 Qy 2351 GAAGTAATCACCTCGATTTTATTTTCAAGAAACCGATTCTTTTGGTTAAATGGATAAAGTG 2410
 Db 70818 AAATTAATTAATTTATTTTCTTACTTAATTTTCTTACTTAATTTTCTTACTTAATTTTGAATTA 70759
 Qy 2411 AAAAAAATGA 2420

```
Db 70758 TGATAAATTA 70749
|||||
Query Match 1.4%; Score 37.8; DB 6; Length 1624;
Best Local Similarity 45.7%; Pred. No. 4.9;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

RESULT 11
US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVEN, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD.309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: US/09/531,120
; PRIOR APPLICATION NUMBER: 2000-03-17
; PRIOR FILING DATE: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Query Match 1.4%; Score 38; DB 7; Length 1082144;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 95; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 2231 AAAACAGCTCCCTTCAGAAAATCAAAACGAATCTTCTTTAGGATCTGAATATCCG 2290
Db 937718 AGAGTAGATGTTTAAATAGATCATGAATGAATATATCTTATTACTAGAGAAAATCT 937777

Qy 2291 GTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCGCAAGAGCATAAATATA 2350
Db 937778 CACGCACTTTGAATTAATATAATATCAATGCAACATTTGTGCTAAGCATACATATC 937837

Qy 2351 GAAGTAATACCCCTGATTTTATTCAGAAACCGATTTCTTTGCGTTAATGATAAAAGTG 2410
Db 937838 AAATTAATTAATTAATTTCTTACTTAAATTTTGTCTTAGTATTTATGAAATTAATAA 937897

Qy 2411 AAAAATGA 2420
Db 937898 TGATAAATTA 937907

RESULT 12
US-10-750-185-29572/c
; Sequence 29572, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29572
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Bovine 19866880413136
US-10-750-185-29572

Query Match 1.4%; Score 37.6; DB 6; Length 1908;
Best Local Similarity 49.0%; Pred. No. 6;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 2397 AATGGATAAAAGTCAAAATAATGATTTATCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 715 AATGGCATATGATATACTGAATCATTTTACTGCCACAGAAAATTTAACACACATTTGT 774

Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATACAGAAATACATGTCACATGCAATT 2516
Db 775 AAATCACTGTAITTCATTTTCAATTTAAAAATAAATAAATGTTAACTTCCACTTCACTACTGA 834

Qy 2517 GGCCCATCCCTATACGCAATTTAGTAATGAAGAAGAGCGCTGTTGCAAGAAACAGAAC 2576
Db 835 GGCACATGCAATTTTGAAGAGGGGTACCTGAAAAAATCACCACATCTCCAGTTGGCAGAA 894

Qy 2577 CGCTATTTCGAATAGATAGAATA 2600
Db 895 CCACAAATAAATGGTGGTGTGA 918

US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.6; DB 6; Length 1908;
Best Local Similarity 49.0%; Pred. No. 6;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 2397 AATGGATAAAAGTCAAAATAATGATTTATCCGGTGAAGAAAAATTTATCGGCAATGGA 2456
Db 715 AATGGCATATGATATACTGAATCATTTTACTGCCACAGAAAATTTAACACACATTTGT 774

Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATACAGAAATACATGTCACATGCAATT 2516
Db 775 AAATCACTGTAITTCATTTTCAATTTAAAAATAAATAAATGTTAACTTCCACTTCACTACTGA 834

Qy 2517 GGCCCATCCCTATACGCAATTTAGTAATGAAGAAGAGCGCTGTTGCAAGAAACAGAAC 2576
Db 835 GGCACATGCAATTTTGAAGAGGGGTACCTGAAAAAATCACCACATCTCCAGTTGGCAGAA 894

Qy 2577 CGCTATTTCGAATAGATAGAATA 2600
Db 895 CCACAAATAAATGGTGGTGTGA 918

US-10-750-185-59339
; Sequence 59339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59339
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Bovine 19866880404878
US-10-750-185-59339

Query Match 1.4%; Score 37.8; DB 6; Length 1624;
Best Local Similarity 45.7%; Pred. No. 4.9;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 2000 AAAAAGGAAATATACAAAGAGGTAAATTTCTTTGATGAATTAATAATTCAAATTCGCAG 2059
Db 733 AAAATAGGAAATATGATCACAATGCTTATTTATTTTAGGAAAAAAGCCCTACTTTCAGATT 674

Qy 2060 CCAAAAGTTTCACATGTTGTCAAATGGAACGAGAAAGAGAGCAGTTATACAAAAATAAAT 2119
Db 673 AAATATGTTTAAATTTTATATACTAATAAATTAATAATTAATAATTTTAAATTTTAAAT 614

Qy 2120 CATTTGAAAGTGGTTCGTGTCGGTGATTCGATCCGTCGGGTATTTTGTCTAAGCCACGAAG 2179
Db 613 ACCACTAATTAATACATTTTGGAGATTCAGATTTATAAATACATTTCTAAGACAAACAAA 554

Qy 2180 AGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATATAGCCGACTTTGAAGAAAAACAGCT 2239
Db 553 ATCCTATAAAACATTCGACTATAAAGAGATACATTTCTAGTTATTTTAAAAATTTATTTC 494

Qy 2240 CCCTTTTCAGAAAAATCAAAACGAATCTTCTTTAGGATCTGAAATATC 2288
Db 493 GAATTTTATTAGTAAGAAATACAGACTCTGTCTCATTAATAATTAATC 445
```

RESULT 14
US-11-117-187-210/c
; Sequence 210, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 50959
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-210

Query Match 1.4%; Score 37.6; DB 7; Length 50959;
Best Local Similarity 49.6%; Pred. No. 34;
Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
QY 2249 AAAAAACAAAACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
DB 14717 AATTATATATTTAAATTTAGAAATTCCTAAATTCCTGATTTTCTGATTTTAAATCCAAACCC 14658
QY 2309 TACAAGATACGATATCAGAAATATGCCGAAGAGCATAAATATAGAAAGTAATCACCCTGATT 2368
DB 14657 TATATTATTAATTTCTAAAGTTTAACTTTTGTGCTCAACTTAAATAATTTAAATCATAAAAAAT 14598
QY 2369 TTTATTTCAGAAACCGATTCTTTTGGTTAATCGATATAAAGTCAAAAAAATGATTATTCG 2428
DB 14657 TATATTATTAATTTCTAAAGTTTAACTTTTGTGCTCAACTTAAATAATTTAAATCATAAAAAAT 14598
QY 2369 TTTATTTCAGAAACCGATTCTTTTGGTTAATCGATATAAAGTCAAAAAAATGATTATTCG 2428
DB 14657 TATATTATTAATTTCTAAAGTTTAACTTTTGTGCTCAACTTAAATAATTTAAATCATAAAAAAT 14598
QY 2429 GTGAAAGAAAAATTTTATGCGCAATGGAGGTTTAAAGTTTATCATGATTTTAAAAAATAAAC 2488
DB 14538 GCGAAACAATAATAGACAATAAATGTTCTTAAATCTTTTGGCTACTTTTGAATATATAC 14479
QY 2489 AATCAGAA 2496
DB 14478 ATGAAGCA 14471

RESULT 15
US-11-117-187-206/c
; Sequence 206, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 72600
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-206

Query Match 1.4%; Score 37.6; DB 7; Length 72600;
Best Local Similarity 49.6%; Pred. No. 41;

Matches 123; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
QY 2249 AAAAAACAAAACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGGCAAGAACCA 2308
DB 14717 AATTATATATTTAAATTTAGAAATTCCTAAATTCCTGATTTTCTGATTTTAAATCCAAACCC 14658
QY 2309 TACAAGATACGATATCAGAAATATGCCGAAGAGCATAAATATAGAAAGTAATCACCCTGATT 2368
DB 14657 TATATTATTAATTTCTAAAGTTTAACTTTTGTGCTCAACTTAAATAATTTAAATCATAAAAAAT 14598
QY 2369 TTTATTTCAGAAACCGATTCTTTTGGTTAATCGATATAAAGTCAAAAAAATGATTATTCG 2428
DB 14597 TTTAATTTGGCATCTAATTTTTTTTTCATCTCCCTTAAATTTGTCAGAACTAAA-ATTGG 14539
QY 2429 GTGAAAGAAAAATTTTATGCGCAATGGAGGTTTAAAGTTTATCATGATTTTAAAAAATAAAC 2488
DB 14538 GCGAAACAATAATAGACAATAAATGTTCTTAAATCTTTTGGCTACTTTTGAATATATAC 14479
QY 2489 AATCAGAA 2496
DB 14478 ATGAAGCA 14471

Search completed: December 14, 2005, 06:50:56
Job time : 939 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 23:36:00 ; Search time 1950 Seconds
(without alignments)
11640.740 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcggaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2745	100.0	2745	3 US-09-817-514A-5	Sequence 5, Appli
2	2653.8	96.7	2748	7 US-10-609-113-45	Sequence 45, Appl
3	1442.2	52.5	2817	7 US-10-609-113-48	Sequence 48, Appl
4	1440.6	52.5	2817	7 US-10-706-424-15	Sequence 15, Appl
5	1440.6	52.5	2817	8 US-10-754-115-57	Sequence 57, Appl
6	1004.6	36.6	2883	7 US-10-706-424-11	Sequence 11, Appl
7	1004.6	36.6	2883	7 US-10-609-113-46	Sequence 46, Appl
8	1004.6	36.6	2883	8 US-10-754-115-46	Sequence 46, Appl
9	962	35.0	3132	6 US-10-262-794A-60	Sequence 60, Appl
10	962	35.0	3132	7 US-10-609-113-44	Sequence 44, Appl
11	962	35.0	3132	8 US-10-754-115-25	Sequence 25, Appl
12	957.2	34.9	2850	7 US-10-706-424-13	Sequence 13, Appl
13	957.2	34.9	2850	7 US-10-609-113-47	Sequence 47, Appl
14	730.8	26.6	2889	8 US-10-754-115-50	Sequence 50, Appl
15	730.8	26.6	2889	10 US-11-020-848-3	Sequence 3, Appli
16	730.8	26.6	2947	8 US-10-754-115-53	Sequence 53, Appl
17	730.8	26.6	2947	10 US-11-020-848-8	Sequence 8, Appli
18	730.8	26.6	7508	8 US-10-754-115-54	Sequence 54, Appl
19	730.8	26.6	7508	10 US-11-020-848-9	Sequence 9, Appli
20	666	24.3	3048	8 US-10-753-901-15	Sequence 15, Appl
21	666	24.3	3048	8 US-10-754-115-15	Sequence 15, Appl
22	666	24.3	3051	7 US-10-609-113-21	Sequence 21, Appl
23	666	24.3	39005	8 US-10-753-901-6	Sequence 6, Appli

C

C	24	666	24.3	39005	8	US-10-754-115-6	Sequence 6, Appli
	25	599	21.8	38258	7	US-10-365-319-1	Sequence 1, Appli
	26	368.4	13.4	2793	6	US-10-609-113-12	Sequence 12, Appl
	27	368.4	13.4	2793	8	US-10-754-115-41	Sequence 41, Appl
	28	368.4	13.4	2862	8	US-10-754-115-55	Sequence 55, Appl
	29	368.4	13.4	33521	7	US-10-609-113-1	Sequence 1, Appli
	30	216.2	7.9	2823	6	US-10-365-742-63	Sequence 63, Appl
	31	148.6	5.4	858	7	US-10-609-113-40	Sequence 40, Appl
	32	57.4	2.1	7442	7	US-10-221-714A-409	Sequence 409, App
	33	53.8	2.0	6419	6	US-10-311-455-240	Sequence 240, App
	34	53.6	2.0	1062	8	US-10-425-115-120013	Sequence 120013
	35	52.4	1.9	3673778	6	US-10-312-841-2	Sequence 2, Appli
	36	51.8	1.9	6292	7	US-10-221-714A-461	Sequence 461, App
	37	51.6	1.9	11745	6	US-10-240-453-206	Sequence 206, App
	38	51.4	1.9	14006	6	US-10-311-455-1931	Sequence 1931, Ap
	39	51.4	1.9	410846	9	US-10-481-613-1	Sequence 1, Appli
	40	51	1.9	6334	6	US-10-311-455-1186	Sequence 1186, Ap
	41	51	1.9	11745	6	US-10-240-453-205	Sequence 205, App
	42	50.8	1.9	3683	8	US-10-473-126-339	Sequence 339, App
	43	50	1.8	573	4	US-09-925-065A-23123	Sequence 23123, A
	44	49.6	1.8	634	8	US-10-425-115-85320	Sequence 85320, A
	45	49.6	1.8	6048	7	US-10-433-793-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-817-514A-5

; Sequence 5, Application US/09817514A

; Patent No. US20020078478A1

; GENERAL INFORMATION:

; APPLICANT: ffrench-Constant, Richard

; APPLICANT: Bowen, David

; APPLICANT: Rocheleau, Thomas

; APPLICANT: Waterfield, Nicholas

; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS

; FILE REFERENCE: 61645

; CURRENT APPLICATION NUMBER: US/09/817,514A

; CURRENT FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: US 60/191806

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 2745

; TYPE: DNA

; ORGANISM: Photorhabdus luminescens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2745)

US-09-817-514A-5

Query Match	100.0%	Score 2745;	DB 3;	Length 2745;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2745;	Conservative	0;	Mismatches	0; Gaps 0;
Qy	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAGACCCCTCGATTAAAGGTATTAGATAAC	60	
Db	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAGACCCCTCGATTAAAGGTATTAGATAAC	60	
Qy	61	AGGAATTAATAGTACGTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGTAT	120	
Db	61	AGGAATTAATAGTACGTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGTAT	120	
Qy	121	GAATTAATACGTTCTATGAGTTCAATATTCGGGATTTTCAGTAAACACCGATCCT	180	
Db	121	GAATTAATACGTTCTATGAGTTCAATATTCGGGATTTTCAGTAAACACCGATCCT	180	
Qy	181	CGTAAATAAATAAACACGACGCGCCCAATTTTCATTCGTTGTTCTTTTAACTTTGCGGTCAA	240	
Db	181	CGTAAATAAATAAACACGACGCGCCCAATTTTCATTCGTTGTTCTTTTAACTTTGCGGTCAA	240	

Qy	241	GT	TTTACGTGAAGAAAGTGTGTGATGCGCGTGCAGCTATTACCCCTCAATGATATTGAAAGT	300
Db	241	GT	TTTACGTGAAGAAAGTGTGTGATGCGCGTGCAGCTATTACCCCTCAATGATATTGAAAGT	300
Qy	301	CG	CCGGGTGTGATCATCAATGAACCGGTGTCGCGCAAAACCATCTGTTATGAAGATAAC	360
Db	301	CG	CCCGGTGTGTGATCATCAATGAACCGGTGTCCGCAAAACCATCTGTTATGAAGATAAC	360
Qy	361	ACC	TTTCCCGGTGCTGTGCTTCGCTATCACCGAACAAGTACAGGCAGAGAGAAAAACGACC	420
Db	361	ACC	TTTCCCGGTGCTGTGCTTCGCTATCACCGAACAAGTACAGGCAGAGAGAAAAACGACC	420
Qy	421	GA	CGTCTTATCTGGGCGCGGCAATACGCCCGCAAGAAAAAGATTCAACTTCGCGGTGAG	480
Db	421	GA	CGTCTTATCTGGGCGCGGCAATACGCCCGCAAGAAAAAGATTCAACACTTCGCGGTGAG	480
Qy	481	TG	TGTCGCGCAATACGATACGGCGGAGACTTACTCAACTCAATAGCCTTCTCTGGGTGGC	540
Db	481	TG	TGTCGCGCAATACGATACGGCGGAGACTTACTCAACTCAATAGCCTTCTCTGGGTGGC	540
Qy	541	GT	CGTGTCTATCACAACTCTCAACAACTGCTTACCGATAACCAAGATGCCGACTTGGACAGGT	600
Db	541	GT	CGTGTCTATCACAACTCTCAACAACTGCTTACCGATAACCAAGATGCCGACTTGGACAGGT	600
Qy	601	GA	AGACAGAGCCTCTGGCAACAAAAACTGAGTAGTGATGCTATATACACCCAAAGTAAC	660
Db	601	GA	AGACAGAGCCTCTGGCAACAAAAACTGAGTAGTGATGCTATATACACCCAAAGTAAC	660
Qy	661	ACT	GATGCCACCGGGCTTACTGACCCAGACCGATGCCAAAGGCACACTTACGCGGCTG	720
Db	661	ACT	GATGCCACCGGGCTTACTGACCCAGACCGATGCCAAAGGCACACTTACGCGGCTG	720
Qy	721	GC	CTATGATGTGGCGGGCAGCTAAAAAGGAGTTGGTTAACTCAAAGCTCAGGCGGAA	780
Db	721	GC	CTATGATGTGGCGGGCAGCTAAAAAGGAGTTGGTTAACTCAAAGCTCAGGCGGAA	780
Qy	781	CAG	TGATTATCAAATCGTAACTCTACCGCGCGGGCAAAAATTAACGTGAAGAGCAC	840
Db	781	CAG	TGATTATCAAATCGTAACTCTACCGCGCGGGCAAAAATTAACGTGAAGAGCAC	840
Qy	841	GG	TAAACGGGATTGCTACTGAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATT	900
Db	841	GG	TAAACGGGATTGCTACTGAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATT	900
Qy	901	ACC	ACTCGCCGTCCATCAGACCGCAAGGTGTTGAAGACCTACGCTATCAATATGACCCA	960
Db	901	ACC	ACTCGCCGTCCATCAGACCGCAAGGTGTTGAAGACCTACGCTATCAATATGACCCA	960
Qy	961	GT	AGCAATGTCAATTAATATCCGTATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	961	GT	AGCAATGTCAATTAATATCCGTATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	1021	AA	GTAGCCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGGCGCAC	1080
Db	1021	AA	GTAGCCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGGCGCAC	1080
Qy	1081	GG	CGCGAAATGGCCAAATATCGGTGAGCAAAACCAACTTCCTCCCTCGCTGCTACCT	1140
Db	1081	GG	CGCGCGAAATGGCCAAATATCGGTGAGCAAAACCAACTTCCTCCCTCGCTGCTACCT	1140
Qy	1141	TCT	GACAACTACCTACACTATCTCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Db	1141	TCT	GACAACTACCTACACTATCTCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Qy	1201	CT	GACGCAAAATCGGCACAGCTCGCAGCTACCCAGAACAACTACACCGTGGCTATCACC	1260
Db	1201	CT	GACGCAAAATCGGCACAGCTCGCAGCTACCCAGAACAACTACACCGTGGCTATCACC	1260
Qy	1261	CT	CTCAAAACCGCAGCAATCGGGGTGTTCTCAGTAGCGTTAAACCGATCAAATCAAGTG	1320
Db	1261	CT	CTCAAAACCGCAGCAATCGGGGTGTTCTCAGTAGCGTTAAACCGATCAAATCAAGTG	1320
Qy	1321	GAT	AGTGTGTTTGTGTCGCGGTGGTCACCAAAACCAAGTTATTATACCGGACAGACATTTATC	1380

Db	1321	GATACGTTGTTGATGCCGGTGGTCA	CMAACGAGTTTATTACCGGACAGACATTATC	1380
Qy	1381	TGGACACCAAGAGAGTTAAAGCAGGTTAA	TAAATGGCCCCGGGAAATGAGTGGTACC	1440
Db	1381	TGGACACCAAGAGAGTTAAAGCAGGTTAA	TAAATGGCCCCGGGAAATGAGTGGTACC	1440
Qy	1441	TACGACAGCAACGGCATGAGACACACTG	AAAGTGAGTGAACGCCAACCCAGAACTACTAG	1500
Db	1441	TACGACAGCAACGGCATGAGACACACTG	AAAGTGAGTGAACGCCAACCCAGAACTACTAG	1500
Qy	1501	CAGCAACACGGGTAACTTATTTGCCGGAC	TGGAGCTACGCACAAACCCAGACCAACGCC	1560
Db	1501	CAGCAACACGGGTAACTTATTTGCCGGAC	TGGAGCTACGCACAAACCCAGACCAACGCC	1560
Qy	1561	ACAACAACGGAAGAGTTACACGTTATCAC	ACTTCGTTGAAGCCGGTCCGCACACAGGTACGG	1620
Db	1561	ACAACAACGGAAGAGTTACACGTTATCAC	ACTTCGTTGAAGCCGGTCCGCACACAGGTACGG	1620
Qy	1621	GTGTTGCACTGGGAGAGCGGTAAAGCCAG	AAGATGTCAACAAATCAACTACGTTACAGC	1680
Db	1621	GTGTTGCACTGGGAGAGCGGTAAAGCCAG	AAGATGTCAACAAATCAACTACGTTACAGC	1680
Qy	1681	TACGATAAATCTGATCGCTCCAGCCAGCTT	GAACTCGACAAACCAAGACAAAATTAATCAGC	1740
Db	1681	TACGATAAATCTGATCGCTCCAGCCAGCTT	GAACTCGACAAACCAAGACAAAATTAATCAGC	1740
Qy	1741	GAGGAAGAGTATTATCCATTTTGGCGGAC	CAGCGCTGTGGCAGCAACAGCCAAACAGAA	1800
Db	1741	GAGGAAGAGTATTATCCATTTTGGCGGAC	CAGCGCTGTGGCAGCAACAGCCAAACAGAA	1800
Qy	1801	GCCAGCTATAAAACGATTCGCTATTC	CGGCAAGAACGAGATGCCACCGGGTTGTATTAT	1860
Db	1801	GCCAGCTATAAAACGATTCGCTATTC	CGGCAAGAACGAGATGCCACCGGGTTGTATTAT	1860
Qy	1861	TACGGTTATCGTTATTACCAACCGTGGCG	GGGCGAGATGGTTAAGCGCGACCCGGCAGGA	1920
Db	1861	TACGGTTATCGTTATTACCAACCGTGGCG	GGGCGAGATGGTTAAGCGCGACCCGGCAGGA	1920
Qy	1921	ACCATTTGATGGGCTGAATCTATACCGAAT	TGGTAAGAAATAATCCTGTGAGTTTACAAGAT	1980
Db	1921	ACCATTTGATGGGCTGAATCTATACCGAAT	TGGTAAGAAATAATCCTGTGAGTTTACAAGAT	1980
Qy	1981	GAAAAATGGATTAAGCCGCAAGAAAAGG	GAATAATACCAAGAGGTAAATTTCTTTGATGAA	2040
Db	1981	GAAAAATGGATTAAGCCGCAAGAAAAGG	GAATAATACCAAGAGGTAAATTTCTTTGATGAA	2040
Qy	2041	TTAAAAATTCAAATTCGCGCAAGAAAGT	TCACATGTTGTCAAAATGGAAACGAGAAGACAGC	2100
Db	2041	TTAAAAATTCAAATTCGCGCAAGAAAGT	TCACATGTTGTCAAAATGGAAACGAGAAGACAGC	2100
Qy	2101	AGTTATACAAAAATAAATCAITTTGAAAG	TGGTTCTGTGCGGTGATTCGATCCGTCGGGT	2160
Db	2101	AGTTATACAAAAATAAATCAITTTGAAAG	TGGTTCTGTGCGGTGATTCGATCCGTCGGGT	2160
Qy	2161	TATTTGCTAAGCCAGAAAGATTAATAAAG	GTATAGAAAAAGTCAAAATCATATATAGC	2220
Db	2161	TATTTGCTAAGCCAGAAAGATTAATAAAG	GTATAGAAAAAGTCAAAATCATATATAGC	2220
Qy	2221	CGACTTTGAAGAAACAGCTCCCTTTT	CAGAAAAATCAAAAACGATCTTTCTTTAGGATCT	2280
Db	2221	CGACTTTGAAGAAACAGCTCCCTTTT	CAGAAAAATCAAAAACGATCTTTCTTTAGGATCT	2280
Qy	2281	GAAATATCCGGTTATATGGCAAGAAAC	CAATACAAGATA CGATATCAGAAATATGCCGAAGAG	2340
Db	2281	GAAATATCCGGTTATATGGCAAGAAAC	CAATACAAGATA CGATATCAGAAATATGCCGAAGAG	2340
Qy	2341	CATAAATATAGAAGTAAATCAACCTGAT	TTTTTATTCAGAAAACCGATTTCTTTGGCTTAATG	2400
Db	2341	CATAAATATAGAAGTAAATCAACCTGAT	TTTTTATTCAGAAAACCGATTTCTTTGGCTTAATG	2400
Qy	2401	GATAAAAAGTGAAAAAATGATTTTCCGGT	TGAAGAAAAATTTATCGGCAATGAGGTT	2460

Db 2401 GATAAAGTGAAGAAATGATTATTCGGTGAAGAAAAATTTATGCGGCAATGGAGTT 2460
Qy
2461 AAGTTTATCATGATTATTAAGAAATTAACAATCAGAATTACATGTCAACTATGCAATGGCC 2520
Db
2461 AAGTTTATCATGATTATTAAGAAATTAACAATCAGAATTACATGTCAACTATGCAATGGCC 2520
Qy
2521 CATCCCTATACGAATTGAGTAATGAAGAAAGCGCTGTGCAAGAAACAGAACCCGCT 2580
Db
2521 CATCCCTATACGAATTGAGTAATGAAGAAAGCGCTGTGCAAGAAACAGAACCCGCT 2580
Qy
2581 ATTGCAATAGATAGAAATTAATTTCAAAGGTGTTGGCAAAATTCCTGACAAATGAAGCA 2640
Db
2581 ATTGCAATAGATAGAAATTAATTTCAAAGGTGTTGGCAAAATTCCTGACAAATGAAGCA 2640
Qy
2641 ATTAAGAAATCATGAAAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Db
2641 ATTAAGAAATCATGAAAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Qy
2701 CGCTCTGGGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745
Db
2701 CGCTCTGGGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 2

US-10-609-113-45
; Sequence 45, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-45

Query Match 96.7%; Score 2653.8; DB 7; Length 2748;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2688; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
Qy 1 ATGAGCAGTTACAAATCTGCAATGACCAAAAGACCCCTCGATTAAAGTTATAGATAAC 60
Db 1 ATGAGCAGTTACAAATCTGCAATGACCAAAAGACCCCTCGATTAAAGTTATAGATAAC 60
Qy 61 AGGAAATTAATGCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT 120
Db 61 AGGAAATTAATGCTAGCTACTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT 120
Qy 121 GAATTAATTAACGTTCTATGAGTTCAATATTTCCGGGATTTTCAAGTAAAGACCCGATCCT 180
Db 121 GAATTAATTAACGTTCTATGAGTTCAATATTTCCGGGATTTTCAAGTAAAGACCCGATCCT 180
Qy 181 CGTAAAAATAAAAACGAGCGGCCCAAAATTTCAATGCTGTTTAAATCTTGGCGGTCAA 240
Db 181 CGTAAAAATAAAAACGAGCGGCCCAAAATTTCAATGCTGTTTAAATCTTGGCGGTCAA 240
Qy 241 GTTTTACGTGAAGAAAGTTGATGCGGTCGGGACTATTACCCCTCAATGATATTGAAGT 300
Db 241 GTTTTACGTGAAGAAAGTTGATGCGGTCGGGACTATTACCCCTCAATGATATTGAAGT 300

Qy 301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC 360
Db 301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC 360
Qy 361 ACCCTTCCCGGTGCTGCTATCAGCAACAGTACAGGACGAGAGAGAAACGACC 420
Db 361 ACCCTTCCCGGTGCTGCTATCAGCAACAGTACAGGACGAGAGAGAAACGACC 420
Qy 421 GAAAGCTTTATCTGGGCGGCAATACGCCGCAAGAAAAAGATTACAACCTCGCGGTGAG 480
Db 421 GAAAGCTTTATCTGGGCGGCAATACGCCGCAAGAAAAAGATTACAACCTCGCGGTGAG 480
Qy 481 TGTGTCGGCCATACGATACCGGGGACTTACTCAACTCAATAGCCTTCTCTGGGTGGC 540
Db 481 TGTGTCGGCCATACGATACCGGGGACTTACTCAACTCAATAGCCTTCTCTGGGTGGC 540
Qy 541 GTGCTGCTATCAAACTCTCAAACTGCTTACCGATAACGAGATGCCGACTCGACAGGT 600
Db 541 GTGCTGCTATCAAACTCTCAAACTGCTTACCGATAACGAGATGCCGACTCGACAGGT 600
Qy 601 GAAGACGAGGCTCTGGCAACAAAACTGAGTGTGATGTCTATATACCCCAAGTAAAC 660
Db 601 GAAGACCAAGGCTCTGGCAGCAAACTGAGCAGTGATGTCTATACCCCAAAATAA 660
Qy 661 ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTGACGGCTG 720
Db 661 GCGGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCAACATTGACGGCTG 720
Qy 721 GCTATGATGTGGCGGGCAGCTAAAAGGGAGTTGTTAACTAACACTCAAGGTGAGGGGAA 780
Db 721 GCTACGAGTGTGGCGGGCAGCTAAAAGGGAGTTGTTAACTAACACTCAAGGTGAGGGGAA 780
Qy 781 CRAAGTATTATCAAAATCGCTAACTACTCGCGCGCGGCAAAATTTACGTGTAAGACAC 840
Db 781 CRAAGTATTATCAAAATCGCTAACTACTCGCGCGCGGCAAAATTTACGTGTAAGACAC 840
Qy 841 GGTACGGGATGTCTACTGAATACAGCTAGCAACCGGAAACCCCAAGGCTTATCGGAT 900
Db 841 GGTAAACGGGTTTATCACTGAATACAGCTATGAACCAAGAAACCCCAAGGCTTATCGGAT 900
Qy 901 ACCACTCGCGCTCCATCAGACGCGCAAGGTGTTGCAAGACTACGCTATCAATATGACCA 960
Db 901 GCCACCGCGCTCCGTCAGACGCGCAAGGTGTTGCAAGACTACGCTATCAATATGACCG 960
Qy 961 GTAGGCAATGTCAATTAATATCGTAAATGATGCGGAAAGCCACTCGCTTTTGGCGCAAT 1020
Db 961 GTAGGCAATGTGATCAATATCGTAAATGATGCGGAAAGCCACTCGCTTTTGGCGCAAT 1020
Qy 1021 AAAGTAGCCCCGAGAAATAGCTATACCTAGATTTCCCTGTATCAGCTTATCAGCGCAC 1080
Db 1021 AAAGTAGCCCCGAGAAATAGCTATACCTAGATTTCCCTGTATCAGCTTATCAGCGCAC 1080
Qy 1081 GGGCGGGAATGGCTAATATAGGTGAGCAAAATAACCAACTGCCCCCTCGCGCTACCT 1140
Db 1081 GGGCGGGAATGGCTAATATAGGTGAGCAAAATAACCAACTGCCCCCTCGCGCTACCT 1140
Qy 1141 TCTGACAAACATACCTACACTACTACTCGCAGCTACAGCTATGATCAGCTGGTAAAT 1200
Db 1141 TCTGACAAACATACCTACACTACTACTCGCAGCTACAGCTATGATCAGCTGGTAAAT 1200
Qy 1201 CTGACGCAAAATTCGGCAGCTGCGCAGCTACCCAGAAACATACACCGTGGCTATCAC 1260
Db 1201 CTGACGCAAAATTCGGCAGCTGCGCAGCTACCCAGAAACATACACCGTGGCTATCAC 1260
Qy 1261 CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCAGCTCAAAATCAAGTG 1320
Db 1261 CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCAGCTCAAAATCAAGTG 1320
Qy 1321 GATACGTTGTTGATGCGCGGTGCTACCAACAGTTTATACCCGAGACAGACTTATC 1380
Db 1321 GATACGTTGTTGATGCGCGGTGCTACCAACAGTTTATACCCGAGACAGACTTATC 1380
Qy 1381 TGGACACACGAGGAGAGTTAAAGCAGGTTAAATGATGGCCCGGGAATGAGTGGTACCGC 1440

[illegible]

Db	2461	AGGTTTATCATGATTTTAAAAATAAACAAATCAGAAATTACATGTCAACTATGATTCGGCC	2522
Qy	2521	CATCCCTATACGCAATTGAGTAAATGAAGAAAGAGCGCTGTTGCAAGAAAACAGAACCCGCT	2580
Db	2521	CATCCCTATACGCAATTGAGTAAATGAAGAAAGAGCGCTGTTGCAAGAAAACAGAACCCGCT	2580
Qy	2581	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAGAACA	2640
Db	2581	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAGAACA	2640
Qy	2641	ATTAAAAATCATTTGAAGAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATATT	2700
Db	2641	ATTAAAAATCATTTGAAGAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATATT	2700
Qy	2701	CGCTCTGCGGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA	2745
Db	2701	CGCTCTGCGGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA	2745
RESULT 3			
US-10-609-113-48			
; Sequence 48, Application US/10609113			
; Publication No. US20040110184A1			
; GENERAL INFORMATION:			
; APPLICANT: Bintrim, Scott			
; APPLICANT: Bavan, Scott			
; APPLICANT: Zhu, Baolong			
; APPLICANT: Merlo, Donald J.			
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtained			
; TITLE OF INVENTION: Paenibacillus Species			
; FILE REFERENCE: DAS-101XC2			
; CURRENT APPLICATION NUMBER: US/10/609,113			
; CURRENT FILING DATE: 2003-06-27			
; PRIOR APPLICATION NUMBER: US 60/392,633			
; PRIOR FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: US 60/441,647			
; PRIOR FILING DATE: 2003-01-21			
; NUMBER OF SEQ ID NOS: 49			
; SOFTWARE: Patent in version 3.2			
; SEQ ID NO 48			
; LENGTH: 2817			
; TYPE: DNA			
; ORGANISM: Photorhabdus strain w14			
US-10-609-113-48			
Query Match 52.5%; Score 1442.2; DB 7; Length 2817;			
Best Local Similarity 82.9%; Pred. No. 0;			
Matches 1664; Conservative 0; Mismatches 328; Indels 15; Gaps 1;			
Qy	21	AATTGACAAAAGACCCCTCGAATTAAGGTATTAGATACAGGAAATTAATGTACGTAC	80
Db	21	ACTTATACCATACATCGCCTACCGTCAGTGTTCAGATAACCGTGGACTAGCTATCCGTAA	80
Qy	81	TTTAGAATATCTACGCACTCAAGCTGACGAAAAACAGTGATGAATTAATTACGTTCTATGA	140
Db	81	TATTAGTTTTCACCGCACTACCGCAGAGCAATACCGATACCGTATTACCCGCATCA	140
Qy	141	GTTCAATATTCCGGGATTTCCAGGTAAAGACCCGATCTCTCGTA-----A	185
Db	141	ATATAATGCCGGCGGATATTTGAACCAAGCAATTGATCTCTCGCTGATGACGCAAAACA	200
Qy	186	AAATAAAAACGAGCGCGCCAAATTTTCATTCGTGCTTTTAAATCTTCGCGGTCAAGTTT	245
Db	201	GACTTAAACAACGCTGTACAAACCGAATTTTATCTGGCGACATAAATTGACCGGCAATATCCT	260
Qy	246	ACGTGAAGAAGTGTTCATGCGGTCCGAGCTATTACCCCTCAATGATATTGAAAGTCGCCC	305
Db	261	CGGAACAGAGAGCGTCAATCCCGTCCGACGATTTACCTCAACGATATTGAAGGCCGCC	320
Qy	306	GGTGTTCATCAATCAACCGGTGTCGCGCCAAAACCATCTGTTATGAAGATACACCT	365
Db	321	GGTGTTCATCAATCAATCAGCCGGTGTCCGCGAAAACCATCGTACGAAGATACACCT	380

366 TCCGGTCTGCTCGCTATCACCAGAACAGTACAGCAGGAGAGAGAAAACGACCGAAGC 425
Db |||||
381 GCCGGTCTGCTCGCTATCAGGAACAGGACAGCAGAGAGAGAAAACGACCGAGCG 440
Qy |||||
426 TCTTATCGGCGCGCAATACGCGCAAGAAAAGATTACAACTCTCGCGGTCAAGTGTGT 485
Db |||||
441 CCTTATCTGGCGCGCAATACGCGCAAGAAAAGAACCAACACTTGGCGGTCAAGTGTGT 500
Qy |||||
486 CCGCATACGATACGCGGAGCTTACTCACTCAATAGCCTTCTTCTGCTGGCTGCTGT 545
Db |||||
501 CCGCATACGATACGCGGAGCTTACTCACTCAACAGCCTTGGCTTGAACGCGCGCGT 560
Qy |||||
546 GCTTATCACAATCTCAACAACTGTTACCGATAACCCAGGATGCCAGCTTGGACAGGTGA 605
Db |||||
561 TCTATCACAATCTCAACAACTGTTACCGATAACCCAGGATGCCAGCTTGGACAGGTGA 620
Qy |||||
606 CCAGAGCTCTGGCAACAAACAACTGAGTACTGATGTCTATATCAACCAAAAGTAACTGA 665
Db |||||
621 CCAGAGCTCTGGCAACAAACAACTGAGTACTGATGTCTATATCAACCAAAAGTAACTGA 680
Qy |||||
666 TGCACCGGGCTTACTGACCCAGACCGATGCGAAAGCAACATTCAGCGGCTGGCCTA 725
Db |||||
681 TGCACCGGGCTTACTGACCCAGACCGATGCGAAAGCAACATTCAGCGGCTGGCCTA 740
Qy |||||
726 TGATGTGGCGGCGAGCTAAAGGGAGTGTGTTAACTCAAGGTCTAGCGGCAACAGGT 785
Db |||||
741 TGATGTGGCGGCGAGCTAAAGGGAGTGTGTTAACTCAAGGTCTAGCGGCAACAGGT 800
Qy |||||
786 GATTATCAAACTCGTAACTACTCCGCGCGGCGCAAAATACGTGAAGAGCACCGTAA 845
Db |||||
801 GATTATCAAACTCGTAACTACTCCGCGCGGCGCAAAATACGTGAAGAGCACCGTAA 860
Qy |||||
846 CGGATGTCACTGAAATACAGCTACGAAACCGGAAACCCAAAGCTTATCGGCAATACCA 905
Db |||||
861 CGGATGTCACTGAAATACAGCTACGAAACCGGAAACCCAAAGCTTATCGGCAATACCA 920
Qy |||||
906 TCCCGTTCATCAGACCGCAAGGTGTGCAAGCCTACGCTCAATATGACCCAGTAGG 965
Db |||||
921 TCCCGTTCATCAGACCGCAAGGTGTGCAAGCCTACGCTCAATATGACCCAGTAGG 980
Qy |||||
966 CAATGTCAATTAATCGTAAATGATCGGAAGCACCTCGCTTTTGGCGCAATCAGAAAGT 1025
Db |||||
981 CAATGTCAATTAATCGTAAATGATCGGAAGCACCTCGCTTTTGGCGCAATCAGAAAGT 1040
Qy |||||
1026 AGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACCGGGG 1085
Db |||||
1041 AGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACCGGGG 1100
Qy |||||
1086 CGAAATGGCCCAATATCGGTGAGCAAAACCAACCTTCCCTCCCTGCGGTACCTTCTGA 1145
Db |||||
1101 CGAGATGGCCCAATATCGGTGAGCAAAACCAACCTTCCCTTCCGCGCGCTACCTTCTGA 1160
Qy |||||
1146 CAACAATACCTACACTAACTATCTCGCAGCTACGCTATGATCAAGTGGTAACTCTGAC 1205
Db |||||
1161 TAAACAATACCTACACAATATCTCGCAGCTTATCTTATGACCGGTGGCGCAATTTGAC 1220
Qy |||||
1206 GCAAAATTCGCGCACAGCTCGCGAGTACCCAGAACAACTACACCGTGGCTATCACCCCTCTC 1265
Db |||||
1221 GAAATTCAGCATAGTTTACACGCGCGGCAAAATACCTACACGCGATATACGGTTTC 1280
Qy |||||
1266 AAACCGCAGCAATCGGGGTGTTCTAGTACGCTAACACCGATCCAAATCAAGTGGATAC 1325
Db |||||
1281 AAATTCGAGCAACCGGCGGTACTCAGCACAATTTGACCGGAGATCCAACTCAAGTCGATGC 1340
Qy |||||
1326 GTTGTGTTGATCGCGGTGTTACCAACAGTTTATACCGGAGACAGACATCTCTGGAC 1385
Db |||||
1341 CTTATTGATGCGGGAGGCCATCAACACAGCTTGTATTCCGCGCAAGTTCTTAATCTGGAC 1400
Qy |||||
1386 ACCACGAGGAGGTAAAGCAGGTGTTAATATGCGCGGAAATGAGTGGTACCGTACGA 1445
Db |||||
1401 ACCGCGAGGCGAATTGAAACAGCCCAACATACGCGGAGGAAATGAGTGGTATCGCTACGA 1460
Qy |||||
1446 CAGCAACGGCATGAGACAACTGAAAGTGTGTAACAGCCCAACCCAGAAATCTACGCGACA 1505

Db |||||
1461 TAGCAACGGCATACGCCAGCTAAAGTGAATGAACAAACTCAGATATATCCCGCAACA 1520
Qy |||||
1506 ACAACCGGTAAATCTATTTCCCGGACTGGAGCTACGCAAAACCCAGAGCAACCCCAAC 1565
Db |||||
1521 ACAACCGGTAACTTATCTACCGGGCTGGAAATACGTACAAACCCAGCAACCCCAAC 1580
Qy |||||
1566 AACGGAAGAGTTACAGCTTATCACACTCGGTGAGCGGTGCGGACAGGTACGGGTGTT 1625
Db |||||
1581 AACAGAAGAGTTACAGCTTATCACACTCGGTGAGCGGTGCGGACAGGTACGGGTGTT 1640
Qy |||||
1626 GCACTCGGAGAGCGGTAAAGCAGAGATGTCAACAAATATCAACTACGTTTACAGCTACGA 1685
Db |||||
1641 GCATTGGAGAGCGGTAAACCAAGATATTAATAAATACAGCTTCTGTTTACAGCTACGA 1700
Qy |||||
1686 TAATCTGATCGGCTCCAGCCAGCTTGAATGACCAACCAAGGACAAATATATCAGCGAGGA 1745
Db |||||
1701 TAATCTTATTTGGCTCCAGCCAACTTCAATTAGATAGCAGCGACAAATATATCAGTGAAGA 1760
Qy |||||
1746 AGAGTATTTATCAATTTGGCGGACAGCGCTGCGGAGCAAAACAGCCAAACAGAACCCAG 1805
Db |||||
1761 AGAATATTTATCAATTTGGTGTACAGCGCTGCGGCGGCAAGGAATCAAAACCGAAGCCAG 1820
Qy |||||
1806 CTATAAAACGATTCGCTATTCCGGCAACAAACAGAGATGCCACGGGTCTGTTATTATACGG 1865
Db |||||
1821 CTATAAAACGATTCGCTATTCTGGTAAAGAGCGGATGTTACCGGCTGTATTATTATGG 1880
Qy |||||
1866 TTATCTTATTTATCAACACCGTGGCGGACAGATGCTTAAAGCGCGGACCCGCGAGAACCAT 1925
Db |||||
1881 CTACCGTATTATCAACACCGTGGCGGACAGATGTTAAAGTGCAGACCCGCGAGAACCAT 1940
Qy |||||
1926 TGATGGCTGGAATCTATATACCGAATGGTAAAGAAATTAATCTGTGAGTTTACAAGATGAAA 1985
Db |||||
1941 TGATGAGCTGGAATTTATATCGCATGCTGAGAAATTAACCCGCTGACGCAATTTGATGTCA 2000
Qy |||||
1986 TGGATTAGCGCCAGAAAAGGGAATA 2012
Db |||||
2001 GGGATTATCACCGGCCAACAGAACAGA 2027

RESULT 4
US-10-706-424-15
; Sequence 15, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2814)
US-10-706-424-15

Query Match 52.5%; Score 1440.6; DB 7; Length 2817;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 329; Indels 15; Gaps 1;
Qy 21 AATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAACAGGAAATTAATATGTACGTAC 80
Db 21 ACTTTATCACCATAACCGCTACCGTTCAGTGTTCACGATAACCGTGGACTAGCTATCCGTAA 80
Qy 81 TTTAGAAATATCTACCGCACTCAAGCTGACGAAACAGTGAATTAATTACGTTCTATGA 140
Db 81 TATTAGTTTTCACCGCACTACCGCAGAGCAAAATACCGATACCCGTTATTATCCCGCATCA 140

141 GTTCAATATTCGGGATTTTCAGGTAAGGACACCGATCCTCGTA-----A 185
 141 ATATAATGCGGCGGATATTTGAACCAAGACATGTATCCTCGCTGTATGACGCAACA 200
 186 AAATAAAGACAGAGCGGCGCAATATTCATTCGTGTCTTTAAATCTTGCCTGCAAGTTTT 245
 201 GACTAACACGCTGTACAAACCGAATTTATCTGGGACATAATTTGACCGCAATATCCT 260
 246 ACGTGAAGAAGTGTGATGCGGTCGGACATTTACCTCAATGATATTTGAAGTGTGCCC 305
 261 GCGAACAGAGAGGCTGATGCGGTCGGACGATTTACCTCAACGATATTTGAAGCGCGCCC 320
 306 GGTGTTGATCATCAATCGAACCGGTGTCGCGCAAAACCATCGTTTATCAAGATACACCT 365
 321 GGTGTTGACCATCAATGACGCGGTGTCGCGCAAAACCATCGCTACCAAGATACACCT 380
 366 TCCCGGTGCTGCTCGCTATCACCGAACAAAGTACAGGACGAGAGAGAAACGACCGAAG 425
 381 GCGCGTGGCTGCTCGCTATCACGGAACAAAGGACAGGACAGAGAAACGACCGAGCG 440
 426 TCTTATCTGGGCGGCAATACGCGCAAGAAAGATTAACAACCTCGCGGTGCTAGTGTGT 485
 441 CCTTATCTGGGCGGCAATACGCGCAAGAAAGACCAACCTTGCCTGCTCAGTGCCT 500
 486 CCGCATATGATACCGGCGGACTTACTCACTCAATAGCTTTCTCTGCTGCGCTCGT 545
 501 CCGCATATGATACCGGCGGACTTACTCACTCAACAGCTTGCCTGACCGCGCGCT 560
 546 GCTATCAAACTCTCAAACTGCTTACCGTAACAGGATGCCAGTCCGACTGGACAGTGAAGA 605
 561 TCTATCAAACTCTCAAACTGCTTACCGTAACAGGATGCCAGTCCGACTGGACAGTGAAGA 620
 606 CCAGAGCTCTGGCAACAAACCTGAGTGTGCTATATCAACCAAGATTAACCTGA 665
 621 CCAGAGCTCTGGCAACAAACCTGAGTGTGCTATATCAACCAAGATTAACCTGA 680
 666 TGCCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTGGCCTA 725
 681 TGCCACCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTGGCCTA 740
 726 TGATGTGCGCGGCGAGCTTAAAGGGAGTGTGTTAACTCAAGCTCAGGCGGAACAGGT 785
 741 TGATGTGCGCGGCGAGCTTAAAGGGAGTGTGTTAACTCAAGCTCAGGCGGAACAGGT 800
 786 GATTATCAAACTCGCTAACTACTCGCGCGCGGCAAAATTAACGTAAGAGCAAGGTAA 845
 801 GATTATCAAACTCGCTAACTACTCGCGCGCGGCAAAATTAACGTAAGAGCAAGGTAA 860
 846 CCGGATTTGCTCATGATACAGCTACGACCGGAACCCCAACGGCTTATCGGCAATTCAC 905
 861 CCGGATTTGCTCATGATACAGCTACGACCGGAACCCCAACGGCTTATCGGCAATTCAC 920
 906 TCGCGCTCCATCAGACGCGCAAGGTGTGCAAGACCTAGCTATCAATATGACCCAGTAGG 965
 921 TCGCGCTCCATCAGACGCGCAAGGTGTGCAAGACCTAGCTATCAATATGACCCAGTAGG 980
 966 CAATGTCTAATATTCGCTAATATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAAGAGT 1025
 981 CAATGTCTAATATTCGCTAATATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAAGAGT 1040
 1026 AGCCCGGAGATAGCTATACCTAGATTCCTGTATCAGCTTATCAGCGCGCACCGGGCG 1085
 1041 AGCCCGGAGATAGCTATACCTAGATTCCTGTATCAGCTTATCAGCGCGCACCGGGCG 1100
 1086 CGAATGCGCAATATCGGTCAGCAAAACCAACCTTCCCTCCCTGCGCTACCTTCTGA 1145
 1101 CGAGATGCGCAATATCGGTCAGCAAGCAACCACTTCCCTCCTCGGCGCTACCTTCTGA 1160
 1146 CAACAAATACCTACCTAATCTATCTCGAGCTACAGCTATGATACAGTGTGTAATCTGAC 1205
 1161 TAACAATACCTACCACTAATCTATCTGCACTATATCTTATACCTGCGGCAATTTTAC 1220

1206 GCAAAATTCGGCA CAGCTCGCCAGCTACCCAGAAACAACTACACCGTGGCTATACCCCTCTC 1265
 1221 GAAATTCAGCATAGTTTACACGAGCGCGCAAAATAACTACACGAGGATATAACCGTTTC 1280
 1266 AAACCGCAGCAATCGGGGTGTTCTCAGTACGCTTACCACCGATCCAAATCAAGTGTGATAC 1325
 1281 AAATCGCAGCAACCGCGGTACTCAGCACATTTGACCGCAGATCCAACTCAAGTTCGATGC 1340
 1326 GTTGTGTTGATGCGGTGGTGCACCAACCAAGTTTATTTACCGGACAGACACTTATCTGGAC 1385
 1341 CTTATTTGATGCGGAGGCCATCAACCAAGCTTGTATTCGGCCAGTTCTAATTTGGAC 1400
 1386 ACCACGAGGAGAGTTAAAGCAGGTTAATAATGCGCCGGAAATGAGTGTGATACGCTACGA 1445
 1401 ACGCGAGGCGAATTGAAACAAAGCCAACTAATAGCGCAGGAAATGAGTGTATCGCTACGA 1460
 1446 CAGCAACCGCATGAGACAACTGAAGTGTGAAAGCCAAAGCCAACTTACTACGAGCA 1505
 1461 TAGCAACGGCATAACGACGCTAAAGTGAATGAACAAACAACTCAGAAATATCCCGCAACA 1520
 1506 ACAACGGGTAATCTATTTGCGGACTGGAGCTAGCACAACCCAGAGCAACGCCCAAC 1565
 1521 ACAAGGGTAATCTTATACCGGGCTGGAATAGCTACAAACCCAGCAACGCCCAAC 1580
 1566 ACGGAGAGAGTTACAGCTTATCACACTCGGTGAAGCCGTGCGGCAACAGGTACGGTGT 1625
 1581 ACAGAGAGTTTACAGCTTATCACACTCGGTGAAGCCGCGCGCGCAAGTCCGAGTAT 1640
 1626 GCACTGGGAGAGCGTTAAGCCAGAGATGTCAACATTAATCAACTACACTAGCTTACAGCTACGA 1685
 1641 GCATTCGGAGAGCGGTAAACCCAGAGATTAATAACAATCAACTCAGTTCGTTACAGCTACGA 1700
 1686 TAATCTGATCGGCTCCAGCGCAGCTTGAACCTGGCAACCAAGGACAAATATCAGCGAGGA 1745
 1701 TAATCTTATTTGGCTCCAGCCAACTTCAATTAGTAGCAGGACAAATATCAGTGAAGA 1760
 1746 AGAGTATTATCCATTTTGGGGGACAGCGCTGTGGGAGCAAAAACAGCAAAACAGAAAGCCAG 1805
 1761 AGAATATTATCCATTTTGGTGTACAGGCTGTGGGCGGCAAGGAATCAAAACCGAAGCCAG 1820
 1806 CTATAAAACGATTCGCTATTTCCGGCAAGAAACAGAGATGCCACCGGGTGTATTTATACGG 1865
 1821 CTATAAAACCATTCGTTATTTCTGTTAAGAGCGGGATGTTTACCGGGCTGTATTTATATGG 1880
 1866 TTATCGTTATTACCAACCGTGGCGGCGAGATGTTTAAAGCGGAGCCCGGCGAGAAACAT 1925
 1881 CTACCGTTATTACCAACCGTGGCGGCGAGATGTTTAAAGTGTGAGTGTTCACAGATGAAA 1985
 1926 TGATGGCTGAATCTATACCGAATGGTAAGAAAATAATCTCTGTGAGTTTACAGATGAAA 1995
 1941 TGATGGCTGAATTTATATCGCATGGTGAAGAAATAACCGGTCAGCGCAATTTGATGTTC 2000
 1986 TGAATTAGCGCCAGAAAGGGAATA 2012
 2001 GGGATTATCACCGGCCAACAGAACAGA 2027

RESULT 5
 US-10-754-115-57
 ; Sequence 57, Application US/10754115
 ; Publication No. US20040208907A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hey, Timothy
 ; APPLICANT: Schleper, Amanda
 ; APPLICANT: Bevan, Scott
 ; APPLICANT: Bintim, Scott
 ; APPLICANT: Mitchell, Jon
 ; APPLICANT: Li, Ze Sheng
 ; APPLICANT: Ni, Weiting
 ; APPLICANT: Zhu, Baolong
 ; APPLICANT: Merlo, Don
 ; APPLICANT: Apel-Birkhold, Patricia
 ; APPLICANT: Meade, Thomas

; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens strain W14
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2817)
US-10-754-115-57

Query Match 52.5%; Score 1440.6; DB 8; Length 2817;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 1663; Conservative 0; Mismatches 329; Indels 15; Gaps 1;

Qy 21 AATGACAAAGACCCCTCGATTAAAGGTATTAGATAACAGGAAATTAATGTACGTAC 80
Db 21 ACTTTATCACCATACGCTACCGTCAGTGTTCAGGATAACCGTGGACTAGCTATCCGTAA 80

Qy 81 TTTAGAATATCTACGCACTCAAGCTGACGAAACAGTGATGAATTAATTACGTTCTATGA 140
Db 81 TATTAGTTTTACCGCACTACCGCAGAGCAATACCGATACCGGTATTAACCGCCATCA 140

Qy 141 GTTCAATATTCCGGGATTTGAGTAAAGACCGGATCCTCGTA-----A 185
Db 141 ATATAATGCCGGGGATTTTGAACCAAGCATTTGATCCTCGCCTGTATGACGCCAACA 200

Qy 186 AATAAAAAACAGAGCGGCCAAATTTTCAATTCGTGTCTTTAAATCTTCGCGGTCAAGTTT 245
Db 201 GACTAACAGCTGTACACCGGAATTTTATCTGGCGACATAATTTGACCGGCAATATCCT 260

Qy 246 ACSTGAAGAAAGTTGTGATCCGCTCGGACTATTACCCCTCAATGATATTGAAAGTCGCC 305
Db 261 GCGAACAGAGAGCGTGCATGCCGTGGACGATTAACCTCAACGATATTGAAGCGCGCC 320

Qy 306 GGTGTTGATCATCATGCAACCGGTGTCCGCCAAACCATCGTTTATGAAGATTAACCCCT 365
Db 321 GGTGTTGACCATCAATGACGCGGTGTCCGCCAAACCATCGTTTATGAAGATTAACCCCT 380

Qy 366 TCCGGTCTGCTGCTCTATCACGAAACAGTACAGCGAGGAGAGAAACGACCGAACG 425
Db 381 GCCCGTCCGCTGCTCTGCTATCAGCGAAACAGGACAGGACAGAGAAACGACCGAGCG 440

Qy 426 TCTTATCTGGGCGGCAATACGCCGAAGAAAAAGATTACAACCTCGCCGCTCAGTGTGT 485
Db 441 CCTTATCTGGGCGGCAATACGCCGAAGAAAAAGATTACAACCTTGCCCGTTCAGTGTGT 500

Qy 486 CCGCATTAAGATACCGCGGACTTACTCAACTCAATPAGCCTTTCTCTGCTGCGGTGCT 545
Db 501 CCGCATTAAGATACCGCGGACTTACTCAACTCAACAGCCTTTGCCCTGACCGCGCGCT 560

Qy 546 GCTATCAATCTCAACAACTGCTTACCGATACCAGATGCCGACTGGACAGGTGAGA 605
Db 561 TCTATCAATCTCAACAACTGCTTACCGATACCAGATGCCGACTGGACAGGTGAGA 620

Qy 606 CCAGAGCTCTGGCAACAAAACTGAGTAGTGTCTATATCACCCAAAAAGTAACACTGA 665
Db 621 CCAGAGCTCTGGCAACAAAACTGAGTAGTGTCTATATCACCCAAAAAGTAACACTGA 680

Qy 666 TGCCACCGGGCTTTTACTGCCACCGATGCGAAAGCAACATTCAGCGGCTGGCCTTA 725
Db 681 TGCCACCGGGCTTTTACTGCCACCGATGCGAAAGCAACATTCAGCGGCTGGCCTTA 740

Qy 726 TGATGCGCGGCGAGCTTAAAGGGAGTTGGTTAACTCAAGGTCAGCGGCAACAGGT 785
Db 741 TGATGCGCGGCGAGCTTAAAGGGAGTTGGTTAACTCAAGGTCAGCGGCAACAGGT 800

Qy 786 GATTATCAAAATCGCTAACCTACTCCGCGCGCGGCAAAAATTAAGTGAAGACGACGTAA 845
Db 801 GATTATCAAAATCGCTAACCTACTCCGCGCGCGGCAAAAATTAAGTGAAGACGACGTAA 860

Qy 846 CGSGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGGCTTATCGGCATTACCAC 905
Db 861 CGSGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGGCTTATCGGCATTACCAC 920

Qy 906 TCGCCGTCCATCAGACGCCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG 965
Db 921 TCGCCGTCCATCAGACGCCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGG 980

Qy 966 CAATGTCATTAATATCCGTAATGATCGGAAGCCACTCGCTTTTGGGCGCAATCAGAAAGT 1025
Db 981 CAATGTCATTAATATCCGTAATGATCGGAAGCCACTCGCTTTTGGGCGCAATCAGAAAGT 1040

Qy 1026 AGCCCGGAGAGATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGGCGCAACCGGCG 1085
Db 1041 AGCCCGGAGAGATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGGCGCAACCGGCG 1100

Qy 1086 CGAAATGGCCCAATATCGGTACGAAACCAACCAACTTCCCTCCCTCGCTACCTTCTGA 1145
Db 1101 CGAGATGGCCCAATATCGGTACGAAACCAACCAACTTCCCTCTCGGCGCTACCTTCTGA 1160

Qy 1146 CAAACAATACCTACATACTACTCGAGCTACAGCTATGATACAGTGGTAAATCTGAC 1205
Db 1161 TAACAATACCTACATACTACTCGCACTTATCTATGACCGTGGCGGCAATTTGAC 1220

Qy 1206 GCAAAATTCGGCAGAGCTCGCCAGTACCAGAACACTACACGCTGGCTATCACCTCTC 1265
Db 1221 GAAAAATTCAGCATAGTTCACAGCGCGCAAAATAACTACAGCGGATATAACGGTTTC 1280

Qy 1266 AAACCCGAGCAATTCGGGGTGTCTCAGTACGCTTAAACACCGATCCAAATCAAGTGGATAC 1325
Db 1281 AAATCGAGCAACCGCGGCTACTCAGACATTTGACCGGAGATCCAACTCAAGTCGATGC 1340

Qy 1326 GTTGTGTTGATGCGGTTGTCACCAAAACCAAGTTTATACCGGAGACAGACTTATCTGGAC 1385
Db 1341 CTTATTTGATGCGGAGGGCCATCAAAACCAAGTTTATACCGGCAAGTTCTAACTTTGGAC 1400

Qy 1386 ACCACAGAGAGTTAAAGCAGTTTAAATGCCCCGGGAAATGAGTTCACGCTACGA 1445
Db 1401 ACCGAGGCGGAATTTGAAACCAAGCCAACTAATAGCGAGGAAATGAGTGGTATCGCTACGA 1460

Qy 1446 CAGCAACCGGATGAGACAACTGAAAGTGAGTGAACCGCAACCCAGAAATACTACGACGA 1505
Db 1461 TAGCAACCGGATACGCGGCTAAAGTGAATGAACAACTCAGATATCCGCGNACA 1520

Qy 1506 ACAACGGGTAATCTATTTGCGGAGCTGAGCTACGCAACCCAGACCAAGCCCAAC 1565
Db 1521 ACAAGGGTAACTTATCTACCGGGCTGGAAAATACGTACAAACCCAGAACCAACCAAC 1580

Qy 1566 AACGGAAGAGTTACAGTTTATCACCTCGGTGAAGCGGTGCGGCAAGCTACGGGTGTT 1625
Db 1581 AACAGAAGAGTTACAGTTTATCACCTCGGTGAAGCGGTGCGGCGGCAAGCTACGGGTATT 1640

Qy 1626 GCATTCGGAGAGCGGTGAAGCCAGAGATGTCAACAATAATCAACTACGTTTACAGCTACGA 1685
Db 1641 GCATTCGGAGAGCGGTGAAGCCAGAGATTAATAACAATCAGCTTCGTTTACAGCTACGA 1700

Qy 1686 TAATCTGATCGGCTCCAGCGAGCTTGAACTGGACAAACCAAGGCAAAATTAATCAGCGAGGA 1745
Db 1701 TAATCTTATTGGCTCCAGCCAACTTCAATTTAGATAGCGGACAAATTAATCAGTGAAGA 1760

Qy 1746 AGAGTATTATCCATTTTGGGCGGAGACGCGTGTGGGAGCAACAGCCAAACAGAACCCAG 1805
Db 1761 AGAATATTATCCATTTTGGTGGTACAGCGCTGTGGGCGGCAAGGAATCAAAACCGAAGCCAG 1820

Qy 1806 CTATAAAACGATTCGCTATTTCGCGCAAGAAACGAGATGCCACCGGTTGTTATTATTACGG 1865
Db 1821 CTATAAAACGATTCGCTATTTCGTTAAAGAGCGGGATGTTTACCGGCTGTATTATTATGG 1880

Qy 1866 TTATCGTTATTACCAACCGGTGGGCGGAGATGTTTAAAGCGCGGACCCCGGAGAACCAT 1925

Db 1881 CTACCGTTATTACCAACCGTGGCGGCAGATGTTAGGTGCAGACCCGGCAGGAACCAT 1940
Qy 1926 TGATGGGCTGATCTATACCGAATGGTAAGAAATAAATCCTGTGAGTTTACAGATGAAA 1985
Db 1941 TGATGSACTGAATTTATATCGCATGGTGAGAAATAACCCGGTGACGCAATTTGATGTTCA 2000
Qy 1986 TGGATTAGCGCCAGAAAAGGGAATA 2012
Db 2001 GGGATTATCACCGGCCAACAGACAGA 2027

RESULT 6
US-10-706-424-11
; Sequence 11, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: french-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10706.424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2880)
US-10-706-424-11

Query Match 36.6%; Score 1004.6; DB 7; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;

Qy 1 ATGAGCAGTTACAAATCTGCAATTTGACCAAGACCCCTCGATTAGGTATTAGATAAC 60
Db 1 ATGAAAAACATTTGATCCCAAACTTTATCAAAAAACCCCTACTGTGAGGTTTACGATAAC 60
Qy 61 AGGAAATTAATGATGACGTACTTTAGAAATATCTAGCACTCAAGCTGACGAAACACAGTGAT 120
Db 61 CGTGGTCTGAATAATCCGTAACATCGATTTTCATCGTACTACCGCAATGGTGATCCCGAT 120
Qy 121 GAATTAATAGCTTCTATGATTTCAATATCCGGGATTTACGGGATTTACGAAACACCGATCCT 180
Db 121 ACCGGTATTACCCGCCATCAATAGCATATTCACGGACACCTTAAATCAAAAGCATCGATCCG 180
Qy 181 CGTAAATAAATAAACCA-----GAGCGGCCCAAAATTTTCATTCGTGCTTT 225
Db 181 GGCCTATATGAAGCAAGCAACCAACAAATACGATCAAAACCAATTTTCITTTGGAGTAT 240
Qy 226 AATCTTCGCGGTCAAGTTTACGTGAAGAAAGTGTGATGCGGTGCGGACTATTACCCCTC 285
Db 241 GATTTGACCGGTATCCCTTATGTACAGAGAGCATTTGATGAGTGCAGCTGTCACTTG 300
Qy 286 AATGATATTGAAGTCGCCCGGTGTGATCATCAATGCAACCGGTGTCGCCCAAAACCAT 345
Db 301 AATGATATTGAAGCGCGTCCGCTACTAACGGTGACTGCAACAGGGGTTTATACAAATCGA 360
Qy 346 GTTATGAAGATACACCCCTTCCCGTCTGCTCGCTATCACCGAACAGTACAGGCA 405
Db 361 CAATATGAACCTTCTTCCCTCGCGGTCTGTTTATCTGTTGCGGAACAAACACCCGAG 420
Qy 406 GGAGAGAAA-----ACGACCGAAGCTTATCTGCGCGCGCAATACGCCCAAGAAAAA 459
Db 421 GAAAAACATCCCGTATCACCGAAGCCCTGATTTGGGCTGGCAATACCGAAGCAGAGAAA 480
Qy 460 GATTACAACCTCGCGGTGATGTCGCGCAATACGATACCGGGGACTTACTCAATC 519
Db 481 GACCATAACCTTGCGCGCAGTGGTGGTCTCACTATGACACGGCGGAGTTTACCCGGTTA 540

Qy 520 AATAGCCTTTCTCTGGCTGGCGTGTGCTATCACAATCTCAACCAACTGCTTACCGATAAC 579
Db 541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACCTATTGATCGACACT 600
Qy 580 CAGGATGCCGACTGGACAGGTGAAGACCAAGAGCCTCTGGCAACAAACACTGAGTAGTAT 639
Db 601 CAAGAGCAAACTGGACAGGTGATAACGAAACCGTCTGGCAAAACATGCTGGCTGATGAC 660
Qy 640 GTCTATATCACCCAAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCC 699
Db 661 ATCTACACAACCTGAGCACCTTCGATGCCACCGGTCTTACTGACTCAGACCGATGCG 720
Qy 700 AAAGGCAACATTCAGCGGCTGGGCTATGATGTGGCGGCGAGCTAAAAAGGAGTTGGTTA 759
Db 721 AAAGGNAACATTCAGAGACTGGGCTTATGATGTGGCGGCGAGCTAAACGGGAGTGGCTA 780
Qy 760 AACTCAAAGGTGAGCGGAAACAGGTGATTTATCAAAATCGCTAACCTACTCTCGCGCGGG 819
Db 781 AACTCAAAGGCCAGACGGAAACAGGTGATTTATCAAAATCCCTGACTACTCTCGCGCGCGA 840
Qy 820 CAAAATTTAGGTGAAGACGACGCTAACGGGATTTGCTCACTGAATACAGCTACGAAACCGGAA 879
Db 841 CAAAAATTTAGGTGAGGAACACGCGCAATGATTTATCAGCAATACAGTTTATGAACCCGAA 900
Qy 880 ACCCAACGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTTGCAAGAC 939
Db 901 ACCCAACGGCTGATCGGTATCAAAACCCGCGTCCGTGACACACTAAAGTGTCTACAAGAC 960
Qy 940 CTACGCTATCAATATGACCCAGTAGCAATGTCTTAATATTCGTGAATGATGCGGAAGCC 999
Db 961 CTGCGCTATGAATATGACCGGTAGGCAATGTCTATCAGCATCGGTATATGACGCGGAAGCC 1020
Qy 1000 ACTCGCTTTTGGCGCAATCAGAAAGTAGCCCCGGAGAAATAGCTATACCTACGATTCCTG 1059
Db 1021 ACCCGCTTTTGGCACCAATCAGAAAGTAGTCCGGAACAACTTATACCTACGATTCCTG 1080
Qy 1060 TATCAGCTTATCAGCGCCACCGGCGGCAATGGCCAATATCGGTGAGCAAAACCAACAA 1119
Db 1081 TATCAGCTTATCAGCGCCACCGGCGGCAATGGCGNAATATAGTCAACAAAGTCAACAA 1140
Qy 1120 CTTCCCTCCCTCGCTTCTCTGACAAACAATCTCTACACTAACTATATCTCGCAGGTAC 1179
Db 1141 TTTCCCTCACCGCTCTACCTCTGATACCAACACCTTATACCACTATACCCGCTACTTAT 1200
Qy 1180 AGCTATGATCACAGTGTGATCTGACGCAATTTCCGACAGCTCGCCAGCTACCCAGAC 1239
Db 1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCAGCACAGTTTCCCGGCGACGCAAAAC 1260
Qy 1240 AACTTACACCGTGGCTATCACCTCTCAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTA 1299
Db 1261 AACTTACACCAACCAATATCAGGTTTCAAATCGCAGCAACCGCGCAGTACTCAGCACATTG 1320
Qy 1300 ACCACCGATCCAAATCAAGTGGATAGTGTGTTGATGCCGGTGGTCAACCAACAGTTTA 1359
Db 1321 ACCGAGATCCGGCGCAAGTAGATGCTTTGTTGATGACGGCGGACATCAGAACACCTTG 1380
Qy 1360 TTACCCGGACAGACACTTATCTGCAACCAACGAGGAGAGTTAAGCAGGTTAATAATGGC 1419
Db 1381 ATATCAGGACAAAACCTGAACTGGAATCTCGTGGTGAACCTGCAACAAAGTAACACTGGTT 1440
Qy 1420 CCGGAAATCAG-----TGGTACCGCTACGACAGCAACCGCATG 1458
Db 1441 AAACGGGAAGGGCGCAATGATGTCGGGAATGGTATCGTTATAGCGGTGACGGAAGA 1500
Qy 1459 AGCAACTGAAAGTGAAGCAAGCCAAACCCAGAAATACTACGACGAACCAACCGGTAAATC 1518
Db 1501 AGGATGTTAAAAATCAATGAACAGCAGCGCCAGCAACAAACGCTCAAAACACACGCTGACT 1560
Qy 1519 TATTTGCGGAGCTGAGCTACGCAACACCGCAGGCAACGCCACAAACGAGAGCTTA 1578
Db 1561 TATTTGCGGAACTTAGAACTTCGTCTTAACACAAACAGCAGCGGCCAACCGAAGATTG 1620

QY 1579 CACGTTATCACATCGGTGAAGCGGTCCGCGCACAGGTACGGGTGTGCACTCGGAGAGC 1638
Db 1621 CAAGTTATATCCCTAGCGAAGCGGCGCGGCGCACAGGTACGAGTATTTACATTCGGAGAGC 1680
QY 1639 GGTAAAGCCAGAAGATGTCACCAATATCACTCACTACGTTTACAGCTACGATATCTGATCGGC 1698
Db 1681 GGTAAACCGGAAGATATCGACAATATCAGTTGGTTATAGTTACGATATCTTATCGGT 1740
QY 1699 TCAGCCAGCTTGAATCGGACCAACCAAGGACAAATATATCAGCGAGGAAGATATATCCA 1758
Db 1741 TCCAGTCAACTTGAATTAGATAGCAAGGACAAATATATCAGTGAAGAAGATATATCCC 1800
QY 1759 TTTGSCGGGACAGCGTGTGGGACGACCAACAGCAGCAACAGACCCAGCTATATAACGATT 1818
Db 1801 TATGGTGGAAACAGCATTTATGGGCGCGCAGGAATCAGACAGAACCCAGTTATATAAATCATC 1860
QY 1819 CGCTATTTCCGGCAAGAAACAGAGATGCCACCGGTGTGTTATTTATACGTTATCGTTATTAC 1878
Db 1861 CGTTATTCAGCAAGAGCGGGATGCCACCGGCTATTTATCTACCGGCTATCGGTATTAC 1920
QY 1879 CAACCGTGGCGGGCAGATGGTTAAGCGGACCCCGCAGAACCCATTTGATGGGCTGAAT 1938
Db 1921 CAACCGTGGATAGACGGTGGTTAAGCTCCGATCCGCGCAGGAACAATCGATGGCTGAAT 1980
QY 1939 CTATACCGAATGTAGAAATAATCTGTGAGTTTACAGATGAAATAATGATTAGCGCCA 1998
Db 1981 TTATATCGGATGTGAGGAATAATCCAGTTACCTCTGATCCTGATGGATTAATGCCA 2040
QY 1999 GAAAAGGGAATAATACCAAGAGGTAAA 2027
Db 2041 ACAATTCAGACGCATAGCAGCACTAAA 2069

RESULT 7

US-10-609-113-46
; Sequence 46, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-46

Query Match 36.6%; Score 1004.6; DB 7; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;
QY 1 ATGAGCAGTACAAATTCGAATTCACCAAGGACCCCTCGATTAAAGTTATAGATAC 60
Db 1 ATGAAAAACATTCATCCCAACCTTTATCAAAAAACCCCTACTGTCAGCGTTACGATAAC 60
QY 61 AGCAATTAATATGTCAGTACTTTAGAAATATCTACGCACTCAAGCTCAGCAAAAACAGTGAT 120
Db 61 CGTGGTCTGTAATCCGTAACATCGATTTTCATCTGTAACCGCAATATGTTGATCCCGAT 120
QY 121 GAATTAATTAATCGTTCTATGATGTTCAATATTTCCGGGATTTTCAGGTAAAAAGCACCGATCCT 180

Db 121 ACCCGTATTATCCCGCCCATCAATACGATATTTACGGACACCTAAATCAAAGCATCGATCCG 180
QY 181 CGTAAAAATAAAACCA-----GAGCGGCCCCAAATTTCAATTCGTGTCTTT 225
Db 181 CGCTATATGAAGCCAAGCAAAACAATACGATCAAAACCAATTTTCTTTGGCAGTAT 240
QY 226 AATCTTGGCGGTCAAGTTTTCGTGAAGAAAGTTGTGATGCCGTCGGTACGATATTTACCTC 285
Db 241 GATTTGACCGGTAAATCCCTATATGTACAGAGACGATTTGATGCAAGTCCGATCTGTCACCTTG 300
QY 286 AATGATATTGAAAGTCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAAAACCAT 345
Db 301 AATGATATTGAAAGCGCTCCGCTACTAACGGTGACTGCAACAGGGGTATACAACTCGA 360
QY 346 CGTTATGAAGATAAACCCCTTCCCGTCTGCTCTCTATCACCGAACAAGTACAGGCA 405
Db 361 CAATATGAAACTTCTTCCCTGCCCGTCTGTTATCTGTTGCCGAAACAACACCCGAG 420
QY 406 GGAGAGAAA-----ACGACCGGAACGTCTTATCTGGCGCGGCAATACGCGGCAAGAAAA 459
Db 421 GAAAAAACATCCCGTATCACCGAAACGCTGATTTGGGCTGGCAATACCGAAGCAGAGAA 480
QY 460 GATTACAACCTCGCGGTCAAGTGTGTCGCCATTACGATACCGCGGACTTACTCAACTC 519
Db 481 GACCTAACCTTCCCGGCGCAGTGTGCTGCTATCTCAATCCAGCCAATATTGATCGACACT 540
QY 520 AATAGCCTTTCTCTGCTGGCGTCTGCTATCACAACTCTCAAACTGCTTACCGATAAC 579
Db 541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAATATTGATCGACACT 600
QY 580 CAGGATGCGGACTGGAACAGGTGAAGACAGAGCTCTCGGCAACAAAACTGAGTAGTGAT 639
Db 601 CAAGAGGCAAACTGGACAGGTGATACGAAACCGTCTGGCAAAACATGCTGGCTGATGAC 660
QY 640 GTCTATATCACCCARAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACGCGATGCC 699
Db 661 ATCTACAACTCTGAGCACCTTCGATGCCACCGGTCTTACTGACTCAGACCGATGCG 720
QY 700 AAAGGCAACATTCAGCGGCTGGCTATGATGTGGCGGGCAGCTAAAGAGGAGTTGGTTA 759
Db 721 AAAGGCAACATTCAGAGACTGCTTATGATGTGGCGGGCAGCTAAACGGGAGCTGGCTA 780
QY 760 ACACCTAAAGGTGAGCGGAAACAGGTGATTAATAATCGCTAACCTATCTCCGCGCGGG 819
Db 781 ACACCTAAAGGCGCAGACGGAACAAGTATTAATAATCCCTGACTACTCCGCGCGCGA 840
QY 820 CAAAAATTACGTGAAGACGACCGGTAAAGGATGTCTACTGAAATACAGCTACGACCGGAA 879
Db 841 CAAAAATTACGTGAGGAACACCGCAATGATTTATCCGGAATACAGTTATGAACCGGAA 900
QY 880 ACCCAACGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTGCAAGAC 939
Db 901 ACCCAACGGCTGATCGGTATCAAAACCCCGCTCCGTGAGACACTAAAGTGTACAAAGAC 960
QY 940 CTACGCTATCAATATGACCCAGTAGGCAATGCTAATAATATCGTAAATGATCGGAAGCC 999
Db 961 CTGCGCTATGAATATGACCCGTTAGGCAATGTCATCAGCATCCGTAAATGACGCGGAAGCC 1020
QY 1000 ACTCGCTTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGCTATATACCTACGATTCCTG 1059
Db 1021 ACCCGCTTTTGGCAATCAGAAAGTAGTCCCGGAAAAACACTTTATACCTACGATTCCTG 1080
QY 1060 TATCAGCTTATCAGCGCCACCGGGCGGAAATGGCCAATATCGGTGAGCAAAAAACCA 1119
Db 1081 TATCAGCTTATCAGCGCCACCGGGCGGAAATGGCGAATATAGTTCACAAAGTCAACAA 1140
QY 1120 CTTCCCTCCCTCGCTACCTTTCTGACAACTATACCTACACTATATCTCAGCTAC 1179
Db 1141 TTTCCCTCACCCTCTACCTTTCTGATAACAACACCTATACCAACTATACCCGTACTTAT 1200
QY 1180 AGCTATGATCAGAGTGTAAATCTGACGCAAAATTCGGCAGAGCTCCGCCAGTACCCAGAAC 1239
Db 1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCACAGTTTCAACCGCGCAGCAAAAC 1260

```
Qy 1240 AACTACACCGTGGCTATCACCTCTCAAAACCGCAGCAATCGGGTGTCTCAGTAGCCTA 1299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1261 AACTACACCAACCAATATCACGGTTTCANATCGCAGCAACCGCGAGTACTCAGCACTTG 1320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1300 ACCACCGATCAAAATCAAGTGGATACGTTGTTGATCCGGTGGTCAACCAACAGTTTA 1359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1321 ACCGAGATCGGGCGCAAGTAGTCTTTGTTGATCGAGCGGACATCAGAACACCTTG 1380
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1360 TTATCCGGACAGACATTTATCTGTGACACACAGGAGAGTTAAGCGAGTTAATATGGC 1419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1381 ATATCAGGACAAAACCTGAATCTGGAATACTCGTGGTGAACCTGCAACAAGTAACACTGGTT 1440
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1420 CCGGGAATGAG-----TGGTACCGCTACGACAGCAACGCGCATG 1458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1441 AAACGGGAGAGGGCGCAATGATGTCGGGAATGGTATCGTTATACGGTGACGGHAGA 1500
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1459 AGACAACTGAAAGTGAAGAACAGCCAAACCCAGAAATACTACGCAAGCAACACGGTAAATC 1518
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1501 AGGATGTTAAATCAATGAACAGCAGGCCAGCAACACGCTCAAAACACAAACGTTGACT 1560
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1519 TATTTGCGGAGCTGGAGCTACGCACAACCCAGAGCAACGCCACAACAACGGAAGATTGA 1578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1561 TATTTGCGGAACCTTAGAACTTCGTCTAAACAAACACGACGCGCCACAACCGGAAGATTG 1620
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1579 CACGTTATCACACTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTTGCACTGGGAGAGC 1638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1621 CAAGTTATACCGGTAGCGGAAGCGGGCGGGGCAAGGTACGATTAATCATTTGGGAGAGC 1680
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1639 GGTAAAGCCAGAAAGTGTCAACAAATCAACTACGTTTACAGCTACGATAATCTGATCGGC 1698
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1681 GGTAAACCGGAAGATATCGCAATAATACGTTGCGTTATAGTTACGATAATCTTATCGGT 1740
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1699 TCCAGCCAGCTTGAATCTGGACAACCAAGGACAAATTAATCAGCGAGGAAGATTATTCGA 1758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1741 TCCAGTCAACTTGAATTAGATAGCGAAGGACAAATTAATCAGTGAAGGAAGAAATATTATCCC 1800
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1759 TTTGGCGGACAGCGCTGTGGGACAGCAACAGCCAAACAGAGCCAGCTATAAACAGATT 1818
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1801 TATGGTGAACAGCATTTATGGGCGCCAGGAATCAGACAGAACCCAGTTATAAACATATC 1860
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1819 CGCTATTTCGGCAAGAACAGAGTGCCACCGGGTGTATTATTATTCAGGTATTCGTTATTAC 1878
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1861 CGTTATTTCAGCAAGAGCGGGATGCCACCGGCTATATTACTACGGCTATCGGTATTAC 1920
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1879 CAACCGTGGCGGCGAGATGTTTAAGCGCGAACCCCGCAGGAACCATTTGATGGCTGAAT 1938
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1921 CAACCGTGGATAGACCGGTGTTAAGCTCCGATCCGCGCAGGAACAATCGATGGGCTGAAT 1980
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1939 CTATACCGAATGTTAAGAAATAATCTCTGTGATTTACAAGATGAATGGAATGATAGCGCCA 1998
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1981 TTATATCGATGGTGAGGAATAATCCAGTTACCCTCTCTGTATCTGTATGGAATTAATGCCA 2040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1999 GAAAAAGGAAATATACCAAGAGGTAAA 2027
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2041 ACATTCGAGAACGCATAGCAGCACTAAA 2069
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 8

```
US-10-754-115-46
; Sequence 46, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
```

```
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2880)
US-10-754-115-46
```

```
Query Match 36.6%; Score 1004.6; DB 8; Length 2883;
Best Local Similarity 69.3%; Pred. No. 1.4e-250;
Matches 1433; Conservative 0; Mismatches 594; Indels 42; Gaps 3;
```

```
Qy 1 ATGAGCAGTTACAATTCTGCAATTGACAAAGACCCCTCGATTAAAGTTATTAGATAAC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 AGGAATTAATAGTACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 CGTGGTCTGATAATCCGTAACTCGATTTTTCATCTGATACCGCAATGGTGATCCCGAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 GAATTAATTAAGTCTTATGAGTTCAATATTTCCGGGATTTTCAGGTAAAAAGCACCGATCCT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 ACCGTTATTACCGCCCATCAATACGATATTTACGGGACACCTAAATCAAGCATCGATCCG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 CGTAAAAATAAAACCA-----GAGGGGCCAAATTTTCATTCGTGTCCTTT 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 CGCTATATGAAGCCAGCAACCAACAATAACGATCAAAACCCAAATTTCTTTGGCAGTAT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 AATCTTGGCGGTCAAGTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCCTC 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 GATTTGACCGGTAAATCCCTATGTAAGAGAGCATTTGATGACGTTGCACTGTCCACTTG 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 AATGATATTGAAAGTCCCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAAAACCAT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 AATGATATTGAAGCCGTCCGCTACTAACCGTCACTGCAACAGGGGTTATACAAACTCGA 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 346 CGTTATGAAGATAAACCTTCCCGGTCTGCTGCTGCTATACCCGAAAGATACAGGCA 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 CAATATGAAACTTCTTCCCTGCGCGTCTGTTATCTGTTGCCGAAACACACCCGAG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 406 GGAGAGAAA-----ACGACCGGAACGCTTATCTGGGCGGCAATACGCCCAAGAAAAA 459
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 421 GAAAAAACATCCCGTATTCACCGAACCGCTGATTTGGGCTGGCAATACCGAAGCAGAAA 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 460 GATTACAACCTCGCCGTCAGTGTGTCGCGCATTAACGATACCGCGGAGTTTACTCAATC 519
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 481 GACCAATACCTTGGCGGCAAGTGGTCCGTCATCATGACACGGCGGAGTTACCGGTTA 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 520 AATAGCCTTTCTCTGGTGGCGTCTGCTGATATCAATCTCAACAACTGCTTACCGATAAC 579
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 541 GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACTATTGATCGACACT 600
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 580 CAGGATCCGACTGGACAGGTGAAGACAGAGCTCTGGCAACAAACAACTGAGTAGTAT 639
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 601 CAAGAGGCAAACTGGACAGGTGATAACGAAACCGTCTGGCAAAACATCTGGCTGATGAC 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 640 GTCTATATCAACCAAGTAACACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCC 699
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 661 ATCTACACAACCTTGAGACCTTCGATGCCACCGTCTTTTACTGACTCAGACCGATGCG 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 700 AAAGGCAACATTCAGCGGCTGGCCTATGATGTGGCGGGCAGCTAAAGGAGGATGTGTTA 759
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 721 AAAGGGAACATTCAGAGACTGGCTTATGATGTGGCGGGCAGCTAAACGGGAGCTGGCTA 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

760 ACACTCAAGGTGAGCGGAGCAAGGTGATTAATCAAACTCGTAACTACTCCGCGCGCGG 819
Db |||||
781 ACACTCAAGGCGAGAGCAAGGTGATTAATCAAACTCGTAACTACTCCGCGCGCGG 840
Qy |||||
820 CAAAAATACGTGAGAGCAAGGTGATTAATCAAACTCGTAACTACTCCGCGCGG 879
Db |||||
841 CAAAAATACGTGAGAGCAAGGTGATTAATCAAACTCGTAACTACTCCGCGCGG 900
Qy |||||
880 ACCCAAGGCTTATCGGCAATACCACTCGCGGTCATCAGAGCCCAAGGTGTCAGAG 939
Db |||||
901 ACCCAAGGCTGATCGGCAATACCACTCGCGGTCATCAGAGCCCAAGGTGTCAGAG 960
Qy |||||
940 CTAAGCTTATCAATATGACCGGAGGAGTATGATTAATCAAACTCGTAACTACTCCG 999
Db |||||
961 CTGGCTATGATATGACCGGAGGAGTATGATTAATCAAACTCGTAACTACTCCG 1020
Qy |||||
1000 ACTCGCTTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGTATACCTACGATTCCTG 1059
Db |||||
1021 ACCCGCTTTTGGCACAATCAGAAAGTAGCCCGGAGAAATAGTATACCTACGATTCCTG 1080
Qy |||||
1060 TATCAGCTTATCAGCGCCACCGGCGGAAATGCGCAATATCGTCAAGCAAAACCA 1119
Db |||||
1081 TATCAGCTTATCAGCGCCACCGGCGGAAATGCGCAATATAGTCAAAAGTCAAC 1140
Qy |||||
1120 CTTCCCTCCCTCGCTACCTCTGACAAATACCTACACTAATATATCTCGCAGCTAC 1179
Db |||||
1141 TTTCCCTCACCGCTCTACTCTGATACCAACCTATACCACTATACCCGTAAT 1200
Qy |||||
1180 AGTATGATCAGAGTGGTATCTGACGCAAAATTCGGGACAGCTCGCCAGTACCCAG 1239
Db |||||
1201 ACTTATGACCGTGGCGCAATCTGACCAAAATCCAGACAGTTCACCGCGAGCAAA 1260
Qy |||||
1240 AACTACACCGTGGCTATCACTCTCAAAACCGCAGCAATCGGGTCTCTCAGTACG 1299
Db |||||
1261 AACTACACCAATATCAGGTTTCAAAATCGCAGCAACCGCGAGTACTCAGCATTG 1320
Qy |||||
1300 ACCACGATCAAAATCAAGTGGATAGTGTGTTGATCGCGGTGGTCAACAAACAGTT 1359
Db |||||
1321 ACCGAGATCCGCGCAAGTAGATGCTTTGATGCGCGGACATCAGAACACCTTG 1380
Qy |||||
1360 TTACCCGCGAGACATTTATCTGACACCAAGAGGAGTTAAAGCAGGTTAATATGC 1419
Db |||||
1381 ATATCAGGCAAAACCTGAATCTCGTGGTGAATCTGCAACAAAGTAACTCGTT 1440
Qy |||||
1420 CCGGGAATGAG-----TGCTACGCTACACAGCAGCGCATG 1458
Db |||||
1441 AAACGGGCAAGGCGCAATGATGATCGGGAATGGTATCGTTATAGCGGTGACGGA 1500
Qy |||||
1459 AGACAACTGAAAGTGAAGTGAAGCAAGCAACCCAGAACTACTACGAGCAACAAAGGTA 1518
Db |||||
1501 AGATGTTAAATCAATGACAGAGCGGCGGCAACACGCTCAACACAACTGTGACT 1560
Qy |||||
1519 TATTCGCGGAGTGAAGTGAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1578
Db |||||
1561 TATTCGCGAATCTAGAACTCTGCTTAACAAACAGCAGCGCCCAACCGAAGATTG 1620
Qy |||||
1579 CAGTTATCACTCGGTGAGCGGTGCGGACAGGTACGGGTGTTGCACTGGGAGAGC 1638
Db |||||
1621 CAGTTATCACTCGGTGAGCGGTGCGGACAGGTACGGGTGTTGCACTGGGAGAGC 1680
Qy |||||
1639 GGTAAAGCAGAAATGTCAACAAATCAACTACGTTACAGCTACGATTAATCTGATCGG 1698
Db |||||
1681 GGTAAAGCAGAAATGTCAACAAATCAACTACGTTACAGCTACGATTAATCTGATCGG 1740
Qy |||||
1699 TCAGCCAGCTTGAATGGAACCAAGGCAAAATATATCAGCAGGAGGAGGATTAATCCA 1758
Db |||||
1741 TCAGTCAACTTGAATGGAACCAAGGCAAAATATATCAGTGAAGGAGGATTAATCCC 1800
Qy |||||
1759 TTTGGCGGAGCAGGCTGTTGGGAGCAACAGCAGCAACAGCAGCAGCTTAATAACGAT 1818
Db |||||
1801 TATGGTGAACAGCATTTATGGCGCGGAGGAAATCAGACAGAGCCAGTTATAAATCATC 1860

1819 CGCTATTCGGCAAGAACAGATGCCACCGGGTGTATATTTACCGGTTATCGTTATTAC 1878
Db |||||
1861 CGTTATTCAGGCAAGAGCGGATGCCACCGGGTGTATATTTACCGGTTATCGTTATTAC 1920
Qy |||||
1879 CAACGTCGGCGGAGATGGTTAAGCGCGGACCGGAGGAAACCAATTCGATGGGCTGAAT 1938
Db |||||
1921 CAACGTCGGTAGGACGGTGGTTAAGCTCCGATCCGCGAGGAAACAATCGATGGGCTGAAT 1980
Qy |||||
1939 CTATCCGAATGGTAAGAAATATCTGTGAGTTTACAAGATGAAATCGATTCGATTCG 1998
Db |||||
1981 TTATATCGGATGGTGAAGAAATATCCAGTTACCTCTCTTGATCCCTGATGATTAATGCCA 2040
Qy |||||
1999 GAAAGGGAATATACCAAGAGGTAAA 2027
Db |||||
2041 ACAATTGCAGAACGCATAGCAGCACTAAA 2069

RESULT 9

US-10-262-794A-60
; Sequence 60, Application US/10262794A
; Publication No. US20030207806A1
; GENERAL INFORMATION:
; APPLICANT: Ensign, Gerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapingda, Kitisri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/262,794A
; FILING DATE: 02-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,567
; FILING DATE: 03-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-10-262-794A-60

Query Match      35.0%; Score 962; DB 6; Length 3132;
Best Local Similarity 72.2%; Pred. No. 1.8e-239;
Matches 1323; Conservative 0; Mismatches 470; Indels 39; Gaps 4;

Qy 205 CCAATTTTCATTCTGTCGTTTAAATCTTCCCGGTCAAGTCTTTACGTGAAGAAAGTGTGAT 264
Db      |||||
Qy 220 CCTAATTTTGTCTGGCAGCATGATCTGCCGGTCTATGCCCTGGCGACAGAGAGTGTGAT 279
Db      |||||
Qy 265 GCGGTGCGGACTATTACCTCAATGATATTGAAGTATGCGCGGTGTTGATCATCATGCA 324
Db      |||||
Qy 280 GCTGTCGTACTGTTGCAATGAATGATATTGAAGTCTGTTGCGTAAATGCAATGAATGCG 339
Db      |||||
Qy 325 ACCGGTCTGCCCAAAACCATCGTTATGAAGTAAACACCTTCCCGGTCTGTCGCTCGCT 384
Db      |||||
Qy 340 ACCGGTGTCTGTCAGACCCGTCGCTATGAAGGCAACACCTTGGCCCGGTCTGTTATCT 399
Db      |||||
Qy 385 ATCACCGAAACAAGT-----ACAGGCAGGAGAGAAAACGACCGAACGTCCTTATCTGGGCC 438
Db      |||||
Qy 400 GTGAGCGAGCAAGTTTCAACCAAGAGAGTGTCTAAGTGACAGAGCGCTTTATCTGGGCT 459
Db      |||||
Qy 439 GGCATATGCGCGCAAGAAAAGATTACAACTCTCCCGGTGAGTGTGTCGCGCATTAGCAT 498
Db      |||||
Qy 460 GGGAAATCAACCTCGGAGAAAGAGTATAAACCCTCTCCGGTCTGTGTATACGCCACTACGC 519
Db      |||||
Qy 499 ACCGCGGACTTACTCAACTCAATAGCTTTCTCTGGCTGGCGTCTGCTATCAATCT 558
Db      |||||
Qy 520 ACAGCGGAGTGACCCGGTTGATGATCAGTCACTTGGCGGCGCATGCTATCCCAATCT 579
Db      |||||
Qy 559 CAACAACTGCTTACCGATAACAGGATGCCAGTCCGACGTGAGAGTGAAGACCAAGAGCTCTGG 618
Db      |||||
Qy 580 CACCAATTTGCTGGCGGAAGGCGAGGAGCTAACTGGAGCGGTGACGAGCAACTGTCTGG 639
Db      |||||
Qy 619 CAACAAAACTGAGTAGTGATGCTATATACCCAAAGTAACTATGATGCCACCGGGCT 678
Db      |||||
Qy 640 CAGGGAATGCTGGCAAGTGAGTCTATACGACACAAAAGTACCACTAATGGCCATCGGGCT 699
Db      |||||
Qy 679 TTACTGACCCAGACCGATGCCAAGGCAACATTACAGCGGCTGGCTATGATGTGCGCGGG 738
Db      |||||
Qy 700 TTACTGACCCAAACCGATGCCAAGGCAATATTACAGCTCTGGCTTATGACATTTGCCGCT 759
Db      |||||
Qy 739 CAGCTAAAGGGAGTGTGTTAACTACTCAAGGTTCAGGCGGAACAGGAGTATATCAAAATCG 798
Db      |||||
Qy 760 CAGTTAAAGGGAGTGTGTTGACCGGTGAAGGCCAGAGTGAACAGGTGATTTGTTAAGTCC 819
Db      |||||
Qy 799 CTAACTACTCCGCGCGCGGCAAAAATTACGTGAAGAGCAAGTAAACCGGATTTGTACT 858
Db      |||||
Qy 820 CTGAGCTGGTCAGCGCGAGGTCTATAAATTTGGTGAAGAGCACGGTAAACCGGCTGTTACG 879
Db      |||||
Qy 859 GAATACAGCTACGAACCGGAACCAACCGCTTATCGGCATTTACCACTCGCC-----910
Db      |||||
Qy 880 GAGTACAGTTATGAGCGGGAACCAACGCTCTGATAGGTATCACCAACCGCGGTGCCGAA 939
Db      |||||
Qy 911 ----GTCCATCAGACGCCAAGGTGTGCAAGACCTTACGCTATCAATATGACCCAGTAGGC 966
Db      |||||
Qy 940 GGGAGTCAATCAGGAGCCAGAGTATTGACGATCTACGCTATAGTATGATCCGGTGGG 999
Db      |||||
```

RESULT 10
US-10-609-113-44
; Sequence 44, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2002-06-28, 633
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 3132
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-44

Query Match 35.0%; Score 962; DB 7; Length 3132;
Best Local Similarity 72.2%; Pred. No. 1.8e-239; Mismatches 470; Indels 39; Gaps 4;
Matches 1323; Conservative 0;

QY	205	CCAAATTCATTCGTGCTTTAATCTTGCCTGCAAGATTTTACGTGAAAGAAAGTGTGAT	264
DB	220	CTTAATTTGCTGGCAGCATGATCTGCCGGTCATGCCCTCGGACAGAGTGTGAT	279
QY	265	GCCGGTGGCAATTAACCTCAATGATATTGAAGTGCCTGCTGATCATCAATGCA	324
DB	280	GCTGCTGCTACTGTCATTTGAATGATATTGAAGTGTGCTGCTGATGAATGCAATGCG	339
QY	325	ACCGGTGTCGCCAAACCATCTGATGAAGATAACACCTTCCCGTGTCTGCTCGCT	384
DB	340	ACCGGTGTTGCTCAGACCCGCTGCTATGAAGCAACACCTTGCCTGCTGCTGCTGCT	399
QY	385	ATCACCGCAACAGT-----ACAGGAGGAGAGAGAAACGACCAAGTCTTTATCTGGGC	438
DB	400	GTGAGCGGCAAGTTTCAACCAAGAGAGTGCTAAAGTGACAGCGCTTTATCTGGCT	459
QY	439	GGCAATAACCGCGCAAGAAAGATTACAACTCCCGGTCAGTGTGTCGCCCAATTACGAT	498
DB	460	GGGAATACAACTCCGGAGAAAGATATAACCTCTCCGGTCTGTGTATACGCCACTACGAC	519
QY	499	ACCGCGGACTTACTCAACTCAATAGCTTTCTCTGCTGGCTGCTGCTATCAATCT	558
DB	520	ACAGCGGGAGTGACCGGGTGTGATGAGTCAGTCACTGCGCGGCCCATGCTATCCCAATCT	579
QY	559	CAACAACCTGCTTACCGATACCAAGATGCGCATGAGACAGGTGAAGACAGAGCCTCTGG	618
DB	580	CACCAATTGCTGCGGAGGCGGAGGAGGTAACTGAGCGGTGACACGAACTGTCTGG	639
QY	619	CAACAAAACTGATGATGATGCTATATACCCAAAGTAAACACTGATGCCACCGGGCT	678
DB	640	CAGGGAATGCTGCAAGTGAAGTCTATACGACAAAGTACCACCTAATGCCATCGGGCT	699
QY	679	TTACTGACCCAGACCGATGCCAAAGCAATTCAGCGGCTGCTGCTATGATGTCGGCGG	738
DB	700	TTACTGACCCAAACCGATGCCAAAGCAATTTTACGCGTCTGCTGCTATGACATTCGGCT	759
QY	739	CAGTAAAGGGAGTGTGTTAACTCAACTCAAGGTGAGCGGAAACAGGTGATTATCAATCG	798
DB	760	CAGTAAAGGGAGTGTGTTGAGCGGTGAAAGGCGAGAGTGAACAGGTGATTGTTAAGTCC	819
QY	799	CTAACCTTACTCCCGCGCGGCAAAATTAACGTGAAGAGCACCGGTAAACGGGATGTCACT	858

DB	820	CTGAGCTGTGTCAGCCGCGAGGTCAATAAATTGCGTGAAGAGACGGTAACGGCGTGTGTTACG	879
QY	859	GAATACAGCTACGAACCGGAAACCCAAACGGCTTTATCGGCATTACCACTTCGCC-----	910
DB	880	GAGTACAGTTATGAGCGCGGAAACTCAACGCTCTGATAGGTATACCAACCGCGCTGCCGAA	939
QY	911	----GTCCATCAGACGCCCAAGGTGTGCAAGACCTTACGCTATCAATATGACCCAGTAGGC	966
DB	940	GGAGTCAATCAGGAGCCAGAGTATTGCAAGGATCTACGCTATAAGTATGATCCGGTGGG	999
QY	967	AATGTCAATTAATATCCGTATGATCGGAAGCCACTTCGCTTTTGGCGCAATCAGAAGTA	1026
DB	1000	AATGTTATCAGTATCCATATGATCGGAAGCTACCCGCTTTTGGCGTATCAGAAGTG	1059
QY	1027	GCCCCGAGATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCACCGGCGC	1086
DB	1060	GAGCGGAGATCGCTATGTTATGATCTCTGTATCAGCTTATGATGCGACAGGCGT	1119
QY	1087	GAATGGCCAAATATCGGTGAGCAAAACAAACCACTTCCTCCCTG-----CGTACCT	1140
DB	1120	GAATGGCTAATATCGGTGAGCAAAACCAACCTTCCTCCCTACCCCTTATACCTGTCT	1179
QY	1141	TCTGACAAACATACCTACACTAATATCTCCGAGCTACAGCTATGATCAGCTGTGTAAT	1200
DB	1180	ACTGACGACAGCACCTTATACCAATTAACCTTCGTACCTATATCTTATGACCGTGGCGTAAT	1239
QY	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGAAACATACACCGTGGCTATCAC	1260
DB	1240	TGGTTCAATATCGACACAGTTCACCCGGAGCTCAAAATAGTTTACACACAGATATCAC	1299
QY	1261	CTCTAAACCGCAGCAATCGGGTGTTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320
DB	1300	GTTCACGCGCAGTAACCGGGCGGTATTGAGTGACATTAACGACAGATCCAAACCGAGTG	1359
QY	1321	GATACGTTTGTGTCGCTGTCACCAACCGAGTTTATACCCCGACAGACATATATC	1380
DB	1360	GATGCGCTATTGATTCGCGCGGTATCAGAAGATGTTAATACCGGGGCAAAATCTGGAT	1419
QY	1381	TGACACCAACGAGGAGAGTTAAAGCAGGT-----TAATATGCGCCGGGA	1425
DB	1420	TGGATATTCGGGGTGAATTGCAACGAGTCAACCGGTGACCGTGAATAATAGCAGTGAC	1479
QY	1426	AATGAGTGTGTCGCTACGACAGCAACGGCATGAGACAACTGAAAGTGTGAGTGAACGCCA	1485
DB	1480	AGTGAATGTTATGCTATAGCAGTGATGCTGCGCTGCTAAAGTGTGAGTGAACGACAG	1539
QY	1486	ACCGAATATCTACGACAGCAACCGGTTATCTATTGCGCGGACTGAGCTACGACACA	1545
DB	1540	ACGGGCAACAGTACTCAAGTACAAACCGGTGACTTATCTGCGGGATTAGAGCTACGGACA	1599
QY	1546	ACCGAGCAACCGCACAAACGGAAGAGTTACAGTTATACACTTCGTTGAAGCGGT	1605
DB	1600	ACTGGGGTTCAGATTAACAAACCGGAAGATTTCAGGTGATTTACGGTAGGTGAAGCGGT	1659
QY	1606	CGCGCACAGTACGGGTGTGCACTGGGAGAGCGGTAAAGCCAGAGATGTCAACAATAAT	1665
DB	1660	CGCGCACAGTAAAGGTATTGCACTGGGAAAGTGTGTAAGCCGACAGATATTGACACAAT	1719
QY	1666	CAACTAGCTTACGCTACGATTAATCTGATCGGCTCCAGCAGCTTGAACCTGGCAACCAA	1725
DB	1720	CAGGTGCGCTACAGCTACGATTAATCTGCTTGGCTCCAGCCAGCTTGAACCTGGTAGCGAA	1779
QY	1726	GGACAATTTATCAGCGGAGAGATTAATCCATTTTGGGGGACAGCGCTGCGGACGA	1785
DB	1780	GGCAGATTCTCAGTCAGGAAGAGTATTATCCGTAAGCGGTACGGCGATATGGCGGCG	1839
QY	1786	AACAGCCAAACAGAACCCAGCTATAAAACGATTCGCTATTTCGGCAAAAGAACGAGATGCC	1845
DB	1840	AGNAATCAGACAGAACCCAGCTACAAATTTATTCGTTACTCCGGTAAAGACCGGATGCC	1899
QY	1846	ACCGGTTGTATTTATCGGTTATCGTTATACCAACCGTGGCGGCGAGATGCTTAAAGC	1905
DB	1900	ACTGGATTGTATTTATACGCTACCGCTATTATCAACCTTGGGTGGGTGCTGATGCTT	1959

QY 1666 CAACACTAGTTACAGCTACGATATCTGATCGGCTCCAGCGAGCTTGAACTGGACAAACCAA 1725
|||
Db 1720 CAGGTGGCTACAGCTACGATATCTGCTGGCTCCAGCGAGCTTGAACTGGATAGCGAA 1779
|||
QY 1726 GGCACAAATATCAGCGAGGAGGATATATCCATTTTGGCGGACAGCGCTGTGGCGAGCA 1785
|||
Db 1780 GGGCAGATTTCTAGTCAGGAGAGATATATCCGATATGGCGGTACGGCGATATGGCGGGC 1839
|||
QY 1786 AACAGGCAACAGAGCCAGCTATATAAAACGATTCGCTATTTCCGGCAAGAAACGAGATGCC 1845
|||
Db 1840 AGAATCAGACAGAGCCAGCTACAAATTTATTCGTTACTCCGGTAAAGCGGGATGCC 1899
|||
QY 1846 ACCGGTGTGATTTATTCGGTTATCGTTATATACAAACCGTGGCGGCGAGATGTTAAGC 1905
|||
Db 1900 ACTGGATTTGATTTATTCAGCTACCGTTATATCAACCTTGGGTGGTCCGATGGTTGAGT 1959
|||
QY 1906 GCGGACCGCGCAGGACCACTTGATGGCTGAATCTATACCGATGCTAAGAAATATACCT 1965
|||
Db 1960 GCTGATCCCGCGGGAACCGGTGGATGGCTGAATTTGTACCGAATGGTGAAGAAATACCCC 2019
|||
QY 1966 GTGAGTTTACAGATGAAATGATGATTAGCGCC 1997
|||
Db 2020 ATCAGATTGACTGACCATGACGATTTAGCACC 2051
|||

RESULT 12

US-10-706-424-13
; Sequence 13, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: ffrrench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 52878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2847)
US-10-706-424-13

Query Match 34.9%; Score 957.2; DB 7; Length 2850;
Best Local Similarity 68.6%; Pred. No. 3.1e-238;
Matches 1398; Conservative 0; Mismatches 598; Indels 42; Gaps 4;

QY 21 AATTGACCAAAACCCCTCGATTAAAGGTATTAGATTAACAGAAATTAATGATAGTAC 80
|||
Db 21 ACTTTATCAACATACGCCCAACCGTTAAAGTCTACGATAACCGTGGCTGACCAATTCGTAA 80
|||
QY 81 TTTAGAAATATCTAGCACTCAAGCTCAGCAAAAACAGTGATGAATTAATACGTTCTATGA 140
|||
Db 81 CATCGACTTTCACCGTGAGCTCGCGGAGCGGATACAGATATCTCGTTATTACCCGCCACCA 140
|||
QY 141 GTTCAATATTCGGGATTTTCAGTAAAGCAACCGATCTCTCGTA-----A 185
|||
Db 141 ATATGATACCCGAGGACATTTGAGCCAAAGCAATTGATCCACGGCTGTATGACGCCAAACA 200
|||
QY 186 AAATAAAACAGAGCGGCCAAATTTTCATTCGTGTCTTTAAATCTTGGCGGTCAAGTTT 245
|||
Db 201 AACCAATAACTCGACAAACCCCAACTCTCTCGGCAATACAAATCTCACCGGCGACACTTT 260
|||
QY 246 ACCTGAAGAAAGTTGATCCCGGTGGACTATTTACCTCAATGATATTGAAAGTCGCC 305
|||
Db 261 GCGGACAGAAAGTTGATGATCCCGGCGGTACCGTAGCCCTCAATGATTTGAAGCGGTCA 320
|||
QY 306 GGTGTTGATCATCAATGCAACCGGTGTCCGCCAAACCATCGTTATGAAGATAACACCT 365
|||

Db 321 AGTGTGATTGTAAACCGCAACCGGGCCATTAGACCCGACAAATATGAAGCCAATACCT 380
|||
QY 366 TCCCGTCTCTCTCGCTATCACCGAAACAAGTACAGGCGAGGAGAAAC-----GAC 419
|||
Db 381 GCCCGTCTCTATTATTCGTAAGTGAACAAGCCCGGAGAACAGACTCCCGCGGTAC 440
|||
QY 420 CGAAGCTCTTATCTGGCGCGGCAATACGCCGCAAGAAAGATTTACAACTCCCGCGGTCA 479
|||
Db 441 TGAGCATTTTATTTGGGCTGGTAAATACAGGCGGAGAAAGATCATTAATCTTTGCGCGCCA 500
|||
QY 480 GTGTGTCGCCCAATAGATACCGGGGACTTACTCAACTCAATAGACTTTCTCTGCTGG 539
|||
Db 501 GTATGTCGCCCACTACGACACAGAGGAGTACGCAACTGGAAAGCCTGTCTATTGACAGA 560
|||
QY 540 CGTCTGCTATCACAACTCTCAACCTGCTTACCAGATAACCCAGGATGCCGACTGGACAGG 599
|||
Db 561 AAACATCTTATCTCAATCCCGTCAGTTATTAGCCGACGGTCAGGAAGCAGACTGGACAGG 620
|||
QY 600 TGAAGACAGAGCCTCTGGCAACAAAACTAGTAGTAGTGTCTATATCACCCCAAAGTAA 659
|||
Db 621 TAAAGATGAACCTCTGCGCAGACCAAACTCAATAGCGAAACTTACACGACACAAAGCAC 680
|||
QY 660 CACTGATGCCAGCGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTTACAGCGCT 719
|||
Db 681 CTTTGATGCTACCGCGCTTTGCTGACCCAAACCGATGCAAAAGGCAACATGCAACGTCT 740
|||
QY 720 GGCCTATGATGCGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAGGTGAGCGGA 779
|||
Db 741 GGTTCACACGTGGCGAGCAATTAACAGTAGTGGCTGACATTTGAAAACCAAGTGA 800
|||
QY 780 ACAGGTGATTATCAATCGCTAACTCTCCCGCGCGGCAAAAATTAAGTGAAGAGCA 839
|||
Db 801 GCAAGTCAATTGCAATCCCTGACCTATTCCGCGCAGCGCCAGAAATTCGCGTGAAGAACA 860
|||
QY 840 CGGTAAAGGATGTCACCTAGATACAGTACGAAACCGGAACCCACGCGCTTATCGCAT 899
|||
Db 861 CGGTAAAGGCTTATCACTGAATACAGCTATGAACCGGAACCTCTACGATTGATCGGTAC 920
|||
QY 900 TACCCTCGCGCTCCATCAGAGCCAAAGGTGTTGCAAGACCTACGCTATCAATATGACCC 959
|||
Db 921 CACTACTCGCGCTCAATCAGATAGCAGAGGTGTTACAGATCTACGCTATGACATGATCC 980
|||
QY 960 AGTAGCAATGTCAATTAATATCCGTAATGATCGGAAGCCACTCGTTTTGGCGCAATCA 1019
|||
Db 981 TGTAGGGAATATTATTAGTGTCCGTAATGATGCAAGAGCCACCGCTTCTGGCGCAATCA 1040
|||
QY 1020 GAAAGTAGCCCGGAGATAGCTATACCTACGATTCCTGTTATCAGCTTATCAGCGCCAC 1079
|||
Db 1041 GAAATATAGTCCCTGAAAATACCTACACCTACGATTCCCTGTATCAGCTTATCAGTCAAC 1100
|||
QY 1080 CGGGCGGAAATGGCCCAATATCGTTCAGCAAAACCAACTTCCCTCCCTCC-----TGC 1133
|||
Db 1101 AGACGTGAGATGGCTTAACATCGGCAGCAAGCAACCAACTTCTTCGCAATCATCC 1160
|||
QY 1134 GCTACCTCTGACCAACATACCTACATACTATCTCGCAGCTACAGCTATGATCAGAG 1193
|||
Db 1161 TCTTCCTACTGATGAAAACCTCATATACCAACTATCTCGCAGCTATAATTTACGATCGCG 1220
|||
QY 1194 TGTAAATCTGACGCAAAATTCGGCAGAGCTCGCGAGTACCCAGAACAACTACACCGTGGC 1253
|||
Db 1221 CGGCAATTTGGTTTCAATCCGGCACAGTTTCCCGCGCGCCCAAAATTAACCTACACCAAGA 1280
|||
QY 1254 TATCACCTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAA 1313
|||
Db 1281 TATCACCGTTTGAATCGCAGTAAACCGGCAAGTGTGAGTTGCTTAACCTCAGACCCAC 1340
|||
QY 1314 TCAAGTGGATAGCTGTTGTTGATCGCGGTGGTCAACAAACAGTTTATTTACCCGAGACAG 1373
|||
Db 1341 ACAGGTGGAGGCACTGTTTGTATGCGCGCGGACATCAACAAATTTGTTTACCGGGCAAGA 1400
|||
QY 1374 ACTTATCTCGACACCAAGAGGAGTTAAAGCAGGTTA-----ATAATGG 1418
|||

Db 1401 GCTGAGTTGGAATACACGAGGTGAATAAACAGGTAAACGCCAGTCACTCGCGAGCGC 1460
Qy 1419 CCCEGGAAATGAGTGGTACCGCTACGACAGCAACGGCATAGACAACCTGAAGTGA 1478
Db 1461 CAGCGATCGGGAATGGTATCGTTACCGCAACGACGGCATCGACGGTTAAAGTCA 1520
Qy 1479 ACAGCCAAACAGCAATCTACTGCGAGCAACACGGGTAACTCTATTGGCGGACTGGAGCT 1538
Db 1521 GCAACAGACTGGCAACAGCAGCAGCAGCAACGATGAACCTTCTCCGATCTGGAGCT 1580
Qy 1539 ACGCACAAACCCAGAGCAACGCCCAACCAACGGAAGAGTTACACGTTATCACACTCGGTGA 1598
Db 1581 ACGTACAAACAAATCGGACTACTACATCAGAAGACCTGATGCTATTACCGTGGGAGC 1640
Qy 1599 AGCGGTGGCGACAGTACGGGTGGTGGCTGAGTGGAGAGCGGTAAAGCCAGCAAGATGCAA 1658
Db 1641 AGCAGGCCACGCAACAGTGGGAGTTCTACACTGGGAAACTACGCCACACCGCGGTATCAA 1700
Qy 1659 CAATAATCAACTAGTTACAGCTACGATAATCTGATCGGTCCAGCCAGCTTGAACCTGGA 1718
Db 1701 TAACAATCAGCTTCGCTATAGCTATGATTAATTTGATTTGGTTCAGTCAACTTGAACCTGGA 1760
Qy 1719 CAACCAAGGCAAAATATACGCGAGGAGAGTATTAATCCATTTGGCGGGACAGCGCTGTG 1778
Db 1761 TAAGCAGGACAAATATCAGTCAGGAAGAGTATTAATCCATTTGGCGGCACAGCATTA 1820
Qy 1779 GGCAGCAACAGCCAAACAGAGCCAGCTATAAACGATTCGCTATTCGGGCAAGAACG 1838
Db 1821 GGCAGCAAGAAACCAATAGAACGAGCTACAAATCCTCGTCTACTCAGGTAAAGAACG 1880
Qy 1839 AGATGCCACCGGTGTGATTAATTAACGTTATCGTTTATTAACCAACCGTGGCGGCGCAGATG 1898
Db 1881 CGATGCTACCGGCTCTATTATTAACGCTACCGCTATTAACGCTGGGTGGGTGGTGGT 1940
Qy 1899 GTTAAGCGCGGACCCGCGAGCAACATTTGATGGGCTGAATCTATACCGGAATGGTAAGAAA 1958
Db 1941 GTTAAGCGCGATCCGCTGGAACAACTGATGGACTGAATCTATACCGGATGGTGAAGAA 2000
Qy 1959 TAATCTGTGATTTACAGATGAATGAATGATTAAGCCGCGAGAAAGGGAATATACC 2016
Db 2001 TAATCCGCTCAACTGGTTGATATTTCTGGGCTTGACACTACGAAATACAAATATTTCC 2058

RESULT 13

US-10-609-113-47
; Sequence 47, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-47

Query Match 34.9%; Score 957.2; DB 7; Length 2850;
Best Local Similarity 68.6%; Pred. No. 3.1e-238;
Matches 1398; Conservative 0; Mismatches 598; Indels 42; Gaps 4;

Qy 21 AATTGACCAAGACCCCTCGATTAAAGTATTAGATAAACAGGAAATTAATGTAGCTAC 80
Db 21 ACTTTATCAACATACGCCACACCGTTAAACGTTACGATTAACCGTGGCTGACCAATTGTA 80
Qy 81 TTTAGAATATCTACGACCTCAAGCTGACGAAACACGTGATGAATTAATACGTTCTATGA 140
Db 81 CATCGACTTTACCGTGAGCTCGCGGAGCGGATACAGATCTCGTATTACCGGCCACCA 140
Qy 141 GTTCAATNTTCGGGATTTTCAGGTAAAGACCCGATCTCGTA-----A 185
Db 141 ATATGATACCCGAGGACACTTGGACCAAGCATTTGATCCACGGCTGTATGACGCCAAACA 200
Qy 186 AAATAAAACACAGCGCGCCAAATTTCAATTCGTGCTTTAAATCTTGGCCGCTCAAGTTTT 245
Db 201 AACCAATTACTCGAACAACCCCACTTCTCTGGCAATACAACTCTCACCGGCGACACTTT 260
Qy 246 ACGTGAAGAAAGTGTGATCGCGGTCCGACTATTACCCCTCAATGATATTGAAGTGCACC 305
Db 261 GCGGACAGAAAGTGTGATCGCGGTCCGACTCGGTAGCCCTCAATGATATTGAAGGCCGTC 320
Qy 306 GGTGTTGATCATCAATGCAACCGGTCTCGCCAAACCATCGTTATGATGAATTAACCCCT 365
Db 321 AGTGTGATTTGTAACCGCAACCGCGCCATTTCAGACCCGCAATATGAAGCCAATACCT 380
Qy 366 TCCCGTCTGCTCTCGCTATCACCGAAACAAGTACAGGAGGAGAGAAAC-----GAC 419
Db 381 GCCCGTCTCTATTATTCGTAAGTGAACAAGCCCCGGGAGACAGACTCCCGCGCTTAC 440
Qy 420 CGAACGCTCTTATCTGGCCCGCAATACGCGCAAGAAAGAAAGATTACAACTCCCGCGTCA 479
Db 441 TGAGCATTTTATTTGGCTGGTAAATACACAGGCGGAGAAAGATCATATACTTCCGCGCCA 500
Qy 480 GTGTGTCGGCATTAGCATACCGCGGACTTACTCAACTCAATAGCTTTCTCTGCGCTGG 539
Db 501 GTATGTGCGCACTACGACACAGCAGGAGTGACCAACTGGAAGGCTGTGATTGACAGA 560
Qy 540 CGTGTGTCTATCAACTCTCAACAACTGTTACCGATTAACGAGATGCCGACTGGACAGG 599
Db 561 AAACATCTTATCTCAATTCGGTCACTTATGACCGAGCTCAGGAAGCAGACTGGACAGG 620
Qy 600 TGAAGACCGAGAGCTCTGGCAACAAAGAACTGATGATGTCTATATATCAACCAAGTAA 659
Db 621 TAACGATGAACCCCTCTGGCAGACCAAACTCAATAGCGAAACTTACACGACACAAAGCAC 680
Qy 660 CACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGCT 719
Db 681 CTTTGTATGCTACCGGCGCTTTGCTGACCCAAACCGATGCAAAAGGCAACATGCAACGCT 740
Qy 720 GGCCTATGATGGCGGCGAGCTAAAGGGAGTGTGTTAACTCAACTCAAGGTGAGCGCGA 779
Db 741 GGCCTTACAGCTGGCAGGACAAATTACAGGTAGCTGGCTGACATTTGAAAACCAAGTGA 800
Qy 780 ACAGGTGATTATCAAACTCGCTAACCTACTCCGCGCGCGGCAAAAAATACGTGAAGACA 839
Db 801 GCAAGTCAATTTGTCAAATCCCTGACCTATTCCGCGCGGAGCCAGAAATTTGGGTGAAGAACA 860
Qy 840 CGGTAACGGGATTTGCTACTGAATACAGCTACGAAACCGGAAACCCACCGGCTTATCGCAT 899
Db 861 CGGTAATGGCGTTTATCACTGAATACAGCTATGAACCCGGAACCTCTACGATTTGATCGGTAC 920
Qy 900 TACCCTCGCGCTCCATCAGACCCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCC 959
Db 921 CACTACTCGCGCTCAATCAGATAGCAAGGTGTTACAAGATCTACGCTATGAAATGATGCC 980
Qy 960 AGTAGGCAATGTCAATTAATATCGTAAATGATCGGGAAGCCACTCGCTTTTGGGCGCAATCA 1019
Db 981 TGTAGGCAATATTATTAGTGTCCGTAATGATGAGAAGCCACCCGCTTCTGGGCGCAATCA 1040
Qy 1020 GAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCGCTGTATCAGCTTATCAGCGCAC 1079
Db 1041 GAAAAATAGTCCCTGAAAAATACCTACACCTACGATTCCTGATCAGCTTATAGTGAAC 1100
Qy 1080 CGGGCGGAAATGGCCAAATATCGGTACGCAAAAAACAACCACTTCCCTCCCTCCCTCC 1133

```
Db 1101 AGGACGTGAGATGGCTAAACATCGCCAGCAAGAAACCAACTTCCTTCGCAATATCC 1160
Qy 1134 GCTACCTCTTGACAAACAACTACCTAACTACTCGCAGCTACAGTATGATCACAG 1193
Db 1161 TCTTCTCTACTGTAACAACTCATATACCACTATCTCGCAGCTAATATACGATCGCG 1220
Qy 1194 TGTAAATCTGACGCAATTCGGCAGCTCGCCAGTACCGAGAAACAACTACACCGTGGC 1253
Db 1221 CGGCAATTTGGTTCAAAATCGGCACAGTTCCCGCGCCGCAAAATAAATCTACACCA 1280
Qy 1254 TATCACTCTCAAAACCGGAGCAATCGGGTGTCTCACTAGCTACCTAACCCGATCCAA 1313
Db 1281 TATCACCGTTTGAATCGCAGTAACCGGCGAGTGTGAGTTCGTAACTCAGACCCAA 1340
Qy 1314 TCAAGTGGATACCTGTTGATCCGCTGGTCAACAAACAGTTTATTAACCCGACAGAC 1373
Db 1341 ACAGTGGAGCACTGTTGATCGCGCGGACATCAACAAATTTGTACCGGGCAAGA 1400
Qy 1374 ACTTATCTGGACACCGAGGAGTTAAAGCAGTTA-----ATAATGG 1418
Db 1401 GCTGAGTTGGAATACACGAGGTGAACCTAAACAGGTAAACGCCAGTCAGTCGAGAGCG 1460
Qy 1419 CCGGGAAATGAGTGTACCGCTACGACAGCAACGCGCATGAGCAACTGAAAGTGATGA 1478
Db 1461 CAGCGATCGGGAAATGTTATCGTTACCGCAACGACGCGCATGCGGTTAAAGTCAGTGA 1520
Qy 1479 ACAGCCAAACCCAGAACTACTACGAGCAACAAACGGGTAATCTATTTGCGGAGCTCGAGCT 1538
Db 1521 GCAACAGACTGGCAACGACGAGCAACGACGAACTTAATCTTCCCGATCTGAGCT 1580
Qy 1539 ACACCAACCCAGAGCAACCCCAACAAACGGAAGATTAACAGTTATCACTCGGTGA 1598
Db 1581 ACCTACAAACAAATGGGACTACTACATCAGAAGACCTGATGCTATTACCGTGGAGC 1640
Qy 1599 AGCGGTGCGGCAACAGTACGGTGTGCTGAGTGGAGCGGTAAAGCCAGAAATGTCAA 1658
Db 1641 AGCAGGCCACGCAACAGTGGAGTTCTACACTGGGAACTACGCCACCGCGGTATCAA 1700
Qy 1659 CAATAATCAACTAGTTTACAGCTACGATATCTGATCGGCTCCAGCCAGCTTCAACTGGA 1718
Db 1701 TAACAATCAGCTTCGCTATAGCTATGATAATTTGATTTGTTGCTCACTCACTGAGCTGGA 1760
Qy 1719 CAACCAAGGACAAATATACGAGGAGGAGTATTAATCAATTTGGGGGACAGCGCTGTG 1778
Db 1761 TAAGCAGGACAAATATCAGTCAGGAAGATTAATCCATTTTGGGGCACACGATTAAG 1820
Qy 1779 GGAGCAACAGCCAAACAGAACCCAGCTATAAAAGATTCGCTATTCGGGCAAGAACG 1838
Db 1821 GGCAGCAAGAAACCAATAAGCCAGCTACAAATCTCCGTTACTCAGTTAAAGAACG 1880
Qy 1839 AGATCCACCGGTTGTTATTAATACGTTATCGTTATTAACCAACCGTGGGCGGAGATG 1898
Db 1881 CGATGCTACCGGCTCTATTATTAACGCTACCGCTATTAACGCTGTTGTTGAGGTG 1940
Qy 1899 GTTAAGCGCGGACCGGCGAGAACCAATTAATGAGCTGAATCTATACCGAATGTTAAGAA 1958
Db 1941 GTTAAGCGCGGATCCGCTGGAACATCGATGAGTGAATCTATACCGGATGTTGAGAA 2000
Qy 1959 TAATCTGTGAGTTTCAAGATGAATAATGAGTATAGCCGCAAGAAAGGGAAATATACC 2016
Db 2001 TAATCCGTCAACACTGTTGATATTTCTGGGCTTGCACTACGAAATAACAATATTCCTCC 2058
```

RESULT 14

```
US-10-754-115-50
; Sequence 50, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
```

```
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XCI
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Xenorhabdus bovienii
; US-10-754-115-50
```

```
Query Match 26.6%; Score 730.8; DB 8; Length 2889;
Best Local Similarity 63.9%; Pred. No. 3.5e-179;
Matches 1170; Conservative 0; Mismatches 632; Indels 30; Gaps 3;
```

```
Qy 235 GGTCAAGTTTTACGTGAAGAAAGTGTGATGCGGTCGGAGTATTACCTCAATGATATT 294
Db 247 GGTGATGTCTACGGAACAGAGTGTGGATGCGGCAAACTGTCTATTTTGTAGTGACATC 306
Qy 295 GAAAGTCGCGCGGTGTGATCATCAATGCAACCGGTGTCGCCAAACCATCGTTATGAA 354
Db 307 GAAGGTGCGCGGTACTGAATATCAGTGGATGGGTGTCGTAACACATCGGCAATATGAA 366
Qy 355 GATAACACCTTCCCGTGTCTGCTCATCACCGAAC-----AAGTACAGGACGGA 408
Db 367 GAGAGTACATTGCGGGGCGCTTGTCTGCTGTCAGTGAACGGAAGATGAGGCTTCAACA 426
Qy 409 GAGAAACGACCGAAGCTTTATCTGGGCGGCAATACGCGGCAAGAAAGATTTACAAC 468
Db 427 CCCAAATATTGAACGGTTTATTTGTCGGGAAATAGCCCATCAGAAAAAGATCAAAAT 486
Qy 469 CTCCGCGTCACTGTCTCGCCATACGATACCGCGGAGTACTCAACTCAATAGCCTT 528
Db 487 TTGGCGGAAATATCTTCTGCTATGATATACCGCGGATTAACCCAGCTTAATGCTGTG 546
Qy 529 TCTCTGCGTGGCGTCCGTGCTATCACAACTCTCAACAACTGCTTACCGATACAGGATGCC 588
Db 547 TCTCTGACGAGCTGATCTCTCAATCCCGTCACTTATTCAGGATGATGTCACAGCA 606
Qy 589 GACTGCAAGGTGAAGACAGAGCCCTCTGGCAACAAAACTGATGATGATGCTATATC 648
Db 607 GATTGAGCGGAAGTGAAGTCCAGTCCAGTGAAGACGCACTGAGTAACGACATATTCACA 666
Qy 649 ACCCAAGTAACTGATGACCGCGGCTTTACTGACCGACCGGATGCGCAAGCAAC 708
Db 667 ACCGAAATCAACCGCTGATCGGTGGCAATTTCTGACTCAGAAATGATGCGCAAAAGCAAC 726
Qy 709 ATTACGCGTGGCGCTATGATGCGCGGACAGTAAAGGGAGTGGTTTAACTCAAA 768
Db 727 CAGCAACGATTGCTTATGATGCGGAGGCACTTAAAGCAAGCTGGCTGACGATAAA 786
Qy 769 GGTGAGCGGAAACAGGTGATTAATCAAACTCGTAACTCTCCCGCGCGGCAAAATTA 828
Db 787 GGCCAGAAATGAGCAGGTGATGTTAACTCCCTGACTTACTCCCGCGGCGGCAAACTG 846
Qy 829 CGTGAAGACGCGTAAACGGGATGTCACCTGAATACAGTACGAAACCGGAAACCAACGG 888
Db 847 CGTGAAGAGCAGGTTAAACCGCGTGTCTGCTGAAATCTCTTATGAAGCAAACTCGCGT 906
Qy 889 CTTATCGGCATTACCACTCGCGCTCATCAGACCGCAAGGTGTTGCAAGACCTCAACGCTAT 948
Db 907 TTGATAGGTGTAACGGCTTACCCTGCTCAGTACAGTAAAAAAGATTTGCAAGATCTTGTCTAT 966
```



```
QY 769 GGTGAGCGGAACAGGTGATTATCAATCGCTACCTACTCCGCGCCGGGCAAAATTA 828
Db 787 GGCAGAAATCAGCAGGTGATAGTAACTCCCTGACTTACTCCGCGCGGCGAGAACTG 846
QY 829 CGTGAAGAGCAGCGTAAACGGGATTTGTCACTGAATACAGCTACGAAACCGGAAACCCCAACGG 888
Db 847 CGTGAAGAGCAGGTAAACGGGTTGTCACTGAATACAGCTACGAAACCGGAAACCCCAACGG 906
QY 889 CTTATCGGCATTTACCACTCCGCGTCCATCAGAGCCCAAGGTGTTGAAAGACCTACGCTAT 948
Db 907 TTGATAGGTGTAACGGCTTACCCTGACGTACAGATAAAAAAGATTGCAGGATCTTGTCTAT 966
QY 949 CAATATGACCCAGGTAGGCAATGTCATTAATATCCGTAATGATCGGAGGCACTCCGCTTT 1008
Db 967 AACTATGATCCGGTCGGTAATCTCCGTAATGTCGCAATTAATGAGAGGCAACCCCGTTTC 1026
QY 1009 TGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATACCTTCCCTGTATCAGCTT 1068
Db 1027 TGGCGTAATCAGATAGTAGAACACAGAGAACCACTATGCTTATGACTGCTTATCAACTC 1086
QY 1069 ATCAGCGCCACCGGGCGGAAATGGCCAAATATCGGTGAGCAAAACCAAACTTCCCTCC 1128
Db 1087 ATCAGTGTCTAGTGTGAGAAATCGCCAGTATCGGTGAGCAGGCGAGCGGCTGCCTGTA 1146
QY 1129 CC-----TGGGCTACCTTCTGACAACAATACCTACACTAATCTACTGACAGCTACAGC 1182
Db 1147 CGGATTATTCCTCTCTGCGCAATGAGATGTTTATATCTGCTACACCCGACATATCAC 1206
QY 1183 TATGATCACAGTGTGTAATCTGACGCAAAATTCGCGACAGCTCGCCAGCTACCCAGAAACAAC 1242
Db 1207 TATGATCGCGGTGGAATCTCTGCCAGATCCGGATTCGGGATTCGCTCTGCTACAGATATTAAG 1266
QY 1243 TACACCGTGGCTATCACCTCTCTCAAAACCGCAGCAATCGGGGTGTCTCAGTACGCTAAAC 1302
Db 1267 TACACCAAAAGATCACCGTATCGAATCGTAGTAAATCGTGCAGTATGGGATACCTTGAAC 1326
QY 1303 ACCGATCCAAATCAAGTGGATAGTGTGTTGATCGCGGTGGTCAACCAACAGTTTATTA 1362
Db 1327 ACAGATCCCGCAAGTGGATACCTGTTTGTATCATGGAGGGCATCAACTTCAACTCCAG 1386
QY 1363 CCGGACAGACACTTATCTCGACACACAGGAGAGTTAAAGCAGGTTA----- 1411
Db 1387 TCAGGCCAGACTTATGTTGGAACTATCGGGGTGAACTACAGCAATTAACAAAGATACAG 1446
QY 1412 -----ATAATGCGCGGGAATAGTGTGTACCGCTACGACAGCAACGGCATGAGACAA 1464
Db 1447 CGTGACGAAAACCCGCGAGATAAAGAGCGGTATCGCTATGCTGTGGGGCTGCGCGGTC 1506
QY 1465 CTGAAAGTGAAGTGAACAGCCCACTACAGATATCTACGAGCAACAAACGGGTAATCTATTG 1524
Db 1507 GTGAAAATCAGCACACAGCAGCGGGGGGAAAGCAGCCATGTGCAGCGGTGTTGTTATCTG 1566
QY 1525 CCGGACTGGAGCTACGCAACCCAGAGCAACGCGACACACGGAAGGTTACAGTT 1584
Db 1567 CCGGGTTGGAACCTACGCAACCTACGATGTGCGACATTAATCGAAGACTTACAGGTG 1626
QY 1585 ATCACACTCGGTGAAGCGGTGCGCACAGGTACGGGTGTTGCACTGGGAGAGCGGTAAAG 1644
Db 1627 ATTATCATGGGTGAGCAGACGCTGCTCAGTACGCGTACTTCAATGGGAAATACCACCA 1686
QY 1645 CCAAGAGATGTCACAAATAATCAACTACGTTACAGTTACGATATCTGATCGGCTCCAGC 1704
Db 1687 CCGGATAATCTTAACAATGACTCACTGCGTTACAGCTACGATAGTTGATGGGTTCAGT 1746
QY 1705 CAGCTTGAATGGACACCAAGGACAAATTTATCAGCGAGGAAGAGTATTTCCATTGGC 1764
Db 1747 CAGCTTGAATTTGATGGAGCAGGCGAGATTATTAACGAGGAAGAACTACCCCTATGGA 1806
QY 1765 GGGACAGCGCTGTGGGCGAGCAAAACAGCAAAAGAGGAGCTATAAAACGATTTCGCTAT 1824
Db 1807 GGTACAGCAATATGGGCGGCAAGAAACAGACCCGAGCCAAATTAACAAACCATTCGCTAC 1866
QY 1825 TCCGGCAAGAACAGAGATGCCACCGGGTGTGTTATTAATTAACGTTTATCGTTATTACCAACCG 1884
```

```
Db 1867 TCGGCAAAAGAGCGTGTATGCGACGGGGCTTTATTACTACGGGACCGTTATTATCAGCCG 1926
QY 1885 TGGCGCGGCGAGATGGTTAAAGCGCGGACCCGGCAGGAACCAATTGATGGGCTGAATCTATAC 1944
Db 1927 TGGCTAGGGCGCTGGTTGAGCGCAGATCCGCGCGAAACCGTGGACGGAATCTATAT 1986
QY 1945 CGAATGTTAAGAAATAATCTCTGTGAGTTTACAAGATGAAAATGGATTAGCGCCAGAAAAA 2004
Db 1987 CGAATGTTGAGGAATAAACCCGATTACTTACCGGGATGSCAGATGGGCTTGGCCCGATAGGC 2046
QY 2005 GGGAAATATACCAAGAGGTAAATTTCTTTGA 2036
Db 2047 GATAAGATCAGCGAAGGATTTATAGCCTGA 2078
```

Search completed: December 14, 2005, 06:35:20
Job time : 1965 secs

This Page Blank (2000)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:24:31 ; Search time 497 Seconds
(without alignments)
9817.720 Million cell updates/sec

Title: US-10-647-956A-5
Perfect score: 2745
Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggagaacttca 2745

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NH.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCRU COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2745	100.0	2745	3	US-09-817-514A-5
2	1012.4	36.9	37948	3	US-09-251-645-11
3	962	35.0	3132	3	US-08-851-567B-60
4	56.2	2.0	1039	3	US-09-302-540-1280
5	56	2.0	7218	2	US-08-232-463-14
6	47.4	1.7	147382	3	US-09-949-016-14624
7	46.6	1.7	612	3	US-09-302-540-1357
8	45.6	1.7	314798	3	US-09-949-016-13539
9	45.2	1.6	582	3	US-08-949-016-61868
10	45	1.6	94987	3	US-09-949-016-12510
11	45	1.6	96987	3	US-09-949-016-14429
12	44.2	1.6	1141	3	US-09-806-708B-22
13	44.2	1.6	4005	3	US-08-956-171B-631
14	44.2	1.6	4005	3	US-08-781-986A-631
15	44	1.6	19124	2	US-08-487-826B-13
16	43.4	1.6	640681	3	US-09-790-988-1
17	43.2	1.6	3945	3	US-09-200-650B-6
18	42.6	1.6	1827	3	US-09-270-767-1308
19	42.6	1.6	1827	3	US-09-270-767-16590
20	42.4	1.5	168575	3	US-09-426-290-1
21	42.2	1.5	1676	3	US-09-009-443-1
22	41.6	1.5	601	3	US-09-949-016-37135
23	41.6	1.5	601	3	US-09-949-016-161112
24	41.6	1.5	1350	3	US-09-248-796A-4759

ALIGNMENTS

RESULT 1
US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: firench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

Query Match	100.0%	Score 2745;	DB 3;	Length 2745;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Mismatches	2745;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60		
Db	1	ATGAGCAGTTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60		
QY	61	AGGAAATTAATAGTACGTAATCTTAGAATATCTACGCACTCAAGCTGACGAAACACGTGAT	120		
Db	61	AGGAAATTAATAGTACGTAATCTTAGAATATCTACGCACTCAAGCTGACGAAACACGTGAT	120		
QY	121	GAATTAATACGTTCTATGATGTCATATATCCGGGATTTTCAGGTAAAGACCGATCCT	180		
Db	121	GAATTAATACGTTCTATGATGTCATATATCCGGGATTTTCAGGTAAAGACCGATCCT	180		
QY	181	CGTAAATTAATTAACACGAGCGGCCCAAAATTTTCATTCGTGTCCTTTAATCTTTCGGGTCAA	240		
Db	181	CGTAAATTAATTAACACGAGCGGCCCAAAATTTTCATTCGTGTCCTTTAATCTTTCGGGTCAA	240		
QY	241	GTTTTACGTGAAGAAAGTGTGATGCCGGTCGGACTATTACCTCAATGATATTGAAAGT	300		

Qy	2461	AAGGTTTATCATGATTTAAAAAATAAACATCAGAAATTAATGTCACCACTATGANTGGCC	2520
Db	2461	AAGGTTTATCATGATTTAAAAAATAAACATCAGAAATTAATGTCACCACTATGANTGGCC	2520
Qy	2521	CATCCCTATACGCCAATTGAGTAAATGAAGAAGAGCGCTGTTGCAAGAAAAACAGAAACCGCT	2580
Db	2521	CATCCCTATACGCCAATTGAGTAAATGAAGAAGAGCGCTGTTGCAAGAAAAACAGAAACCGCT	2580
Qy	2581	ATTGCAATAGATAGAGAAATAATTTCAAAGGTTTGGCAAAATCTCTGACAAATGAAAGCA	2640
Db	2581	ATTGCAATAGATAGAGAAATAATTTCAAAGGTTTGGCAAAATCTCTGACAAATGAAAGCA	2640
Qy	2641	ATTAAAAAATCATTTGAAGAGCACATAAAATTAATAGGATATCAACAGAGGCTATTAAATATT	2700
Db	2641	ATTAAAAAATCATTTGAAGAGCACATAAAATTAATAGGATATCAACAGAGGCTATTAAATATT	2700
Qy	2701	CGCTCTCGGCTATCGCTGAGAAATTTAGGAAATCGGAGAACTTCA	2745
Db	2701	CGCTCTCGGCTATCGCTGAGAAATTTAGGAAATCGGAGAACTTCA	2745

RESULT 2

```

US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 11
; LENGTH: 37948
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15171)..(18035)
; OTHER INFORMATION: orf5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23768)..(31336)
; OTHER INFORMATION: hph2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31393)..(35838)
; OTHER INFORMATION: orf2
; US-09-251-645-11

```

Query Match 36.9%; Score 1012.4; DB 3; Length 37948;
Best Local Similarity 69.5%; Pred. No. 3.5e-287;
Matches 1414: Conservative 0; Mismatches 596; Indels 24;

Qy	1	ATGAGCAGTTACAATTTCTGCAATTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60
Db	15171	ATGAAAACATCGATCCTAAACTTTTACAAAAGACCCCTGTCGTCAACATCTTACGATTAAC	15230
Qy	61	AGGAATTAAATCTAGCTACTTTAGTAATATCTACGACTCAAGTTCAGCAAAACAGTGAT	120
Db	15231	CGAGGCTTACGATCCGTAACATCGACTTTTCAACCGTACCACCGCAAAACGGCGATACCGAT	15290
Qy	121	GAATTAATTACGTTCTATGAGTTTCAATATATCCGGGATTTTCAGGTAAAAAGACCCGATCCT	180

15291	ATCCGTTATTACTCGCCATCAATATGACTCTCCCTTGGCAGCCTTAAGCCAAAGACACCGATCCG	15350	
Qy	181	CGTAAAAATAAAAAACAGAGCGGCCAAAATTTCAATTCGTGTCTTTAAATCTTCCCGGTCAA	240
Db	15351	CGTCTATATGAAGCCAAAACAAAACTAACTTTCTCTGGCAGTAGATTTGACCGGTAAT	15410
Qy	241	GTTTTACGTGAAGAAAGTGTTCATGCGCGTGGAGCTATTACCCCTCAATGATATTGAAGT	300
Db	15411	ATTTTGTGTACGAAAGCGTGCATGCTGGTGCACGTGCACCTTGAATGATATTGAAGGC	15470
Qy	301	CGCCCGGTGTGATCATCAATCAACCAACCGGTGTCGCCAAAACCATCGTTTATGAAGATAAC	360
Db	15471	CGTCCGCTACTGACGTAAGTCTGCAACAGGTGTATACAAACCCGACAATATGAAACGTCT	15530
Qy	361	ACCTTTCCGGTCTGTCTGCTCATCACCGAACGAATAC---AGCGAGGAGAGAAAACG	417
Db	15531	TCCCTACCCGGTCTGTGTGTCTGTGTACCGAACAAATACCAAGAAAAACATCCCGTATC	15590
Qy	418	ACCGAAGCTTTATCTGGGCGCGCAATACGCCGCAAGAAAAAGATTACACCTCCCGGT	477
Db	15591	ACCGAAACGGCTGATTTTGGCTGGCAATAGCAAGCAGAGAAAAACCAATAATCTTCCAGC	15650
Qy	478	CAGTGTCTCGCCATTACCATACCGCGGACTTACTCAACTCAATAGCTTTCTCTGGCT	537
Db	15651	CAGTGGTGGCCACTATGACACGGCGGAGTCACCCGATTAGAGAGTTTGTACTGACC	15710
Qy	538	GGCGTCTGTATCAACAATCTCAAAACATCTTACCGATAACACGAGATGCCGACTGGACA	597
Db	15711	GGTACTGTTTTATCTCAATCCAGCCNACTATTGAGGCACCTCAAGAGCTAGCTGGACA	15770
Qy	598	GGTGAAGACAGAGCCTCTGGCAACAAAACTGAGTAGTGTCTATATACCCAAAGT	657
Db	15771	GGTGATAATGAACACCGCTCTGGCAAAACATGCTGGCTGATGACATCTACACAAACCTGAGC	15830
Qy	658	AACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGG	717
Db	15831	GCCTTTGATGCCACCGCGCTTTACTCACTCAGACCGATGCGAAAGGGAACAATTCAGAGG	15890
Qy	718	CTGGCTATGATGTGGCCCGGCGAGCTTAAAGGGAGTTGGTTAACTCAAAAGTTCAGCGG	777
Db	15891	CTAACCTATGATGTGGCCGGGCGAGCTTAACGGGAGCTGGTTAACCTTAAAGACCAACCG	15950
Qy	778	GAACAGGTGATTATCAAAATCGCTAACCTACTCGCGCGCGGGCAAAAAATTACGTGAAGAG	837
Db	15951	GAACAAAGTATTATCAGATCCCTGACCTATTCCGCGCGCGGACAAAAATTACGCGAGGA	16010
Qy	838	CAGGTTAAACGGATTTGTCTAGTACAGTACAGTACCGAACCGGAACCCACGGCTTATCCGC	897
Db	16011	CACGGCAATGGTGTATTACCCGAATACAGTTATGAACCGGAACCCACAGCTTATCCGT	16070
Qy	898	ATTACCACTCGCGTCCATCAGACGCCAAGTGTTCGAAGACCTACGCTATCAATATGAC	957
Db	16071	ACCAAAACCAACCGTCCGTAGATGCCAAAGTTGGCAAGATCTAGTTATGAGTATGAC	16130
Qy	958	CCAGTAGGCAATGTCAATTAATTCGGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAAT	1017
Db	16131	CCGCTAGGCAATGTCAATCAGTATCCGTAATGACGCAAGCCACCGCTTCTGGCACAAT	16190
Qy	1018	CAGAAAGTAGCCCCGAGAAATAGCTATACCTACGATTCCTCTGTACAGCTTATCAGCGCC	1077
Db	16191	CAGAAAGTGCGCGCGGAAAACATTATACCTACGACTCCTCTGTATCAGCTTATCAGCGCA	16250
Qy	1078	ACCGGCGCGAAATGCCAATATCGGTACAGCAAAAACAACTTCCTCCCTCCCTCGGCTTA	1137
Db	16251	ACCGGCGCGAGATGCGGAATATAGGTACGCAAAAGTAAACCACTTCCCTCCCTCACCTTA	16310
Qy	1138	CCTTCTGACAAACATACCTACACTAACTATCTACTCGCAGCTACAGCTATGATCACAGTGT	1197
Db	16311	CCTTCTGATAACAAACCTTACCAACTATACCGGTACTTATCTTATGACCGTGGCGGC	16370
Qy	1198	AATCTGACGCAAAATTCGGCACAGCTCCGACGTACCCAGAACCACTACACCGTGGCTATC	1257
Db	16371	AATTTGACTAAAAATCCAGCAAGCTTCAACGGGAGCGCAAAACAACTACCAACCAACATC	16430

```
Qy 1258 ACCTCTCAAAACCCGACCAATCGGGTCTTCTAGTACGTAACCAACCGATCCAAATCAA 1317
Db 16431 ACGGTTTCTAACCGGAGCAATCGCGAGTACTCTAGCACTCTGACCCGGAAGATCCGGCGCAA 16490
Qy 1318 GTGATACGTTGTTTGTATCGCGTGGTTCACCAACCAAGTTTATTACCGGACAGACACTT 1377
Db 16491 GTAGATGCTTTATTTGTATGAGCGGACNTCAGAACGTTGATATCAGACAAACCTG 16550
Qy 1378 ATCTGGAACACAGAGAGAGTTAAAGCAGGTTTAATATGGCCCGGAAA----- 1427
Db 16551 AACTGGAATACACGCGTGAACATACAATGTGACATTTGGTAAACGGGACAGGGCGCC 16610
Qy 1428 -----TGAGTGGTACCGTACGACAGCAACCGCATGAGACAACCTGAAAGTGA 1476
Db 16611 AATGATGATCGGGAATGGTATCGCTATAGTAGTGACGGGAGAGGATATTTAAATAATCAAT 16670
Qy 1477 GAACAGCAACCCAGAAATACTAGCAGCAACAACCGGTATCTATTTCCGCGGACTGGAG 1536
Db 16671 GAACAGCAGACCGACGAACCTCTCAACACAGAGAAATTAATTTGCCGAGTTAGAA 16730
Qy 1537 CTACGCAACACCCAGAGCAACCGCACCAACAAACGGAAGATTACAGTTTATCACACTCGGT 1596
Db 16731 CTTGCTCTAACACAAACAGCAGCATCACAAACCGAAGATTGCAAGTTATCACAGTAGGA 16790
Qy 1597 GAAGCCGTCGCGCACAGGTACGGGTGTTGCACTGGGAGAGCGTAAAGCCAGAGATGTC 1656
Db 16791 GAAGCCGTCGCGCACAGGTACGAGTATTACATTTGGGATAGCCGTCAACCGGAAGATATC 16850
Qy 1657 AACAAATCACTACGTACAGCTACGATATCTGATCGGCTCCAGCGAGCTTGAAGTCTG 1716
Db 16851 GACAAATCACTACGTATAGCTTATAGCTACGATTAATCTTATCGGTTCCAGTCACTTGAATTA 16910
Qy 1717 GACAACCAAGACAAAATTTATCAGCGAGGAAGAGTATTATCCATTTGGCGGACAGCGCTG 1776
Db 16911 GACACAAAGAGAGAAATTTATGTTAGTGAAGAGTACTATCCCTATGCGGCGACGCATTA 16970
Qy 1777 TGGCAGCAACACGCCAAACGAGCCAGCTATATAAGGATTCGCTATTCGGGCAAGAA 1836
Db 16971 TGGGCAACAAAGAAAGCGGACAGAACCCAGTTTATAAAACCATCCGTTATTCAGSTAAAGAG 17030
Qy 1837 CGAGATGCCACCGGTTGTATTATTACGTTTATCGTTTATACCAACCGTGGCGGCGGAGA 1896
Db 17031 CGGATGCCACCGGACTATATTATACGGTTACGATATATATGACCTTGGGTAGGACGA 17090
Qy 1897 TGGTTAAGCGCGGACCCGCGAGGAACCAATTGATCGGCTGAATCTATACCGAATCGTAAGA 1956
Db 17091 TGGTTAAGTCGGATCCGCGAGGAACAGTAGATGGTTGAATTTATATCGGATCGTAAGG 17150
Qy 1957 AATAATCCTGTGAGTTTACAAGATGAAAATGGATTAGCGCCAGAAAAGGGAAA 2010
Db 17151 AATAATCCGGTTACTCTGCTTGTATCTGATGGATTAATGCCAAACAAATTTGCAGAA 17204
```

RESULT 3

US-08-851-567B-60
; Sequence 60, Application US/08851567B
; Patent No. 6528484

GENERAL INFORMATION:

APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining

APPLICANT: Ciche, Todd A.
APPLICANT: Sukhapingda, Kitiieri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agrosciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seav, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-851-567B-60

Query Match 35.0%; Score 962; DB 3; Length 3132;
Best Local Similarity 72.2%; Pred. No. 5.8e-273;
Matches 1323; Conservative 0; Mismatches 470; Indels 39; Gaps 4;

```
Qy 205 CCAATTTTCATTCGTCTTTAATCTTCCGGTCAAGTTTTCGTGAGAAAGTGTGAT 264
Db 220 CCTAATTTTCTCTGGCAGCATGATCGCCGGTTCATGCCCTCGGACAGAGAGTGCAT 279
Qy 265 GCGGTCGGACTATTACCCCTCAATGATATTGAAAGTCGCCCGGTGTTGATCATCAATGCA 324
Db 280 GCTGGTCGTACTGTTGCATTTGAATGATATTGAAGTCTGTTCCGTAATGACAAATGATCG 339
Qy 325 ACCGGTGTCCGCAAAACCATCGTTATGAAGATAAACCCCTTCCCGGTGCTGCTCGCT 384
Db 340 ACCGGTGTCTCGTCAGACCCCGTCGCTATGAAGGCAACACCTTGGCCGCTCGCTTGTATCT 399
Qy 385 ATACCGAACAAGT-----ACAGGAGGAGAGAAACGACCGCTCTTATCTGGGCC 438
Db 400 GTGAGCGAGCAAGTTTTTCAACCAAGAGAGTGTCTAAAGTGACAGAGCCCTTATCTGGGCT 459
Qy 439 GGCAATACGCCGCAAGAAAGAAATTAACAACCTCGCCGGTCAGTGTGTGTCGCCCATTAACGAT 498
```

Db 460 GGGAAATACAACTCCGAGAAAGAGTATAACCTCTCCGGTCTGTGTATACGCCACTAGGAC 519
Qy 499 ACCCGGGAGTACTCAACTCAATAGCCTTTCTCTGGCTGGCGTCTGTCTATCACAACTCT 558
Db 520 ACAGCGGAGTACCCGGTTGATGAGTCACTGCGGGGCCATGCTATCCCAATCT 579
Qy 559 CAACAACCTGTTACCGATAACCAAGGATGCCAGTGGACAGGTGAAGACAGACCTCTGG 618
Db 580 CACCAATTTGTCGGAAGGCGAGGAGGCTAACTGGAGCGGTGACACGAAACTGTCTGG 639
Qy 619 CAACAAAACTGAGTGTAGTGTCTATATCACCAAAAGTAACTGATGCCACCGGGCT 678
Db 640 CAGGGAATGCTGCGAATGAGTGTCTATACGACAAAGTACCACTAATGCGCATCGGGCT 699
Qy 679 TTAAGTACCCAGACCGATGCAAGGCAAACTTACGCGGTGGCTTATGATGTGGCGGG 738
Db 700 TTAAGTACCCAGACCGATGCAAGGCAAACTTACGCGGTGGCTTATGATGTGGCGGT 759
Qy 739 CAGCTAAAGGAGTGTGTTAACTCACTCAAAAGTACGCGGGAACAGGTGATTCAATCG 798
Db 760 CAGTTAAAGGAGTGTGTTGAGCGGTGAAAGGCCAGAGTGAACAGGTGATTGTTAAGTCC 819
Qy 799 CTAACCTTACTCCCGCGCGGCAAAATTAACGTGAAGAGCACGTAACGCGATTGTCACT 858
Db 820 CTGAGCTGTGACCGGAGGTCAATAATTGCGTGAAGAGCACCGTAACGCGGTGGTTACG 879
Qy 859 GAATACAGCTACGAACCGGAAACCCAAACGGCTTATCGGCATTACCACTCGCC----- 910
Db 880 GAGTACAGTTATGAGCGGAACTCAACGTCGTAGGTATACCAACCGCGGTGCCGAA 939
Qy 911 -----GTCCATCAGACGCGAGGTGTGCAAGACTTACGCTATCAATATGACCCAGTAGGC 966
Db 940 GGGAGTCAATCAGGAGCCAGATATTGACAGATCTACGCTATAAGTATGATCGGTGGGG 999
Qy 967 AATGTCTAATTAATCCGTATGATCGGAGGCACTCGCTTTTGGCGCAATCAGAAAGTA 1026
Db 1000 AATGTTATCAGTATCCATATGATGCGAAGTACCGCGTTTGGCGTAAATCAGAAGTG 1059
Qy 1027 GCCCGGAGAAATAGCTATACCTACGATCTCCCTGTATCAGCTTATCAGCGCACCGGCGC 1086
Db 1060 GAGCGGAGATCGCTATGTTATGATTTCTGTATCAGCTTATGATGCGCACAGGCGGT 1119
Qy 1087 GAAATGGCAATTCGGTCAGCAAAAACAACAACTTCCCTCCCTG-----CGTACCT 1140
Db 1120 GAAATGGCTAATTCGTCAGCAAAAGCAACAACTTCCCTCCCTGTTATACCTGTTCT 1179
Qy 1141 TCTGACAAATACCTACACTACTATCTACGAGCTACAGCTATGATCAGTGTGTAAT 1200
Db 1180 ACTGACGACAGCACTTATACCAATTAACCTTCTGTAACCTTATGATGCGGTGGGTAAT 1239
Qy 1201 CTGACGCAATTCGGCACAGCTCGCCAGCTTACCAGAACTACACCGTGGCTATCACC 1260
Db 1240 TTGGTTCAATTCGCACACATTCACCGGACTCAAAATGTTACACCAAGATATCACC 1299
Qy 1261 CTCTAAACCGCAGCAATCGGGTGTCTCAGTACGCTACCAACCGATCCAAATCAAGTG 1320
Db 1300 GTTTCAGCGCGAGTAAACCGGCGGTATTGAGTACATTAAGGACAGATCCAAACCGAGTG 1359
Qy 1321 GATACGTTGTTGATCGCGGTGTGTCACCAACAGTTTATACCGGACAGACATTATC 1380
Db 1360 GATGCGCTATTGATTTCCGCGGTCTATCAGAAGATGTTATATACCGGGGCAAAATCTGGAT 1419
Qy 1381 TGGACACCAAGAGGAGTTAAAGCAGGT-----TAATATGCCCGGGA 1425
Db 1420 TGGATATTCGGGTGAAATTTGCAACGAGTCAACCGGTGAGCGTGAATAATAGAGTGAC 1479
Qy 1426 AATGAGTGTGATCGCTACGACAGCAACCGGATGAGCAAACTGAAAGTGTGATGAAACGCA 1485
Db 1480 AGTGAATGGTATCGCTATACGATGTGCGATCGCGGTCTAAAGTGTGATGAACAGCAG 1539
Qy 1486 ACCCAGAACTACGAGCAACAAACCGGTAACTTATTTGCGCGGACTGGAGCTACGACAA 1545
Db 1540 ACGGGCAACAGTACTCAAGTACAAACCGGTGACTTATCTGCGCGGATTAGAGCTACGACA 1599

Qy 1546 ACCAGAGCAACGCCCAACAACCGGAAGAGTTTACAGTTTATCACACTCTGGTGAAGCGGT 1605
Db 1600 ACTGGGTTTCAGATAAAACAACCGAAGATTTTCAGGTGATTACGGTAGGTGAAGCGGT 1659
Qy 1606 CCGCACAGGTACGGGTGTTGCACCTGGGAGAGCGGTAAAGCAAGATGTCAACAATAAT 1665
Db 1660 CCGCACAGGTAAAGGATTTGCACCTGGGAAGTGGTAAGCCGACAGATATTGACAACAAT 1719
Qy 1666 CAACTACGTTACAGCTACGATATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAA 1725
Db 1720 CAGGTGGCTACAGCTACGATATCTGCTTGGCTCCAGCCAGCTTGAACCTGGATAGGAA 1779
Qy 1726 GGAACAAATATCAGCGAGGAAGAGTATTATCAATTTGGCGGACACGCGTGTGGGAGCA 1785
Db 1780 GGGCAGATTCTCAGTCAGGAAGAGTATTATCCGTATGGCGGTACGCGCATATGGGCGCG 1839
Qy 1786 AACAGCCAAACAGACGAGCTATATAACGATTTCGCTATTTCGGCAAAAGAACAGATGCC 1845
Db 1840 AGAAATCAGACAGAAAGCCAGCTACAAATTTATTCGTTACTCCGGTAAAGAGCGGATGCC 1899
Qy 1846 ACCGGTCTGATTTATTTACGTTTATCTGTTATACCAACCGTGGCGGCGCAGATGTTAAGC 1905
Db 1900 ACTGGATTGTTATTTACGCTACCGTTATTTATCACTTTGGTGGTTCGATGTTGAGT 1959
Qy 1906 GCGGACCCGCGAGGAACCATTTGATGGCTGAAATCTATACGAATGTAAGAAATAATCCT 1965
Db 1960 GCTGATCCGCGGAAACCGTGGATGGCTGAAATTTGTACGAATGGTGAGGAATAACCCC 2019
Qy 1966 GTGAGTTTACAAGATGAAAATGGAATTAGCGCC 1997
Db 2020 ATCATTGACTGACCATGACGATAGCACC 2051

RESULT 4

US-09-902-540-1280
; Sequence 1280, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1280
; LENGTH: 1039

; TYPE: DNA
; ORGANISM: Myxococcus xanthus

; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(1039)
; OTHER INFORMATION: unsure at all n locations

US-09-902-540-1280

Query Match 2.0%; Score 56.2; DB 3; Length 1039;

Best Local Similarity 42.2%; Pred. No. 8.5e-06;

Matches 307; Conservative 0; Mismatches 420; Indels 0; Gaps 0;

Qy 1974 ACAGATGAAATGGATTAGCGCCAGAAAAGGGAATATACCAAGAGGTAAATTTCTT 2033
Db 277 AAAATAAATAAAAAAATCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 336
Qy 2034 TGATGAATTAATAATTCAAATTCGACCCCAAAAGTTCCACATGTTGTCAAATGGAAACGAGAA 2093
Db 337 ATAAATAAATAAAAAATTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAA 396
Qy 2094 AGAGAGCAGTTATACAAAAAATAAATCAATTGAAAGTGGTTGTCGTGCGTGTGATCCGATCC 2153


```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14624
; LENGTH: 147382
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(147382)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14624

Query Match      1.7%; Score 47.4; DB 3; Length 147382;
Best Local Similarity 45.8%; Pred. No. 0.069;
Matches 243; Conservative 0; Mismatches 281; Indels 7; Gaps 2;

Qy 2161 TATTGCTAAGCCAGAGTACTAAAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Db 137228 TATATAAATATATATAAATATATATAAATAAATAAATAAATAAATAAATAA 137169
Qy 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTTAGGATCT 2280
Db 137168 TAAATAAATATAAATATATAAATATGTAATAACATATATAAATAAATAAATAA 137109
Qy 2281 GAAATATCCGGTTATATGCGAAGAACCATACAAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 137108 AATATATATAAATACATATATAAATATATAAATATATAAATATATAAATAAATATG 137049
Qy 2341 CATAAATATAGN-----GTAATCACCCCTGATTTTATTCAGAACCGGATTTCTTTGGGTT 2396
Db 137048 TATAAATATATAAACAATATATATAAATAAATAAATAAATAAATAAATAAATAAAT 136989
Qy 2397 AATCGATAAAGTGCAAAAAATGATTTATCCGGTGAAGAAAATTTATCGGCAATGGA 2456
Db 136988 TATATATAAATATATGATATATATAAATAATATGTTAATATACATATATAAATAAATA 136929
Qy 2457 GGTTAAGGTTTATCATGATTTAAAAATAAACAATCAGAAATTAACATCTCAACTATGCAAT 2516
Db 136928 TATAAAAAATATATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 136869
Qy 2517 GGCCCATCCCTATACGCAATGAGTAATGAAGAAGAGCGCTGTTCGCAAGAACAGACACC 2576
Db 136868 AATATATAAATAATA- --TATGAACATAATATAAATAAATAAATAAATAAATAAATAA 136812
Qy 2577 CGCTATTGCAATAGATAGAGAAATAAATTTCAAAGGTGTTGGCAAAATTCCTGCAAAATGAA 2636
Db 136811 ATATATAAATAAATATATACAAATATATATAAATAAATAAATAAATAAATAAATAAATAA 136752
Qy 2637 AGCAATTAATAAATCATTTGAAGGACATATAAATAAATTAATAGGATATCAACAGA 2687
Db 136751 ATATATAAATAAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 136701
```

```
RESULT 7
US-09-902-540-1357
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
```

```
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match      1.7%; Score 46.6; DB 3; Length 612;
Best Local Similarity 43.1%; Pred. No. 0.0042;
Matches 220; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

Qy 2177 AAGAGTTACTAAAGGTATAGAAAAGTCAAAATCATATATAGCCGACTTTGAAGAAAACA 2236
Db 12 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 71
Qy 2237 GCTCCCTTTTCAGAAAATCAAAAACGAATCTTTCTTTAGGATCTGAAATATCCGGTTATA 2296
Db 72 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 131
Qy 2297 TGCAGAACCATACAGATACGATATCAGAAATATGCCGAAGAGCATAAATATAGAGTA 2356
Db 132 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 191
Qy 2357 ATCACCTGATTTTATTCAGAAACCGATTTCTTTGCGTTAATGGATAAAAGTGAAAAAA 2416
Db 192 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 251
Qy 2417 ATGATTTATTCGGTGAAGAAAAATTTATGCGGCAATGGAGGTTAAGGTTTATCATGATT 2476
Db 252 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 311
Qy 2477 TAAAAATAAACAATCAGAAATTAACATGTCAACTATGCAATGGCCCATCCCTATACGAAT 2536
Db 312 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 371
Qy 2537 TGAGTAATGAAGAACAGCGCTGTTCGCAAGAACAGACCCGCTATTGCAATAGATAGAG 2596
Db 372 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 431
Qy 2597 AATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAAAATGAAAGCAATTTAAAAAATCATTTGA 2656
Db 432 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 491
Qy 2657 AAGCAGATAAATAAATATAGATATCAACAGA 2687
Db 492 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 522
```

```
RESULT 8
US-09-949-016-13539
; Sequence 13539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13539
; LENGTH: 314798
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
```

```

; LOCATION: (1)...(314798)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13539

Query Match
Best Local Similarity 1.7%; Score 45.6; DB 3; Length 314798;
Matches 144; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 2199 AAAAAGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAA 2258
Db 18841 AAATATATATAAAATATATATAAATATATATAAATATATAAATATATAAATAT 18900
Qy 2259 AACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2318
Db 18901 ATATATAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 18960
Qy 2319 GATATCAGATATATCCGAAGAGCAATAATATAGAAATGTAATCACCCTGATTTTATTTCAGA 2378
Db 18961 TATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 19020
Qy 2379 AACCGATTTCTTCGGTTAATGGATAAAGTGAAGAAAATGATTTATCCGGTGAAGAAA 2438
Db 19021 TATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 19080
Qy 2439 AATTATGCGCAATGAGGTTAAGGTTTATCATGATTTTAAAAATATAAACAATCAGAAAT 2498
Db 19081 TATTAAATATATATATATATATATATATATATATATATATATATATAAATAA 19140
Qy 2499 ACATGTCA 2506
Db 19141 AATTGCCA 19148

```

```

RESULT 9
US-09-949-016-61868
; Sequence 61868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61868
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-61868

```

```

Query Match
Best Local Similarity 1.6%; Score 45.2; DB 3; Length 582;
Matches 143; Conservative 1; Mismatches 164; Indels 0; Gaps 0;

Qy 2199 AAAAAGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAA 2258
Db 12 AAATATATATAAAATATATATAAATATATAAATATATAAATATATAAATATAA 71
Qy 2259 AACGAATCTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2318
Db 72 ATATATAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 131
Qy 2319 GATATCAGATATATCCGAAGAGCAATAATATAGAAATGTAATCACCCTGATTTTATTTCAGA 2378
Db 132 TATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 191

```

```

Qy 2379 AACCGATTTCTTTGCGTTAATGATATAAAGTGAAGAAAATGATTTATCCGGTGAAGAAA 2438
Db 192 TATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATAA 251
Qy 2439 AATTATGCGCAATGAGGTTAAGGTTTATCATGATTTTAAAAATATAAACAATCAGAAAT 2498
Db 252 TATTAAATATATATATATATATATATATATATATATATATATATATAAATAA 311
Qy 2499 ACATGTCA 2506
Db 312 AATTGCCA 319

```

```

RESULT 10
US-09-949-016-12510
; Sequence 12510, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12510
; LENGTH: 94987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12510

```

```

Query Match
Best Local Similarity 1.6%; Score 45; DB 3; Length 94987;
Matches 165; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy 2203 AGTCAATCATATATAGCCGACTTGAAGAAAACAGCTCCCTTTTCAGAAAATCAAAACG 2262
Db 1177 AGGTAAGCCATTAGTACCTTTTAAAAAAGCATACGAGTGCATACAGTAAATAA 1236
Qy 2263 AATCTTTTCTTTAGGATCTGAAATATCCGGTTATATGCGCAAGAACCATACAGATAC 2322
Db 1237 ATGAAAAATTCATCAAGCAATATAAGATACAAACAAAGATCATTAATGAAATCTAGATC 1296
Qy 2323 TCAGATATATCCGAAGAGCATATAATATAGAAATGTAATCACCCTGATTTTATTTCAGAAAC 2382
Db 1297 TCAGGGATTTTCCAAGAGAGATTACTTAAAGGAGAAAACAAGTTTGTTCAGTGGATAAACA 1356
Qy 2383 GATTTCTTTGCGTTAATGGATAAAGTGAAGAAAATGATTTATCCGGTGAAGAAAAT 2442
Db 1357 TTGTTCTATGCGTGAATATAGGAGAGTGAAGATTCCTCATTTTCTAGTTCAGGGAATGT 1416
Qy 2443 TATGCGCAATGAGGTTAAGGTTTATCATGATTTTAAAAATATAAACAATCAGAAATACAT 2502
Db 1417 CATAGATCAGGATGCGCAGAGTTAAACAATATTTCTCTGCTCTCTTAATGGAAGCAT 1476
Qy 2503 GTCAACTATGATGGCCCATCCCTATATACCAATTTGAGTAAATGAAGAAAGAGCGCTGTTG 2562
Db 1477 AAGAAAAATTAGCTTCACTGAAGTTTAAACAAATGGAATTAACAAAGAAAAGAGCTATTT 1536
Qy 2563 CAAGA 2567
Db 1537 AAAAA 1541

```

RESULT 11

US-09-949-016-14429
; Sequence 14429, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 14429
; LENGTH: 96987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14429

Query Match 1.6%; Score 45; DB 3; Length 96987;
Best Local Similarity 45.2%; Pred. No. 0.27;
Matches 165; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 2203 AGTCAATCATATATAGCCGACTTGAAGAAAAACAGCTCCCTTTACAGAAAAATCAAAAACG 2362
DB 51177 AGGTAGCCATTAGTCACCTTTTAAAAAAGCATACGAGTGGATCAAGTAATAACA 51236

QY 2263 AATCTTTCTTTTAGGATCTGAAATATCCGGTTATATGSCAAGAACCATACAGATACGATA 2322
DB 51237 ATGAAAAATTCATCAAGCAATATAAGATACAAACAAAGATCATTAATGAAATCTAGATC 51296

QY 2323 TCAGATATCCGAGAGCATATAATAGAAATTAACACCTGATTTTATTCAGAAACC 2382
DB 51297 TCAGGGATTTTCAAGAGAGATTACTTAAGGAGAAAAACAAGTTTGTTCAGTGGATAAACA 51356

QY 2383 GATTCTTCTCGTTAATGGATAAAGTGAAGAAAAATGATTATTCGCTGAAAGAAAAATT 2442
DB 51357 TTGTTCTATCGTGAATAGGAGATGGAATGGCAATTTCTAGTTCAAGGGATGT 51416

QY 2443 TATCGCGCAATGGAGGTAAAGTTTATCATGATTTAAAAAATAAACAATCAGAAATTACAT 2502
DB 51417 CATAGATCAGGATGGCACAGAGTTAAACACATATTCTCTGCTCTAATGGAAGCAT 51476

QY 2503 GTCACATATGATGGCCCATCCCTATACGCAATTGATGTAATGAAGAGCGCTGTTG 2562
DB 51477 AAGAAAAATTAGCTTCACTGAAGTTTAAACAAAAATGGAATTAACAAAGAAAGAGCTATTT 51536

QY 2563 CAAGA 2567
DB 51537 AAAAA 51541

RESULT 12
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAE1 promoters
US-09-806-708B-22

Query Match 1.6%; Score 44.2; DB 3; Length 1141;
Best Local Similarity 12.3%; Pred. No. 0.032;
Matches 97; Conservative 268; Mismatches 420; Indels 5; Gaps 2;

QY 1956 AAATAATCCTGTGAGTTTCAAGATCAAAATGATTAGCCGAGAAAAAGGGAATATAC 2015
DB 1003 ATNNAMYYATTAAAYAAAKARWAGNNRMRYGAAAGNKGWCAAAATATGWBWADTAGKM 944

QY 2016 CAAAGAGGTAAATTTCTTTGATGAATTAATAATCAAAATGCGCAGCCAAAGTTACATGT 2075
DB 943 CNNNNNTTIDVRRMAMKAKNNNNNNNAYWTACYNRAATNNKATHMKWTHGAHSHKRT 884

QY 2076 TGTCAAAATGGAACGAGAGAGAGAGAGTATACAAAAATAATCATTTGAAAGTGGTTCG 2135
DB 883 HHTRTCRRTKYNNNNNNARTVYVYHHAARRWMAWTRTNNNNNNNNNNNACRTRTWAB 824

QY 2136 TGTGCGTGATTCGGATCCGCTCGGTTATTGCTAAGCCAGAGAGTTACTAAAGGTAT 2195
DB 823 WKHSWCNNNNNNNNNNNNNTWCHYTANABBCYRANNNNAAARMARTCNYYHAAVTTT 764

QY 2196 AGAAAAAAGTCAAAATCATATATAGCCGACTTGAAGAAAAACAGCTCCCTTTACAAAAATC 2255
DB 763 HTDWCYKTMWYWDWMTTMBTTTTTRNMTTSTNNNNNNNNNNNNNNNNNNNNNNNNNN 704

QY 2256 AAAAAAGCAATCTTTCTTTTAGGATCTGAAATAT---CCGGTTATATGCGCAAGAACCATACA 2312
DB 703 HATNNGWCNNNTDARRTNTTVMRRRWMTNTKTRWYSTTRRHHTGATNNNNNNNNNN 644

QY 2313 AGATACGATATCAGAAATATGCGGAGAGCATATAATAGAAATATACACCTGATTTTA 2372
DB 643 NNNNSCCCTTRMTMRMTMGDMTVRKVKWRDTTCTYVDVWADSVWVYANMRCRD 584

QY 2373 TTCAGAAACCGATTTCTTTGCGTTAATGATGATAAGTGAAGAAAAATGATTATTCGCGTGA 2432
DB 583 VTYTRNTYCKSYAHSYWTSNNAMWYRYSARNSSMARWTRNNNNNNNNNNNNNNNNNN 524

QY 2433 AAGAAAAATTTATGCGCAATGGAGTTAAGGTTTATCATGATTTAAAAAATAAACAATC 2492
DB 523 MWRHNNNNNTDTRYVWKKRWBTTTVVDSNCNAKSMWGNMWRAMKMWAAANNNDAGA 464

QY 2493 AGAATATCATCACTATGCTATGCGCCATCCCTATACGCAATTCAGTAATGAGTAAG 2552
DB 463 MDHWTYMGNTTMMRRAMKMMNMAMCRRAYCCNNNNNNRACVWHKHQWRWTKWYMKAA 404

QY 2553 AGCGCTGTTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAGATAATAATTTCAAA-- 2610
DB 403 CNNNNBKAMYMRVAMMYSRDNTTNDMMWTSDBWHWTYVDYTMRRANNNNNNNNNRBC 344

QY 2611 GGTGTTGGCAAAATTCCTGACAAATGAAAGCAATTTAAAAAATCATTTGAAAGGACATAAAAT 2670
DB 343 KTTSSWMMMDHKNTHCTYGNNTWGSAYBMAASMWAAAGASBNBYTYWCHWTYMGKMTN 284

QY 2671 AATAGATATCAACAGAGGCTATTATATTCGCTCTCGCGGCTATCGCTGAGAAATTTAGGA 2730
DB 283 NNNNNKAYYRTKTVAWCNNRYVDVAVTMBKRNKYCYAYBWWYBYMYGKHWHBWWRA 224

QY 2731 ATCGCGAGAA 2740
DB 223 BHRSMNMWV 214

RESULT 13
US-08-956-171E-631/c
; Sequence 631, Application US/08956171E
; Patent No. 6593114

APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 1.6%; Score 44; DB 2; Length 19124;

Best Local Similarity 44.4%; Pred.No. 0.2; Mismatches 1; Gaps 1;
Matches 220; Conservative 0;

QY	2180	AGTTACTAAAAGGTATAGAAAAAGTCAATCATATATATAGCCGACTTGAAGAAAAACAGCT	2239
Db	15410	ATTATATTAAAAAGAAATATAAAACAAATTTATTAAATGAAAAAGAAAAATGAA	15469
QY	2240	CCCTTTTCAGAAAATCAAAACGAATCTTTCTTTTAGGATCTGAAATATCCGGTTATATGG	2299
Db	15470	ATATAAAAAAAATTTATTAAAAATAAAAAAAGGAGAAAAATTTTTT	15529
QY	2300	CAAGACCATACAGATACGATATAGATATGCCGAGCATTAATATAGAGTAATC	2359
Db	15530	AAAAATAATAAAATTTATAATAAAATAAAATTTTGTAGATAAAAAATGAAAAAGAT	15589
QY	2360	ACCTCGATTTTATTCAGAAACCGATTCTTTCGTTTAAATGGATAAAAGTAAAAAAATG	2419
Db	15590	TATCAAAAAAAATTTAAAAAAATTTTATATAAAAAAAATGATTATAAAAAAATAA	15649
QY	2420	ATTATTCGGTGAAGAAAAATTTATGCGGCAATGAGGTTAAGGTTTATCATGATTTAA	2479
Db	15650	AAACAAAAGAGAAAAAAACATTAATAAAAAAAATATATATCAAAAAACAAA	15709
QY	2480	AAATATAACAATCAGA-ATTACATGTCAACTATGCTTGCCCATCCCTATACGCAATTG	2538
Db	15710	AAAAAGAAAAAATATATTTAAATAAATAAATATATATCAATAAATAAAAAAATTTAAA	15769
QY	2539	AGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAGAA	2598
Db	15770	AAATGTTAAAAAATAATATATACATAAATAAAAAATTTTAAATATAAAAAAAT	15829
QY	2599	TATAATTTCAAGGTGTTGGCAAAATTCCTGACAATGAAAGCAATTAAAAAATCAITGAAA	2658

Db	15830	ATAAATAAAAAAATTTAATTAAATAAAAAAATAAATAAATAAATAAATAAATAAATAA	15889
QY	2659	GGACATAAAATTAATA 2674	
Db	15890	AAAAAAAATTAATAA 15905	

Search completed: December 14, 2005, 02:25:44
Job time : 504 secs

Best Available Copy

This Page Blank (uspto)

Best Available Copy

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:10:31 ; Search time 9683 Seconds
(without alignments)
13363.507 Million cell updates/sec

Title: US-10-647-956A-5

Perfect score: 2745

Sequence: 1 atgagcagttacaattctgc.....taggaatcgaggagaacttca 2745

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419.6	15.3	460	9 AQ991476	AQ991476 Rfc02418
2	352	12.8	749	9 AQ991727	AQ991727 Rfc00357F
3	292.6	10.7	605	9 AQ990411	AQ990411 Rfc01179
4	239.8	8.7	494	9 AQ991400	AQ991400 Rfc02327
5	226.8	8.3	406	9 AQ990055	AQ990055 Rfc00763
6	192.6	7.0	594	9 AQ990688	AQ990688 Rfc01498
7	176.8	6.4	878	10 C2547320	C2547320 SRAA-aad7
8	152.6	5.6	547	9 AQ990013	AQ990013 Rfc00707
9	148.8	5.4	312	9 AQ990147	AQ990147 Rfc00869
10	141	5.1	733	1 AQ990147	AQ990147 Rfc00869
11	74.6	2.7	1224	10 CL077121	CL077121 CH216-143
12	71.8	2.6	1299	8 DN705619	DN705619 CLJ60-F02
13	68	2.5	942	10 CNS0186S	AL109318 Drosophila
14	65.4	2.4	1811	10 CG753732	CG753732 P048-4-G0
15	65	2.4	1353	10 CG744812	CG744812 P037-3-B0
16	64.8	2.4	1683	10 AG390417	AG390417 Mus muscu
17	64.4	2.3	1364	8 DN693282	DN693282 CGX87-B03
18	64.2	2.3	1178	10 CL491661	CL491661 SAIL 559
19	63.6	2.3	1101	10 CNS0039G	AL063921 Drosophila
20	63.6	2.3	1137	10 CL080345	CL080345 CH216-158
21	63.4	2.3	1053	5 BU508694	BU508694 AGENCOURT
22	63.4	2.3	1204	8 DN432684	DN432684 LIB4217-0

23	63.2	2.3	644	1 AW901491	AW901491 RCO-NN101
24	63.2	2.3	1843	10 AG435185	AG435185 Mus muscu
25	63	2.3	1134	10 CL073913	CL073913 CH216-130
26	63	2.3	1201	10 CNS0167M	AL106396 Drosophila
27	63	2.3	1256	10 CL119201	CL119201 ISB1-76U1
28	62.8	2.3	2071	8 DR147304	DR147304 49027161
29	62.6	2.3	1433	10 CG745119	CG745119 P037-4-G0
30	61.4	2.2	974	10 CNS001TT	AL075432 Drosophila
31	61.4	2.2	1512	10 CL082685	CL082685 CH216-169
32	61.4	2.2	1528	10 CG753854	CG753854 P049-1-D0
33	61.2	2.2	1330	8 DN705530	DN705530 CLJ60-A10
34	61	2.2	1108	1 AJ926042	AJ926042 AJ926042
35	61	2.2	1167	1 AJ927228	AJ927228 AJ927228
36	61	2.2	1266	10 AJ859745	AJ859745 Braggella
37	61	2.2	1680	10 CL079033	CL079033 CH216-154
38	60.8	2.2	1146	10 CL649333	CL649333 CH213-227
39	60.8	2.2	1531	10 CG748014	CG748014 P041-4-B0
40	60.4	2.2	1055	5 BQ876453	BQ876453 AGENCOURT
41	60.4	2.2	1114	8 DN560777	DN560777 CSC21-A11
42	60.2	2.2	997	10 CNS0134P	AL102403 Drosophila
43	60.2	2.2	1566	10 CG757757	CG757757 P053-1-D0
44	60	2.2	1173	1 AJ926089	AJ926089 AJ926089
45	60	2.2	1558	10 CL491664	CL491664 SAIL_559

ALIGNMENTS

RESULT 1
AQ991476 460 bp DNA linear GSS 14-AUG-2000
LOCUS Rfc02418 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG02418, genomic survey sequence.
ACCESSION AQ991476 GI:9650070
VERSION AQ991476.1
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
REFERENCE 1 (bases 1 to 460)
AUTHORS Bacterla; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
TITLES ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL 10919786
COMMENT Contact: ffrrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES

Location/Qualifiers
1. .460
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02418"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN		source
Query Match 15.3%; Score 419.6; DB 9; Length 460; Best Local Similarity 97.0%; Pred. No. 2.6e-99; Matches 448; Conservative 0; Mismatches 11; Indels 3; Gaps 2;		1. .749 /organism="Photorhabdus luminescens" /mol_type="genomic DNA" /strain="W14" /db_xref="taxon:29488" /clone="PLG00357F" /dev_stage="primary phase variant" /clone_lib="Photorhabdus luminescens strain W14 M13 library" /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
QY 1266 AAACCCGAGCAATCGGGGTCTCTCAGTAGCTAAACACCGATCCAAATCAAGTGGATAC 1325		
DB 1 AAACCCGAGCAATCGGGGTCTCTCAGTAGCTAAACACCGATCCAAATCAAGTGGATAC 60		
QY 1326 GTTGTGTTGATCGCGGTGTCACCAACACAGTTTATTACCCGGAGACAGACTTATCTGGAC 1385		
DB 61 GTTGTGTTGATCGCGGTGTCACCAACACAGTTTATTACCCGGAGACAGACTTATCTGGAC 120		
QY 1386 ACCACGAGGAGAGTTAAAGCAGGTTAATATGCGCCGGGAAATGAGTGGTACGCTACGA 1445		
DB 121 ACCACGAGGAGAGTTAAAGCAGGTTAATATGCGCCGGGAAATGAGTGGTACGCTACGA 180		
QY 1446 CAGCAACGGCATCAGACCACTGAAAGTGAGTGAACGCCAACCCAGAATACTACGCAGCA 1505		
DB 181 CAGCAACGGCATCAGACCACTGAAAGTGAGTGAACGCCAACCCAGAATACTACGCAGCA 240		
QY 1506 ACAACGGGTAATCTATTGTCGGGACTGGAGCTACGCACCAACCCAGACGCAACGCCACAAC 1565		
DB 241 ACAACGGGTAATCTATTGTCGGGACTGGAGCTACGCACCAACCCAGACGCAACGCCACAAC 300		
QY 1566 AACGGAAGAGTTACAGTTATCATCTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTT 1625		
DB 301 AACGGAAGAGTTACAGTTATCATCTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTT 359		
QY 1626 GCACTGGGAGCGGTAAAGCCAGAGATGTCACAAATCACTAGTTTACAGCTACGA 1685		
DB 360 GCACTGGGAGCGGTAAAGCCAGAGATGTCACAAATCACTAGTTTACAGCTACGA 417		
QY 1686 TAATCTGATCGGTCACGACGCTTGAACCTGGACCAACCAAGG 1727		
DB 418 TAATCTGATCGGTTCAACGCTTGGACTGGACACCCNAGG 459		
RESULT 2		
AQ991727/c		749 bp DNA linear GSS 14-AUG-2000
LOCUS		RfC00357F Photorhabdus luminescens strain W14 M13 library
DEFINITION		Photorhabdus luminescens genomic clone PLG00357F, genomic survey sequence.
ACCESSION		AQ991727
VERSION		AQ991727.1 GI:9650223
KEYWORDS		GSS.
SOURCE		Photorhabdus luminescens
ORGANISM		Photorhabdus luminescens
REFERENCE		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
AUTHORS		1 (bases 1 to 749) ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE		A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
JOURNAL		Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED		10919786
COMMENT		Contact: ffrench-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bbsrfc@bath.ac.uk This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Reverse Class: shotgun.
FEATURES		Location/Qualifiers
ORIGIN		
Query Match 12.8%; Score 352; DB 9; Length 749; Best Local Similarity 71.2%; Pred. No. 2.2e-81; Matches 487; Conservative 0; Mismatches 190; Indels 7; Gaps 2;		
QY 267 CGGTCCGACTATTACCCCTCAATGATATTGAAAGTCGCCGGTGTGATCATCAATCAAC 326		
DB 713 CGGTTCGCTGTCNCCTTNAATTATATTGAAGNCCGTCGCTACTACGGGTGNTTCAAC 654		
QY 327 CGGTGTCGCCAAAACCATCGTTATGAAAGATAACACCTTCCCGGTGCTGCTCGGTAT 386		
DB 653 AGGNTTATAC-AAACTGCCAATATGAAATTTTNCCTGCGCGGTGTTGTTATCTGT 595		
QY 387 CACCGAACAGTACAGCGCAGGAGAGAAACG-----ACCGACGCTTATCTGGGCGG 440		
DB 594 TCGCGCAACAAACCCCGAGGAAAAACATCCCGCTATCACCGAACCTTGATTTGGGTGG 535		
QY 441 CAATACCGCGCAAGAAAAAGATTACAACTCGCGGTGTCAGTGTGTCGCCCATTCACGATAC 500		
DB 534 CANTACGAGCAGAGAAAGACCATTAACCTTGCGCCAGTGGCTGCTCACTATGACAC 475		
QY 501 CGCGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGGCTGCTGCTATCAATCTCA 560		
DB 474 GCGGGAGTTACCGGTTANAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAG 415		
QY 561 ACACTGCTTACCGATAACCGAGATCCGACTCGACAGGTGTAAGACAGAGCCTCTGGCA 620		
DB 414 CCAACTATTGATCGACACTCAAGAGGCAAACTGGACAGGTGTAACGAAACCGCTCTGGCA 355		
QY 621 ACAAAACTGAGTAGTGTCTATATCACCCAAAGTAACACTGATGCCACCGGGGCTTT 680		
DB 354 AAACATGCTGGCTGATGACATCTACACAACTTGAGCACCTTCGATGCCACCGGTGCTT 295		
QY 681 ACTGACCCAGACCGATGCCAAAGGCAACATTACAGCGCTGGCCTATGATGTGGCCGGCA 740		
DB 294 ACTGACTCAGACCGATGCGAAAGGGAACATTCAAGAGACTGGCTTATGATGTGGCCGGCA 235		
QY 741 GCTAAAGGGAGTTGGTTAACTCAACTCAAGGTCAAGGCGGACAGGTGATTATCAATCGCT 800		
DB 234 GCTAAAGCGGAGCTGGCTAACTCAAAAGGCCAGACGGAACAAGTATTAATCAATCCCT 175		
QY 801 AACCTACTCCGCGCGGCAAAAATTAAGTGAAGACACGCTAAACGGGATTTGCTACTGA 860		
DB 174 GACTTACTCGCGCGCGGACAAAATTAAGTGAAGACACGCTAAAGTATTAATCAACCGA 115		
QY 861 ATACAGTACGAACCGGAAACCAACGGCTTATCGGCATTTACCACTCGCGGTCCATCAGA 920		
DB 114 ATACAGTTATGAACCGGAAACCAACGGCTATCGGTATCAAAACCGCGCTCGTCAGA 55		
QY 921 CGCCAAAGTGTTCGAAGACCTAGC 944		
DB 54 CACTAAAGTGCTACAAGACCTGCG 31		
RESULT 3		
AQ990411		605 bp DNA linear GSS 14-AUG-2000
LOCUS		RfC01179 Photorhabdus luminescens strain W14 M13 library
DEFINITION		Photorhabdus luminescens genomic clone PLG01179, genomic survey sequence.
ACCESSION		AQ990411

```
VERSION AQ990411.1 GI:9649005
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
          Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 605)
AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
          Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
          Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: fFrench-Constant RH
          Department of Biology and Biochemistry
          University of Bath
          South Building, Bath BA2 7AY, UK
          Tel: (44) 1225 826621
          Fax: (44) 1225 826779
          Email: bssrfc@bath.ac.uk
          This is one of 2,122 random reads from the M13 library. For
          annotation of identified clones (BLASTX, BLASTN and mapping to E.
          coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic
          Acids Res.
          Seq primer: M13 Forward
          Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..605
                /organism="Photorhabdus luminescens"
                /mol_type="genomic DNA"
                /strain="W14"
                /db_xref="taxon:29488"
                /clone="PLG01179"
                /dev_stage="primary phase variant"
                /clone_lib="Photorhabdus luminescens strain W14 M13
                library"
                /notes="Genomic DNA from strain W14 was size selected (1-2
                kb) and then cloned into M13 Janus."
ORIGIN
    Query Match 10.7%; Score 292.6; DB 9; Length 605;
    Best Local Similarity 70.8%; Pred. No. 1e-65; Indels 14; Gaps 2;
    Matches 422; Conservative 0; Mismatches 160;
QY 417 GACCGAACGCTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACCTCCCGCG 476
DB 2 GACAGAGCGCTTATCTGGCGTGGGAATACACCTCGGAGAAAGATTAACCTCTCCGG 61
QY 477 TCAGTGTGTCGCCCATTAATGATACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGC 536
DB 62 TCTGTGTATACGCGCACTAGCACACACGCGGGAGTGACCCGGTTGATCAGTCAGTCACCTGGC 121
QY 537 TGGCGTGTGCTATCAATCTCAACTCAACCTGTTACCGATACCGATACCGATGCGGACTGGAC 596
DB 122 GGGCGGCATGCTATCCCAATCTCACCATTGCTGGCGGAAGGCGCAGGCTTAACCTGAG 181
QY 597 AGGTGAAGACACGAGCGCTCTGGCAACAAACCTGAGTAGTGCTATATACCCCAAG 656
DB 182 CGGTGACGACGAACACTGTCTGGCAGGGAATGCTGGCAAGTAGGTCTTACGACACAAG 241
QY 657 TAACTGATGTCACCGCGGCTTTTACTGACCCAGCGATGCGCAAGGCAACATTCAGCG 716
DB 242 TACCACTAATGCCATCGGGCTTTTACTGACCCAAACCGATGCGAAGGCAATATTTCAGCG 301
QY 717 GCTGGCTATGATGTGGCGGGGAGCTTAAAGGGAGTTGGTTAACTCAAGGTCAAGC 776
DB 302 TCTGGCTTATGACATTTGCCCGTCAGTTAAAGGGAGTTGGTTGACCGGTGAAGGCCAGAG 361
QY 777 GGAACAGGTGATTTATCAATCGTCACTTCTCCCGCGCGGCAAAAATTTAGTGAAGA 836
DB 362 TGAACAGGTGATTTGTTAAGTCCCTGAGCTGGTCAGCGCGCAGGTCAATAATTTGGTGAAGA 421
QY 837 GCACGGTAACGGGATTTGTCACTGTAATACAGCTACGAACCGGAACCCCAACGGCTTATCGG 896
```

```
Db 422 GCACGGTAACGGCGTGGTTACCGAGTACAGTTATGAGCCCGGAAACTCAACGCTCTATAG 481
QY 897 CATTACCCTCCCGCTCCATCA-----GACGCCAAGGTGTTGCAAGACCTAC 943
DB 482 GTATACCACCCCGCGTGGCCCAANGGAGTCAATCANGAGCCAGAGTATTGCGAGGATCTAC 541
QY 944 GTATCAATATGACCCAGT-AGGCAATGTCAATATATATCCGTAATGATGCGGAAGC 998
DB 542 GCTATAAGTATGATCCCGTGGGGAATGATCAGTATTTCATAATGATGCCCNAC 597

RESULT 4
AQ991400/c 494 bp DNA linear GSS 14-AUG-2000
LOCUS Rfc02327 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG02327, genomic survey
          sequence.
ACCESSION AQ991400
VERSION AQ991400.1 GI:9649994
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
          Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 494)
AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
          Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
          Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: fFrench-Constant RH
          Department of Biology and Biochemistry
          University of Bath
          South Building, Bath BA2 7AY, UK
          Tel: (44) 1225 826621
          Fax: (44) 1225 826779
          Email: bssrfc@bath.ac.uk
          This is one of 2,122 random reads from the M13 library. For
          annotation of identified clones (BLASTX, BLASTN and mapping to E.
          coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic
          Acids Res.
          Seq primer: M13 Forward
          Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..494
                /organism="Photorhabdus luminescens"
                /mol_type="genomic DNA"
                /strain="W14"
                /db_xref="taxon:29488"
                /clone="PLG02327"
                /dev_stage="primary phase variant"
                /clone_lib="Photorhabdus luminescens strain W14 M13
                library"
                /note="Genomic DNA from strain W14 was size selected (1-2
                kb) and then cloned into M13 Janus."
ORIGIN
    Query Match 8.7%; Score 239.8; DB 9; Length 494;
    Best Local Similarity 71.9%; Pred. No. 8.8e-52;
    Matches 343; Conservative 0; Mismatches 127; Indels 7; Gaps 2;
QY 276 TATTACCTCAATGATATTGAAAGTCGCCCGGTGTTGATCATCAATGCAACCGGTGTCG 335
DB 476 TGTTCATTGAATGATTGAAGGTCGTTCCGTAATGACAATGAATGCGCCCGGTGTCG 417
QY 336 CCAAAACCATCGTTATGAAGATAACACCCCTTCCCGTCGTCGCTCATCAACCGAACA 395
DB 416 TCAGACCCGTCGTCATGAAGGCAACA-CCTTGGCGGTGCTTGTATTCTGTGAGCGAGCA 358
QY 396 AGT-----ACAGGCGAGGAGAGAAACGACCGCAACGCTTATTCTGGGCGCGCAATACGCC 449
    |||
```


Db 357 AGTTTTCAACCAAGAGAGTCTAAAGTGACAGAGCGCTTTATCTGGGCTGGGAATACAC 298

Qy 450 GCAAGAAAAGATATCAACTCGCGGTCAAGTGTCCGCCATTAAGATACCGCGGACT 509

Db 297 CTCGGAGAAAGATATAAACCCTCCGGTCTGTGTATACGCCACTACGACACAGCGGGAGT 238

Qy 510 TACTCAACTCAATAGCTTTCTCTGGCTGGCGTGTCTATCAATCTCAACAATGCT 569

Db 237 GACCCGGTTGATGAGTCAGTCACCTGGCGGGCGCATCTATCCAAATCTCACCAATGCT 178

Qy 570 TACCGATAACACAGGATGCCAGCTGGACAGGTGAAGACAGAGCCTCTGGCAACAAAAC 629

Db 177 GCGGGAAGGCGAGGAGCTAACTGGAGCGGTGACGACGAACTGTCTGGCAGGGAATGCT 118

Qy 630 GAGTAGTGATCTATATCAACCAAGTAACACTGATGCCACCGGGCTTTACTGACCCA 689

Db 117 GGCAAGTGAGGTCTATACGACACAAAGTACCACTTAATGCCATCGGGGCTTTACTGACCCA 58

Qy 690 GACCGATGCCAAAGGCAACATTACGCGCTGGCTATGATGTGCGCGGCGAGCTAAA 746

Db 57 AACCGATGCCAAAGGCAATATTACGCGTCTGGCTTATGACATTCGCCGTCAGTTAAA 1

RESULT 5
AQ990055
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00763, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
AQ990055.1 GI:9648649
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 406)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: Shotgun.
Location/Qualifiers
1. .406
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00763"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES
source

ORIGIN

Query Match 8.3%; Score 226.8; DB 9; Length 406;
Best Local Similarity 75.5%; Pred. No. 2.3e-48;
Matches 293; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

Qy 1447 AGCAACGGCATGAGACAACTGAAAGTGAAGTGAACAGCCCAACCCAGAAATACTACGCAGCA 1506

Db 1 AGCAACGGCATACGCCAGCTAAAGTGAATGAACAAACAACTCAGAAATATCCGCGAACAA 60

Qy 1507 CAAACGGTAACTCTATTTCGCGGACTGGAGCTACGACAAACCCAGAGCAACGCAACA 1566

Db 61 CAAAGGGTAACTTATCTACCGGGCTGGAATACGTAACAACCCAGAAACGCGCAACA 120

Qy 1567 AGGAAGAGTTACACGTTATCACCTCGGTGAAGCCGGTCGGCCACAGTACGGGTGTTG 1626

Db 121 ACAGAAGAGTTACACGTTATCACCTCGGTGAAGCCGGCGCGCAAGTCCGAGTATTG 180

Qy 1627 CACTGGGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTAGTTACGCTACGAT 1686

Db 181 CATTTGGAGAGCGGTAAACCAAGATATTAATACATCAGCTTCGTTACGCTACGAT 240

Qy 1687 AATCTCATCGGCTCCAGCCAGCTTGAATCTGGCAACCAAGGCAAAATTTACGCG-AGGA 1745

Db 241 AATCTTATTTGGCTCCAGCCAACTTCAATAGATAGCGACGGCAAAATTTATCAAGTGAAGA 300

Qy 1746 AGAGTATTATCCATTTTGGCGGACAGCGCTGTGGGACGAAACAGCAACCAAGCCAG 1805

Db 301 AGAATATTATCCATTTTGGTGTACAAAGCGCTGTGGCGGNAAGGATTAAACCGAACCCAG 360

Qy 1806 CTATAAACGATTCGCTATTCGCGCAAA 1833

Db 361 CTNTTAAACAATTCGTATTTTTGTAAAA 388

RESULT 6
AQ990688/c
LOCUS
DEFINITION

Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01498, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
AQ990688.1 GI:9649282
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 594)
ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: Shotgun.
Location/Qualifiers
1. .594
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01498"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"

FEATURES
source

/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN		FEATURES		source	
Query Match		Location/Qualifiers		1..878	
Best Local Similarity		6.4%; Score 176.8; DB 10; Length 878;		/organism="Strongyloides ratti"	
Matches 351; Conservative 0; Mismatches 239; Indels 3; Gaps 3;		59.2%; Pred. No. 2.7e-39;		/mol_type="genomic DNA"	
				/strain="Isaofemale line ED321 heterogonic"	
				/db_xref="taxon:34506"	
				/dev_stage="infective larval stage (iL3)"	
				/lab_host="GS10"	
				/clone_lib="Strongyloides ratti whole genome shotgun library (SRAAGSS 004)"	
				/note="Vector: pOW13; Site 1: BatX1; Site 2: BatX1; Strongyloides ratti genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 Kb fragments. Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."	
ORIGIN		Query Match		6.4%; Score 176.8; DB 10; Length 878;	
		Best Local Similarity		63.4%; Pred. No. 4.4e-35;	
		Matches 321; Conservative 0; Mismatches 152; Indels 33; Gaps 2;			
QY	1487	CCGAGTAATCTACGCGCAACACCGGGTAATCTATTTGCGGACTTGGAGCTACGCACAA	1546		
DB	815	CCGGTAACAGTACACAGACACAGCGGGTGGTTATCTGCGGGTCTTGGAACTTCG----	761		
QY	1547	CCGAGGACGCCCAACACGAGAGTTACAGTTATCACCTCGGTGAAGCCGGTC	1606		
DB	760	-----CAGCGGAAAGAAATTTATCAGGTGATCTGCGCGGTGTTCCCGGC	714		
QY	1607	CGCCAGGATCGGGTGTGCACTGGGAGCGGTAAAGCCAGAGATGTCACAAATAATC	1666		
DB	713	GGGCACAGTACGGCTGTGCACTGGCGGACGGTAAAAAG-----ATC	669		
QY	1667	AATAGCTTACGCTACGATATCTGATCGGCTCCAGCCAGCTTGAATGGAACAACAA	1726		
DB	668	ACCAGCGTTCAGTTATGGCAATCTGATCGGACAGCGGCTTGGAAACGGATGGGACG	609		
QY	1727	GACAAATATCAGGAGGAGAGTATTCATTTGGCGGACAGCGCTGTGGCAGCAA	1786		
DB	608	GTAAACTGCTGAGTCAGGAGGAATATCTCCGTTCCGCGGACCGGGTGTCTGGTGGCCG	549		
QY	1787	ACAGCCAAACAGAACCCAGCTATAAAAAGATTTCGCTATTCCGCAAAAGAACGAGATGCCA	1846		
DB	548	ATGCGGACAGCGGTATTGACTACAAACCCACCGTTATTCCGCAAAAGAGCGGGATGCCA	489		
QY	1847	CCGGTTGTATTATTACGGTTATCGTTATTACCAACCGTGGCGGCGAGATGTTAAGCG	1906		
DB	488	CCGACTGTATTACTACGGCTACCGCTACTATCAGCCGTGGGCGGCGCTGCTGAGTT	429		
QY	1907	CGGACCGGCGGAGAACCATTTGAGCTGAATCTATACGNAATGGTAAGNAATATCTCTG	1966		
DB	428	CAGACCGGCGGAGAACCGTTGACGGGCTGAATCTGTATTCAATGGTAAAAAATAATCCCG	369		
QY	1967	TGAGTTTACAGATGAAATGGATTA	1992		
DB	368	TCTATTACAGATATTAATGGATTA	343		
RESULT 8		A0990013		547 bp	
LOCUS		A0990013		547 bp	
DEFINITION		Photorhabdus luminescens strain W14 M13 library		GSS 14-AUG-2000	
		Photorhabdus luminescens genomic clone PLG00707, genomic survey			
Query Match		878 bp		DNA	
Best Local Similarity		59.2%; Pred. No. 2.7e-39;		linear	
Matches 351; Conservative 0; Mismatches 239; Indels 3; Gaps 3;		59.2%; Pred. No. 2.7e-39;			
QY	1282	GGTGTCTCAGTACGCTAACCCAGCTCAAAATCAAGTGGATACGTTGTTGATCGCGT	1341		
DB	593	GGTGTCTCAGTACGCTAACCCAGCTCAAAATCAAGTGGATACGTTGTTGATCGCGT	534		
QY	1342	GGTCAACCAACAGTTATTACCCGACAGACACATTTATCTGACACACAGGAGAGTTA	1401		
DB	533	GGTCAACCAACAGTTATTACCCGACAGACACATTTATCTGACACACAGGAGAGTTA	474		
QY	1402	AAGCAGGTTAATAATGCCCGCGGAAATAGTG-GTACCGCTACGACAGCAACGGCATGAG	1460		
DB	473	CHNATGACCAAGTGTATACAGCGCGCGNGAATGGTCCGCTATGACAGTATGGAATGCG	414		
QY	1461	ACAACCTGAAAGTGAGTGAACAGCCCAACCCAGAAATATCTAC-GCAGCAACACCGGTAATCT	1519		
DB	413	GCTTATTGAAATATATGACAGCAACCCATATGCCACTGCAACACACGCGAGTCNCCT	354		
QY	1520	ATTTCGCGGACTGGAGCTACGACAAACCCAGAGCAACGCCACAAACGGAAGAGTTAC	1579		
DB	353	ACCTGCGAGGGTTGGAATATACANACCACTCAAGCGCGCCCAATATCACCGAAGACTTGC	294		
QY	1580	AGTTA-TCACTCGGTGAGCGGTGCGGACAGGTACGGGTGTCACCTGGGAGAGC	1638		
DB	293	AAGTTATTGTCTGTCGACAGCAGNNAGACAAAGTACGGGTTCTCANTGSGNAAAA	234		
QY	1639	GGTAAGCCAGAGATGTCACAAATATCAACTACGTTTACAGCTACGATATCTGATCGGC	1698		
DB	233	GGCCANCCNCTGGNATAGTACNATNAGTCAGTACAGTACGATATCTTNCACAC	174		
QY	1699	TCAGCGAGCTTGAATCGGACCAACCAAGGACAAATTTATCAGGAGGAGAGTATTATCA	1758		
DB	173	AGCAGGAAATAGAACTGNATATGCAAGCGGGTAAATTTATCAGTTGGNAAGATTTACCC	114		
QY	1759	TTTGGCGGACAGCGGTGTGGCAGACACACGCAACGCAACGACGCTATTAACGATT	1818		
DB	113	TATGCGGACCGCAATATGCGNCAAGAAATCAGGTTGAAGCTGTNACAAACCAT	54		
QY	1819	CGTATTTCGCGCAAGACGATGCGCGGTGTTGTTATTATTCGTTATCG	1871		
DB	53	CGTATTTCAGNCAAGCGGTGATGCAACAGGACTGTACTATTACCGCTACCG	1		
RESULT 7		C2547320/c		878 bp	
LOCUS		C2547320/c		878 bp	
DEFINITION		SRAA-aa473b07 b1 Strongyloides ratti whole genome shotgun library		GSS 13-MAY-2005	
		(SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.			
ACCESSION		C2547320			
VERSION		C2547320.1		GI:64683141	
KEYWORDS		GSS.			
SOURCE		Strongyloides ratti			
ORGANISM		Strongyloides ratti			
REFERENCE		Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;			
AUTHORS		Panagrolaimoidea; Strongyloidea; Strongyloides.			
		1 (bases 1 to 878)			
		Mitreva, M., McCarter, J.P., Thompson, F., Viney, M., Pape, D.,			
		Ritter, E., Martin, J., Wylie, T., Dante, M., Waterston, R.H.,			
		Clifton, S.W. and Wilson, R.			
TITLE		Genome Survey sequences from the rat parasitic nematode			
JOURNAL		Strongyloides ratti			
COMMENT		Unpublished (2005)			
		Contact: Mitreva M			
		Washington University in St. Louis			
		Washington University School of Medicine			
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
		Tel: 314 286 1800			

```
sequence.
ACCESSION AQ990013
VERSION AQ990013.1 GI:9648607
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 547)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1. 547
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00707"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
ORIGIN
Query Match 5.6%; Score 152.6; DB 9; Length 547;
Best Local Similarity 76.18; Pred. No. 9.9e-29;
Matches 188; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1753 TATCCATTTTCGGCGGACAGCGCTGTGGCGAGCAACAGCCAGGCGGATATAA 1812
Db 1 TATCCGATGCGCGTACCGCGATATGGCGGAGAAATCAGACAGAGCCAGCTACAA 60
QY 1813 ACGATTGCTATTCGCGCAAGACGAGATGCCACCGGTTGTATTATTACGGTTATCGT 1872
Db 61 TTATTTCGTTACTCCGTAAGAGCGGATGCCACTGGATTGTATTATTACGGCTACCGT 120
QY 1873 TATTACCAACCGTGGCGGCGAGATGGTTAGCGCGGACCGGAGGACCATTTGATGGG 1932
Db 121 TATTATCAACCTTGGGTGGTGGATGGTTGATGCTGATCCGGCGGAAACCGTGGATGG 180
QY 1933 CTGAATCTATACCGAATGGTAAGAAATAATCTGTGAGTTTACAGATGAATAATGGATTA 1992
Db 181 CTGAATTTGATACCGAATGGTGGAGGAATAACCCCATCATTTGACTGACCATGACGGATTA 240
QY 1993 GCGCCAG 1999
Db 241 GCACCG 247
RESULT 9
AQ990147 312 bp DNA linear GSS 14-AUG-2000
LOCUS Rf00869 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG00869, genomic survey
sequence.
sequence.
ACCESSION AQ990147
VERSION AQ990147.1 GI:9648741
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 312)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1. 312
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00869"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
ORIGIN
Query Match 5.4%; Score 148.8; DB 9; Length 312;
Best Local Similarity 71.4%; Pred. No. 8.8e-28;
Matches 222; Conservative 0; Mismatches 82; Indels 7; Gaps 2;
QY 976 AATATCGTAATGATCGGAGCCACTCGCTTTTGGCGCAATCAGAAAGTAGC-CCCGGA 1034
Db 2 AATATTGTAATGATCAGAAAGCAACTCGATTCTGGCGTAATCAGAAATAGTACCCGGA 61
QY 1035 GAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCCACCGGGCGGAAATGGC 1094
Db 62 AATATGGTATACCTATGATTCTGTACCACTTATCATAGCAACCGGCGCGAATGGC 121
QY 1095 CAATATCGGTACGACAAACAACTTCCCTC-----CCCTGGCTACCTTCTGACAA 1148
Db 122 TAACATTAGTCAGCAAGGAGCCAGCTCCCTCTTTAGTTTACCCCTCTTCTACCGATGA 181
QY 1149 CAATACCTACACTATATCTACTCGAGCTACAGCTATGATCAAGTGGTATCTGACGCA 1208
Db 182 CAATACCTATACCTATATCTACTCGCACTTATACCTACGAGTAGCGGCAACCTGACACA 241
QY 1209 AATTCGCGACAGCTCGCCAGTACCAGAACAACTACACCGTGGCTATCACCCCTCTCAAA 1268
Db 242 AATCCCGCATACGCTTCGCGCAGGACATAAATCTNCNCNCCAGATATTACCATTTNAAA 301
QY 1269 CCGCAGCAATC 1279
Db 302 CCGCAATAACC 312
RESULT 10
AW901477/c 733 bp mRNA linear EST 24-MAY-2000
LOCUS AW901477
```


Db 1041 AA 1100

Qy 2613 TGTGGCAATTCCTGACATGAAGCAATATAAAATCATTTGAAAGGACATAAATTA 2672

Db 1101 NNN 1160

Qy 2673 TAGGATATCAACA 2685

Db 1161 AAAAAAAAAAAAAA 1173

RESULT 13

CNS018GS/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC

BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL109318

VERSION

AL109318.1 GI:5629622

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 942)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

1..942

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACN13P09"

/clone_lib="DrosBAC"

/plasmid="pBelobAC11"

/note="end : T7"

ORIGIN

Query Match 2.5%; Score 68; DB 10; Length 942;

Best Local Similarity 35.9%; Pred. No. 2.5e-06;

Matches 182; Conservative 61; Mismatches 264; Indels 0; Gaps 0;

Qy 2174 ACAGAGGTTACTAAAGGTATAGAAAAAGTCAATATATATAGCCGACTTGAAGAAA 2233

Db 593 AAGCAAAAAACGAAARGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 534

Qy 2234 ACAGCTCCCTTCAGAAAAATCAAAACGATCTTCTTTAGGATCTGAATATCCGTT 2293

Db 533 AAAAAATTNGAGACNAACGAAAGAAAAAAGAAAAAAGTAAAGAAAAAAGAAAAA 474

Qy 2294 ATATGGAAGAACATACAGATACGATATCAGATATATGCGGAGAGCATATAATAGAA 2353

Db 473 ANANN 414

Qy 2354 GTAATCACCCCTGATTTTATTCAGAAACCGATTTCTTTGCGTTAAATGGATAAAGTAAA 2413

Db 413 AAMACMBAARAAAAAAMWAAACCGGTARAWTTTAAATGTGAACCAAAATATAAAAAA 354

Qy 2414 AAAAAATGATTTATTCGGTGAAGAAAAATTTATCGCGCAATGGAGGTTTATCATG 2473

Db 353 AAAAAAAMWAAWARTAMWAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 294

Qy 2474 ATTTAAAAATAAACATCAGATTCAGATGTCACTATGATGATGGCCCATCCCTATACGC 2533

Db 293 WAAMRAAAWAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 234

Qy 2534 AATTGAGTAAATGAAGAAAGAGCGCTGTTGCAAGAAACAGAACCCGCTATTGCAATAGATA 2593

Db 233 AAATTTAAATAAANWAAWATGAWAAWATMGTTAAWAAATCGTTAMGAAAAWAAW 174

Qy 2594 GAGATATATTTCAAGGTTGGCAAAATTCCTGCAATGAAGCAATTAATAATCAT 2653

Db 173 AAAMWAAAAATATAWAAWAAWCAAAATTTATGAATTWAAWAAWAAWAAWAAWAA 114

Qy 2654 TGAAGGACATATAATTAATAGATAT 2680

Db 113 WAAAAGTAAMWAAWAAWCGGATTTGRTT 87

RESULT 14

CG753732/c

LOCUS

DEFINITION

P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION

CG753732

VERSION

CG753732.1 GI:37978509

KEYWORDS

GSS.

SOURCE

Pristionchus pacificus

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE

1 (bases 1 to 1811)

AUTHORS

Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.

TITLE

An integrated physical and genetic map of the nematode Pristionchus pacificus

JOURNAL

Mol. Genet. Genomics 269 (5), 715-722 (2003)

COMMENT

12884007

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Classes: BAC ends.

FEATURES

Location/Qualifiers

1..1811

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

Query Match 2.4%; Score 65.4; DB 10; Length 1811;

Best Local Similarity 36.4%; Pred. No. 1.4e-05;

Matches 284; Conservative 0; Mismatches 461; Indels 0; Gaps 0;

Qy 1974 ACAAGATGAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTT 2033

Db 1621 ANAAAAANNAA 1562

Qy 2034 TGATGAATTAATTCAAATTCGACGCCCAAAAGTTTCACATGTTGTCAATGGACGAGAA 2093

Db 1561 AAAAAANNAA 1502

Qy 2094 AGAGACGAGTTATACAAAAATAATCAATTTGAAAGTGGTTGCGTGGTATCCGATCC 2153

Db 1501 AAAAAANNAA 1442

[illegible]

RESULT 15	CG744812/c	CG744812	1353 bp	DNA	linear	GSS 24-OCT-2003
LOCUS						
DEFINITION						P037-3-B03.ya Ppa EcoRI BAC Library <i>Pristionchus pacificus</i> genomic, genomic survey sequence.

FEATURES
SOURCE

```

/db_xref="taxon:54126"
/clone_lib="ppa Ecoli BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

```

ORIGIN

Query Match	2.4%	Score 65	DB 10	Length 1353
Best Local Similarity	38.7%	Pred. No. 1.7e-05		
Matches 287	Conservative 0	Mismatches 454	Indels 0	Gaps 0
Qy	1947	AATGGTGAAGAAATAATCCTGTGAGTTTACAAAGATGAAATGGATTAGCGCCAGAAAGG	2006	
Db	1059	AAANNNAANANANNNNNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANN	1000	
Qy	2007	GAAATATACCAAGAGGTAAATTTCTTTTGATGAATTAAATTCAAATTGGCGACCCAAAAG	2066	
Db	999	AAANNAA	940	
Qy	2067	TTACATGTTGTCAATGGACGACGAGAGACAGTTATACAAAAATAAATCATTTGAA	2126	
Db	939	AA	880	
Qy	2127	AGTGGTTTCGTGCGTGATTCGATCCGATCCGTGCGGTATTTCGTAAGCCACGAAGAGTTACT	2186	
Db	879	AA	820	
Qy	2187	AAAAGGTATGAAAAAGTCAAATCATATATAGCCGACTTGAAGAAAAACAGCTCCCTTTC	2246	
Db	819	AA	760	
Qy	2247	AGAAAAATCAAAACGAATCTTCTTTAGGATCTGGAATATATCCGGTTATATGCGCAAGAAC	2306	
Db	759	AA	700	
Qy	2307	CATACAAGATACGATATCAGAATATGCGAAGAGCATAAATATAGAAGTAAATCACCTGA	2366	
Db	699	NAA	640	
Qy	2367	TTTTTATTCAGAAACCGATTTCTTTGGGTTAAATGGATAAAAGTGAANAAATGATTTTC	2426	
Db	639	AAANAAANNA	580	
Qy	2427	CGGTGAAGAAAAATTTATGCGGCAATGGAGGTTAAGGTTTATCATGATTTAAAAAATAA	2486	
Db	579	AA	520	
Qy	2487	ACAATCAGAAATTAATGTCGAACTATGCAATTTGGGCCATCCCTATACGCAATTGAGTAATGA	2546	
Db	519	AA	460	
Qy	2547	AGAAAGAGCGCTGTGCAAGAAACAGAACCCGCTATTGCAATAGATAGAAATATAATTT	2606	
Db	459	ANNAANNA	400	
Qy	2607	CAAAAGGTGTGGCAAAATTCCTGCAAAATGAAAGCAATTTAAAAAATTCATTTGAAAGGACATAA	2666	
Db	399	AAAAANAAA	340	
Qy	2667	AATTAATAGGATATCAACAGA	2687	
Db	339	AAAAAAAAAAAAAAAAAAAAAAAAA	319	

Search completed: December 14, 2005, 02:17:13
Job time : 9688 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 17:17:29 ; Search time 1489 Seconds
(without alignments)
12286.488 Million cell updates/sec

Title: US-10-647-956A-5
Perfect score: 2745
Sequence: 1 atgagcagttacaattctgc.....taggaatgcggagaacttca 2745

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2745	100.0	2745	6 ABS52585	Abes52585 P. lumine
2	2653.8	96.7	2748	12 ADM61381	Adm61381 Photorhab
3	2329	84.8	2748	10 ACF69438	Acf69438 Photorhab
4	2329	84.8	110000	10 ACF67367_23	Continuation (24 o
5	2329	84.8	110000	10 ACF67367_24	Continuation (25 o
6	2329	84.8	110000	10 ACF65386_4	Continuation (5 of
7	1442.2	52.5	2817	12 ADM61384	Adm61384 Photorhab
8	1440.6	52.5	2817	12 ADR18627	Adr18627 Photorhab
9	1440.6	52.5	2817	13 ADR21537	Adr21537 Photorhab
10	1321.4	48.1	2817	10 ACF69434	Acf69434 Photorhab
11	1321.4	48.1	110000	10 ACF65386_5	Continuation (6 of
12	1013.2	36.9	2811	10 ACF70848	Acf70848 Photorhab
13	1013.2	36.9	110000	10 ACF67367_39	Continuation (40 o
14	1013.2	36.9	110000	10 ACF65388_08	Continuation (9 of
15	1012.4	36.9	37948	2 AAZ06831	Aaz06831 Photorhab
16	1004.6	36.6	2883	12 ADM61382	Adm61382 Photorhab
17	1004.6	36.6	2883	12 ADR18623	Adr18623 Photorhab
18	1004.6	36.6	2883	13 ADR21526	Adr21526 Photorhab
19	989.4	36.0	2913	10 ACF69431	Acf69431 Photorhab

	20	977.4	35.6	2880	10	ACF69421	Acf69421	Photorhab
	21	972.4	35.4	2898	10	ACF71155	Acf71155	Photorhab
C	22	972.4	35.4	110000	10	ACF67367_42	Continuation (43 o	
	23	972.4	35.4	110000	10	ACF65388_05	Continuation (6 of	
	24	962	35.0	3132	2	AAT68850	Aat68850	Photorhab
	25	962	35.0	3132	12	ADM61380	Adm61380	Photorhab
	26	962	35.0	3132	13	ADR21505	Adr21505	Photorhab
	27	960.4	35.0	3132	2	AAV29927	AAV29927	tccC gene
	28	957.2	34.9	2850	12	ADM61383	Adm61383	Photorhab
	29	957.2	34.9	2850	12	ADP18625	Adp18625	Photorhab
	30	930	33.9	3132	10	ACF71170	Acf71170	Photorhab
	31	930	33.9	110000	10	ACF67367_43	Continuation (44 o	
C	32	930	33.9	110000	10	ACF65388_04	Continuation (5 of	
	33	874	31.8	110000	10	ACF65388_05	Continuation (6 of	
	34	730.8	26.6	2889	13	ADR21530	Adr21530	Xenorhabd
	35	730.8	26.6	2889	14	AEB47813	Aeb47813	Native Xp
	36	730.8	26.6	2947	13	ADR21533	Adr21533	Xenorhabd
	37	730.8	26.6	2947	14	AEB47818	Aeb47818	XbaI to X
	38	730.8	26.6	7508	13	ADR21534	Adr21534	Xenorhabd
	39	730.8	26.6	7508	14	AEB47819	Aeb47819	XbaI to X
	40	691.2	25.2	37544	3	AAA50029	Aaa50029	Cosmid cH
	41	666	24.3	3048	13	ADR20366	Adr20366	Recombina
	42	666	24.3	3048	13	ADR21495	Adr21495	Xenorhabd
	43	666	24.3	3051	12	ADM61357	Adm61357	Xenorhabd
C	44	666	24.3	39005	13	ADR20357	Adr20357	Recombina
	45	666	24.3	39005	13	ADR21486	Adr21486	Xenorhabd

ALIGNMENTS

RESULT 1
ABS52585
ID ABS52585 standard; DNA; 2745 BP.
XX
AC ABS52585;
XX
DT 30-DEC-2002 (first entry)
XX
DE P. luminescens (W-14) tccC2 gene.
XX
KW Gene, ds; toxin A; toxin B; TcdA; protoxin; TcdB; TccC2; transgenic;
KW monocot cell; dicot cell; oral toxin; insect; pest; TcBA.
XX
OS Photorhabdus luminescens.
XX
PH Key Location/Qualifiers
FT CDS 1..2745 /*tag= a
FT /product= "TccC2"
FT /partial
FT /note= "No stop codon shown"
XX
PN US2002078478-A1.

XX
PD 20-JUN-2002.
XX
PF 26-MAR-2001; 2001US-00817514.
XX
XX 24-MAR-2000; 2000US-0191806P.
XX
PR (FFRE/) FFRENCH-CONSTANT R H.
PA (BOWE/) BOWEN D.
PA (ROCH/) ROCHELEAU T A.
PA (WATE/) WATERFIELD N R.
XX
PI Ffrench-Constant RH, Bowen D, Rocheleau TA, Waterfield NR;
XX
XX WPI; 2002-655379/70.
DR P-PSDB; ABG32653.
XX
XX Novel nucleic acid sequences which encode genes, tcdB and tccC2 from
PT Photorhabdus luminescens W-14, useful in heterologous expression of

orally active insect toxins.

Claim 3; Page 24-27; 40pp; English.

The invention discloses an isolated nucleic acid that encodes TcdB or TccC2 from *Photobacterium luminescens* W-14. Also disclosed is a transgenic monocot or dicot cell and a transgenic plant (including the seeds) both with genomes comprising tcdB and tccC2 nucleic acids. The nucleic acids are useful for producing Toxin A or B of *P. luminescens* W-14 in a heterologous host and for encoding TcdB or TccC2 for producing an orally active insect toxin in a host, where the host also expresses TcdA or TcdB from *P. luminescens* W-14. Heterologous expression of Toxin A does not afford the level of oral toxicity to insects as that of the native toxin, but the coexpression increases this toxicity. The transgenic plants expressing effective amounts of the toxins protect themselves from insect pests. When the insects feeds on the transgenic plant it also ingests the toxins and this deters the insect from further biting into the plant and may even harm or kill the insect. The sequence presented is the *P. luminescens* (W-14) tccC2 gene

Sequence 2745 BP; 905 A; 623 C; 606 G; 611 T; 0 U; 0 Other;

Query Match 100.0%; Score 2745; DB 6; Length 2745;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGCAGTTACAAATCTGCATTTGACCAAAAGACCCCTCGATTAGGTATTAGATAAC	60
Db	1	ATGAGCAGTTACAAATCTGCATTTGACCAAAAGACCCCTCGATTAGGTATTAGATAAC	60
Qy	61	AGGAAATTAATGATGACGTTTGAATATCTACGCTCAAGCTGACGAAACAGTGAT	120
Db	61	AGGAAATTAATGATGACGTTTGAATATCTACGCTCAAGCTGACGAAACAGTGAT	120
Qy	121	GAATTAATTAAGTTTATGAGTTCAATATTTCCGGGATTTACAGGTAAAAGCACCATCCT	180
Db	121	GAATTAATTAAGTTTATGAGTTCAATATTTCCGGGATTTACAGGTAAAAGCACCATCCT	180
Qy	181	CGTAAAATTAACACGAGCGGCCCAATTTCAATTCGTTCTTTTAAATCTTCCGGTCAA	240
Db	181	CGTAAAATTAACACGAGCGGCCCAATTTCAATTCGTTCTTTTAAATCTTCCGGTCAA	240
Qy	241	GTTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCCTCAATGATATTGAAAGT	300
Db	241	GTTTTACGTGAAGAAAGTTGATGCGCGTCCGACTATTACCCCTCAATGATATTGAAAGT	300
Qy	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCAATCGTTATGAAGATAAC	360
Db	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCAATCGTTATGAAGATAAC	360
Qy	361	ACCTTCCCGTCTGCTGCTGCTATACCGAAACAAGTACGCGAGGAGAGAAACGACC	420
Db	361	ACCTTCCCGTCTGCTGCTGCTATACCGAAACAAGTACGCGAGGAGAGAAACGACC	420
Qy	421	GAAAGTCTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACTCCGCGGTGAG	480
Db	421	GAAAGTCTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACTCCGCGGTGAG	480
Qy	481	TGTTCCGCCATTAACGATACCGCGGACTTACTCAATAGCCCTTCTCGGCTGGC	540
Db	481	TGTTCCGCCATTAACGATACCGCGGACTTACTCAATAGCCCTTCTCGGCTGGC	540
Qy	541	GTCTGTCTATCACAATCTCAACAACTGTTACCGATAACAGGATGCGGACTGACAGGT	600
Db	541	GTCTGTCTATCACAATCTCAACAACTGTTACCGATAACAGGATGCGGACTGACAGGT	600
Qy	601	GAAACACGAGCCCTCTGSCAAACAAAACCTGAGTAGTGATGCTATATCACCACCAAGTAAC	660
Db	601	GAAACACGAGCCCTCTGSCAAACAAAACCTGAGTAGTGATGCTATATCACCACCAAGTAAC	660
Qy	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTG	720
Db	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTG	720

Qy	721	GCCTATGATGTGGCGCGCAGCTAAAGGGAGTTGGTTAACTAACTCAAAAGGTGAGGGGAA	780
Db	721	GCCTATGATGTGGCGCGCAGCTAAAGGGAGTTGGTTAACTAACTCAAAAGGTGAGGGGAA	780
Qy	781	CAGGTGATTATCAAAATCGCTAACTACTCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Db	781	CAGGTGATTATCAAAATCGCTAACTACTCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Qy	841	GGTAACGGGATTTGCTCACTGAATACAGCTAGAAACCGGAAACCCAAAGGCTTATCGGCATT	900
Db	841	GGTAACGGGATTTGCTCACTGAATACAGCTAGAAACCGGAAACCCAAAGGCTTATCGGCATT	900
Qy	901	ACCACCTCGCGCTCATCAGACGCCAAGGTGTTGCAAGACCTAGCTATCAATATGACCCA	960
Db	901	ACCACCTCGCGCTCATCAGACGCCAAGGTGTTGCAAGACCTAGCTATCAATATGACCCA	960
Qy	961	GTAGGCAATGTCTAATTAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	961	GTAGGCAATGTCTAATTAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	1021	AAAGTAGCCCCGGAGAATAGCTATACCTAGATTCCCTGTATCAGCTTATCAGGGCCACC	1080
Db	1021	AAAGTAGCCCCGGAGAATAGCTATACCTAGATTCCCTGTATCAGCTTATCAGGGCCACC	1080
Qy	1081	GGCGCGAAATGCGCAATATCGGTGACGAAACCAACTTCCCTCCCTCGCTACCT	1140
Db	1081	GGCGCGAAATGCGCAATATCGGTGACGAAACCAACTTCCCTCCCTCGCTACCT	1140
Qy	1141	TCTGACAAACAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Db	1141	TCTGACAAACAATACCTACACTAATCTACTCGAGCTACAGCTATGATCAAGTGGTAAT	1200
Qy	1201	CTGACGCAATTCGGCAGCTCGCAGCTACCCAGAACTACACCTACACCTGGGTATCACC	1260
Db	1201	CTGACGCAATTCGGCAGCTCGCAGCTACCCAGAACTACACCTACACCTGGGTATCACC	1260
Qy	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACCTAACCCAGATCCAAATCAAGTG	1320
Db	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACCTAACCCAGATCCAAATCAAGTG	1320
Qy	1321	GATACGTTGTTGATCGCGTGTACCAAAACAGTTTATTTACCCGGACAGACACTTATC	1380
Db	1321	GATACGTTGTTGATCGCGTGTACCAAAACAGTTTATTTATCCCGACAGACACTTATC	1380
Qy	1381	TGACACCAAGAGAGGTTAAAGCAGGTTAAATAGCCCGGGAAATGAGTGGTACCGC	1440
Db	1381	TGACACCAAGAGAGGTTAAAGCAGGTTAAATAGCCCGGGAAATGAGTGGTACCGC	1440
Qy	1441	TACGACGCAACCGCATGACAACTGAAAGTCAAGTGAAACAGCAACCCAGAGCAACGCC	1500
Db	1441	TACGACGCAACCGCATGACAACTGAAAGTCAAGTGAAACAGCAACCCAGAGCAACGCC	1500
Qy	1501	CAGCAACAAACGGGTAATCTATTTGCGGGACTCGAGCTACGCAACCCAGAGCAACGCC	1560
Db	1501	CAGCAACAAACGGGTAATCTATTTGCGGGACTCGAGCTACGCAACCCAGAGCAACGCC	1560
Qy	1561	ACAACAAACGGAAGGTTACGTTTATCACTCGGTGAAGCCGCTCGCGCACAGGTACGG	1620
Db	1561	ACAACAAACGGAAGGTTACGTTTATCACTCGGTGAAGCCGCTCGCGCACAGGTACGG	1620
Qy	1621	GTCTTGCACCTGGGAGAGCGGTAGCCAGAGATGTCAACAATTAATCAACTACGTTACAGC	1680
Db	1621	GTCTTGCACCTGGGAGAGCGGTAGCCAGAGATGTCAACAATTAATCAACTACGTTACAGC	1680
Qy	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAAGTGAACCAACCAAGGACAAATTTATCAGC	1740
Db	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAAGTGAACCAACCAAGGACAAATTTATCAGC	1740
Qy	1741	GAGAGAGAGTATTATCCATTTGGCGGGAAGCGCTGTGGGACGAAACAGCCAAACAGAA	1800
Db	1741	GAGAGAGAGTATTATCCATTTGGCGGGAAGCGCTGTGGGACGAAACAGCCAAACAGAA	1800

Db 301 CGCCGGTGTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC 360
Qy 361 ACCCTTCCCGGTGCTGCTGCTGCTATCACCGAACAAGTACAGGAGAGAGAAACGACC 420
Db 361 ACCCTTCCCGGTGCTGCTGCTGCTATCACCGAACAAGTACAGGAGAGAGAAACGACC 420
Qy 421 GAAGCTGCTTACTCTGGGCGGCAATACGCCGCAAGAAAAGATTACAACCTCGCGGTGAG 480
Db 421 GAAGCTGCTTACTCTGGGCGGCAATACGCCGCAAGAAAAGATTACAACCTCGCGGTGAG 480
Qy 481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGC 540
Db 481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGC 540
Qy 541 GTGCTGCTATCACAACTCTCAACAACTGTTACCGATAACCAAGGATGCCGACTGACAGGT 600
Db 541 GTGCTGCTATCACAATCTCAGCAACTACTGTCGATGATAAAAATGCTGACTGACAGGT 600
Qy 601 GAAGACGAGCCTCTGGCAACAAAACCTGAGTAGTGTATGCTATATACCCAAAGTAAC 660
Db 601 GAAGACAAAAGCCTCTGGCAGCAAAAACCTGAGCAGTGTATATACCCAAAATAAA 660
Qy 661 ACTGATGCCACCGGGCTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG 720
Db 661 GCCGATGCCACCGGGCTTATTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG 720
Qy 721 GCCTATGATGTGGCCGGGAGCTAAAAGGGAGTTGGTTAAACCTCAAAGGTGAGCGGAA 780
Db 721 GCCTACGACGTAGCGGGGAGCTAAAAGGGCTTGGTTGACACTCAAAGGTGAGCGGAG 780
Qy 781 CAGTGATATCAAACTCGCTAACCTACTCCGCCCGGGCAAAAATACGTGAGAGCAC 840
Db 781 CAGTGATATCAAACTCGCTAACCTACTCCGCCCGGGCAAAAATACGTGAGAGCAC 840
Qy 841 GGTAAAGGGATTGTCACTGAATACAGCTACGAACCGGAAACCCAAACCGCTTATCGGCATT 900
Db 841 GGTAAAGGGATTGTCACTGAATACAGCTATGAACAGAAACCCAAACCGCTTATCGGTATT 900
Qy 901 ACCACTCGCGTCACTCAGACGCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA 960
Db 901 GCCACCGCGCTCGCTCAGACGCAAGGTGTGCAAGACTTACGCTATCAATATGACCCG 960
Qy 961 GTAGGCAATGTCAATATCCGTAATGATCGGAGGCCACTCGCTTTTGGCGCAATCAG 1020
Db 961 GTAGGCAATGTCAATATCCGTAATGATCGGAGGCCACTCGCTTTTGGCGCAATCAG 1020
Qy 1021 AAAGTAGCCCGGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
Db 1021 AAAGTGTCCCGGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGTGCACC 1080
Qy 1081 GGGCGGAAATGGCCAAATATCGGTACGAAACCAAACTTCCCTCCCTCGCGTACCT 1140
Db 1081 GGGCGGAAATGGCCAAATATAGGTACGAAATAACCAACTGCGCTCCCTCGCGTACCT 1140
Qy 1141 TCTGACAACTACTACCTAACTATCTCGAGCTACAGCTATGATCAGGTGTAAT 1200
Db 1141 TCTGACAACTACTACCTAACTATCTCGAGCTACAGCTATGATCAGGTGTAAT 1200
Qy 1201 CTGACGCAAAATTCGGCACAGCTCGCCAGTACCCAGAACCACTACACCGTGGCTATCAC 1260
Db 1201 CTGACGCAAAATTCGGCACAGCTCGCCAGTACCCAGAACCACTACACCGTGGCTATCAC 1260
Qy 1261 CTCTCAAAACCGAGCAATTCGGGGTGTCTCAGTAGCTTAACCGATCCAAATCAAGTG 1320
Db 1261 CTCTCAAAACCGAGCAATTCGGGGTGTCTCAGTAGCTTAACCGATCCAAATCAAGTG 1320
Qy 1321 GATACGTTGTTGATCGCGGTGTCACCAACCGAGTTTATACCGGACGACACTTATC 1380
Db 1321 GATACGTTGTTGATCGCGGTGTCACCAACCGAGTTTATACCGGACGACACTTATC 1380
Qy 1381 TGGACACCGAGGAGGTTAAAGCAGGTTAAATGAGGTGAGGAAATGAGTGTACCGC 1440
Db 1381 TGGACACCGAGGAGGTTAAAGCAGGTTAAATGAGGTGAGGAAATGAGTGTACCGC 1440

Qy 1441 TACGACAGCAACGGCATGAGACAACTGAAGTGAGTGAACAGCAACCCCAAGATACTACG 1500
Db 1441 TACGACAGCAACGGCATGAGACAACTGAAGTGAGTGAACAGCAACCCCAAGATACTACG 1500
Qy 1501 CAGCAACAAACGGGTAATCTATTTCGCGGAGCTGAGACTACGCAACAACCCAGAGCAACGCC 1560
Db 1501 CAGCAACAAACGGGTAATCTATTTCGCGGAGCTGAGACTACGCAACAACCCAGAGCAACGCC 1560
Qy 1561 ACAACAAACGGAGAGTTACACGTTATCACTCGGTGAAGCGGTGCGGCACAGGTACGG 1620
Db 1561 ACAACAAACGGAGAGTTACACGTTATCACTCGGTGAAGCGGTGCGGCACAGGTACGG 1620
Qy 1621 GTGTTGCACTGGGAGAGCGGTGAAGCAGAGATGTCAACAATAATCAACTACGTTACAGC 1680
Db 1621 GTGTTGCACTGGGAGAGCGGTGAAGCAGAGATGTCAACAATAATCAACTACGTTACAGC 1680
Qy 1681 TAGCATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAAATTTATCAGC 1740
Db 1681 TAGCATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAAATTTATCAGC 1740
Qy 1741 GAGGAAGAGTATTATCCATTTGGCGGAGACAGCGCTGTGGGACGAAACAGCCAAACAGAA 1800
Db 1741 GAGGAAGAGTATTATCCATTTGGCGGAGACAGCGCTGTGGGACGAAACAGCCAAACAGAA 1800
Qy 1801 GCCAGCTATAAAACGATTCGCTATTTCGCGCAAGACGAGATGCCACCGGGTTGTATTAT 1860
Db 1801 GCCAGCTATAAAACGATTCGCTATTTCGCGCAAGACGAGATGCCACCGGGTTGTATTAT 1860
Qy 1861 TAGCGTTATCGTTATTACAAACCGTGGCGGAGCAGATGTTAAGCGCGGACCCGCGCAGGA 1920
Db 1861 TAGCGTTATCGTTATTACAAACCGTGGCGGAGCAGATGTTAAGCGCGGACCCGCGCAGGA 1920
Qy 1921 ACCATTGATGGGCTGAATCTATACCGAATGGTGAAGAAATAATCCTGTGAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGGCTGAATCTATACCGAATGGTGAAGAAATAATCCTGTGAGTTTACAAGAT 1980
Qy 1981 GAAAAATGATAGCGCCAGAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 1981 GAAAAATGATAGCGCCAGAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Qy 2041 TTAATAATTCAAAATTTGGCAGCCAAAAGTTTCACTGTTGTCAAATGGGAACGAGAAAGAGC 2100
Db 2041 TTAATAATTCAAAATTTGGCAGCCAAAAGTTTCACTGTTGTCAAATGGGAACGAGAAAGAGC 2100
Qy 2101 AGTTATACAAAAATAAATCATTTGAAAGTGGTTGCTGCGTGATTTCCGATCCGTCGGGT 2160
Db 2101 AGTTATACAAAAATAAATCATTTGAAAGTGGTTGCTGCGTGATTTCCGATCCGTCGGGT 2160
Qy 2161 TATTTGCTAAGCCACGAGGTTACTAABAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCACGAGGTTACTAABAGGTATAGAAAAGTCAAAATCATATATAGC 2220
Qy 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
Db 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAAGATACGATATCAGAAATATGCCGAAGAG 2340
Qy 2341 CATATAATAGAAAGTAAATCACCTGATTTTATTCAGAAAACCGATTTCTTTGGGTTAATG 2400
Db 2341 CATATAATAGAAAGTAAATCACCTGATTTTATTCAGAAAACCGATTTCTTTGGGTTAATG 2400
Qy 2401 GATAAAAGTGAATAAATGATTTATTCGGTGAAGAAAAATTTATGCGCAATGGAGGTT 2460
Db 2401 GATAAAAGTGAATAAATGATTTATTCGGTGAAGAAAAATTTATGCGCAATGGAGGTT 2460
Qy 2461 AAGGTTTATCATGTTTAAAAATAAACAATCAAGATTAATGTCAACTATGCAATTTGGCC 2520
Db 2461 AAGGTTTATCATGTTTAAAAATAAACAATCAAGATTAATGTCAACTATGCAATTTGGCC 2520

QY 2521 CATCCCTATACGAATTGAGTAATGAAGAAAGAGCGCTGTTCAGAAACAGAACCCGCT 2580
Db |||||
2521 CATCCCTATACGAATTGAGTAATGAAGAAAGAGCGCTGTTCAGAAACAGAACCCGCT 2580
QY 2581 ATTGCAATAGATAGAGATATATTTTCAAAAGGTGTGGCAAAATTCCTGACAATGAAGCA 2640
Db |||||
2581 ATTGCAATAGATAGAGATATATTTTCAAAAGGTGTGGCAAAATTCCTGACAATGAAGCA 2640
QY 2641 ATTAAAAATCATTTGAAAGGACATATAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Db |||||
2641 ATTAAAAATCATTTGAAAGGACATATAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
QY 2701 CGCTCGCGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745
Db |||||
2701 CGCTCGCGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 3
ACF69438
ID ACF69438 standard; DNA; 2748 BP.
XX AC ACF69438;
XX AC
DT 20-NOV-2003 (first entry)
XX DE
XX DE Photorhabdus luminescens nucleotide sequence #7905.
XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX KW
XX OS Photorhabdus luminescens.
XX PN
XX PN W0200294867-A2.
XX PD
XX PD 28-NOV-2002.
XX PF
XX PF 07-FEB-2002; 2002WO-IB003040.
XX PR
XX PR 07-FEB-2001; 2001FR-00001659.
XX PA (INSP) INST PASTEUR.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX DR
XX DR WPI; 2003-148459/14.
XX PT
XX PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
PS Claim 2; SEQ ID NO 7905; 1205pp; French.
XX CC
XX CC The invention relates to the isolation of genes and their encoded
XX CC proteins from Photorhabdus luminescens. The isolated sequences are
XX CC sources of probes and primers for detecting the genome of P. luminescens
XX CC and related species; to study polymorphisms; for gene analysis and for
XX CC detection/amplification of the genes. Antibodies (Ab) raised against the
XX CC polypeptides encoded by the genes are used for detection/identification
XX CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX CC carry a gene-containing vector are used to select compounds that
XX CC modulate, regulate, induce or inhibit expression of the genes in plants,
XX CC animals or microorganisms other than P. luminescens and are able to alter
XX CC response or sensitivity to toxins and antibiotics produced by P.
XX CC luminescens. Cells transformed to express the genes are useful for
XX CC recombinant production of the proteins, particularly toxins and
XX CC antibacterials useful as insecticides, bactericides and fungicides. The
XX CC genes, proteins, vectors containing the genes and Ab are also useful
XX CC therapeutically (to treat microbial infection by bacteria or fungi that
XX CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
XX CC biopesticides. Other uses of the genes and the proteins are as virulence

CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 2748 BP; 914 A; 606 C; 615 G; 613 T; 0 U; 0 Other;
Query Match 84.8%; Score 2329; DB 10; Length 2748;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 2485; Conservative 0; Mismatches 260; Indels 0; Gaps 0;
QY 1 ATGAGCAGTTTCAATTTCTGCAATTTGACCAAAAGAGACCCCTCGATTAAAGGTATTAGATAAC 60
Db |||||
1 ATGAGCAGTTTCTGTTCTGAAATTTGACAAAAAACACCAATTAATCATGTTATTGGATAAC 60
QY 61 AGGAAATTAATTTAGTACGTACTTTTAGAATATCTACGCACCTCAAGCTGACGAAACACGTGAT 120
Db |||||
61 AGGAGTTTAAATGTTACGTACTTTTAGAATATCTACGTACTCAAGCTGATGAAAAACGTGAT 120
QY 121 GAATTAATTTACGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCATCTCT 180
Db |||||
121 GAATTAATTTACGTTCTATGAGTTCAATATTTCAAGGATTTTGAAGTAAAAAGTACTGATCTCT 180
QY 181 CGTAAAAATAAAAAACCCAGAGCGSCCAAAATTTTCATTCGTGTCTTTTAAATCTTTGCCGCTCAA 240
Db |||||
181 CGTAAAGATAAAAAATCAGAGCGGCCCAATTTTCATTCGGGTCTTTTAAATCTCTCGCGGTGAT 240
QY 241 GTTTTACGTGAAGAAAGTGTGATCGCGGTGCGACTTATTAACCTCAATGATATTGAAAGT 300
Db |||||
241 GTTTTACGTGAAGAAAGTGTGATCGCGGTGCGAACTTATCATCTCAACGATTTTGAAGGT 300
QY 301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCGCAAAACCATCGTTTATGAAGATAAC 360
Db |||||
301 CGCCCGGTATTAAACCATCAATGCAACCGGTGTCGCGCAAGACTTATCACTACGAAGATAAC 360
QY 361 ACCTTCCCGGTGCTGCTGCTACCGCAACAGTACAGCGAGAGAGAAACGAC 420
Db |||||
361 ATCTTACCCCGGTGCTGCTGCTATCACCAGACAGGTGCGAGCAGAGAGAAATGACC 420
QY 421 GAACGCTTTATCTGGCCCGGCAATAGCCGCAAGAAAAAGATTACAACCTCGCGGTGAT 480
Db |||||
421 GAGCGCTTTATCTGGCCCGGCAATAGCCGCAAGAAAAAGATTACAACCTTGTGTTGAT 480
QY 481 TGTGTCGCGCATTAAGATACCGCGGACTTACTCAATCACTCAATGAGCTTTCTCTGGCTGGC 540
Db |||||
481 TGTGTCGCGCATTAAGATACCGCTGAGTCACTCAATCAACAGCGCTTTCTCTGGCTGGC 540
QY 541 GTGCTGCTATCAATCTCAACAGCTTACCGATAACCGGATGCCGACTCGACAGGT 600
Db |||||
541 GTGCTGCTATCAATCTCAACAGCTTACCGATAACCGGATGCCGACTCGACAGGT 600
QY 601 GAAGACGAGCGCTCTGGCAACAAAAAATGAGTAGTGTCTATATCACCCAAAGTAAC 660
Db |||||
601 GAAGATCAAGCGCTCTGGCAGCAGAAAAAATGAGCAGTGTCTATACCCACCAATAGC 660
QY 661 ACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCCAAAGGCAACATTTCAGCGCTG 720
Db |||||
661 ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAGGCAACATTTCAGCGCTG 720
QY 721 GCTATGATGTGGCCCGGCGAGCTTAAAGGGAGTTGGTTAACTCACTCAAGGTGAGCGGAA 780
Db |||||
721 GCTATGATGTGGCCCGGCGAGCTTAAAGGGAGTTGGTTAACTCACTCAAGGTGAGCGGAA 780
QY 781 CAGGTGATTTATCAAAATCGCTTAACTACTCGCCCGCGGCAAAATTTACGTGAAGAGCAC 840
Db |||||
781 CAGGTGATTTATCAAAATCGCTTAACTACTCGCCCGCGGCAAAATTTACGTGAAGAGCAC 840
QY 841 GGTAAACGGAGTTGTCTAGTGAATACAGTACGAAACCGGAAACCCAAACGGCTTTATCGGCAAT 900
Db |||||
841 GGTAAACGGAGTTTATCAACCGGATATACAGTATGAACAGGAAACCCAAACGGCTTTATCGGCAAT 900
QY 901 AACACTCGCGGTGCTTCAACAGCGCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCA 960
Db |||||
901 ACTACCGCGGTGCTTCAACAGGATACCAAGGTGTTGCAAGACCTACGCTATCAATATGATCCG 960

WP	ACF67367_19	1300001	2010000	
WP	ACF67367_20	2000001	2110000	
WP	ACF67367_21	2100001	2210000	
WP	ACF67367_22	2200001	2310000	
WP	ACF67367_23	2300001	2410000	
WP	ACF67367_24	2400001	2510000	
WP	ACF67367_25	2500001	2610000	
WP	ACF67367_26	2600001	2710000	
WP	ACF67367_27	2700001	2810000	
WP	ACF67367_28	2800001	2910000	
WP	ACF67367_29	2900001	3010000	
WP	ACF67367_30	3000001	3110000	
WP	ACF67367_31	3100001	3210000	
WP	ACF67367_32	3200001	3310000	
WP	ACF67367_33	3300001	3410000	
WP	ACF67367_34	3400001	3510000	
WP	ACF67367_35	3500001	3610000	
WP	ACF67367_36	3600001	3710000	
WP	ACF67367_37	3700001	3810000	
WP	ACF67367_38	3800001	3910000	
WP	ACF67367_39	3900001	4010000	
WP	ACF67367_40	4000001	4110000	
WP	ACF67367_41	4100001	4210000	
WP	ACF67367_42	4200001	4310000	
WP	ACF67367_43	4300001	4410000	
WP	ACF67367_44	4400001	4510000	
WP	ACF67367_45	4500001	4610000	
WP	ACF67367_46	4600001	4710000	
WP	ACF67367_47	4700001	4810000	
WP	ACF67367_48	4800001	4910000	
WP	ACF67367_49	4900001	5010000	
WP	ACF67367_50	5000001	5110000	
WP	ACF67367_51	5100001	5210000	
WP	ACF67367_52	5200001	5310000	
WP	ACF67367_53	5300001	5410000	
WP	ACF67367_54	5400001	5510000	
WP	ACF67367_55	5500001	5610000	
WP	ACF67367_56	5600001	5648894	
Query Match				84.8%; Score 2329; DB 10; Length 110000;
Best Local Similarity				90.5%; Pred. No. 0;
Matches 2485; Conservative				0; Mismatches 260; Indels 0; Gaps 0;
Qy	1	ATGAGCAGTTACAAATCTCTGCAATTTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60	
Db	100781	ATGAGCAGTTATCGTTCTGAAATTTGACAAAAAACACCATTAAATCAGTGTATTGGATAAC	100840	
Qy	61	AGGAATTAATGATGCTACTTTAGAAATATCTAGGCACTCAAGCTGACGAAAACAGTGAT	120	
Db	100841	AGGAGGTTAAATGTACGTACTTTAGAAATATCTAGGTAATCTCAAGCTGATGAAAACAGTGAT	100900	
Qy	121	GAATTAATTAAGTTCTATGAGTTCAATATTCCGGGATTTTCAGGTAAAAACCGATCCT	180	
Db	100901	GAATTTGATCACTCTATGAGTTCAATATTCAAGGATTTGAGGTAAAAAGTACTGATCCT	100960	
Qy	181	CGTAAAAATAAAACACAGACGGCCCAAAATTTCAATCGTGTCTTTTAATCTTTGCGGTCMA	240	
Db	100961	CGTAAAGATTAATAATCAGAGGGCCCGAAATTTCAATCGGCTCTTTAATCTCGGGTCAG	101020	
Qy	241	GTTTTACGTGAAGAAAGTTGTGATGCGCGTCGGAATTAACCTCAATGATATTTGAAGT	300	
Db	101021	GTTCACGTGAAGAAAGGTTGATGTCGGGTGGAATTTCAATTTCAAGGATTTGAGGTAAAGT	101080	
Qy	301	CGCCCGGTGTGATCAATCAATGCAACCGGTGTCGGCCAAACCATCGTTATGAAGATAAC	360	
Db	101081	CGCCCGGTATTAACCATCAATCAATGCAACCGGTGTCGGCCAAAGCTATCACTACGAAGATAAC	101140	
Qy	361	ACCTTCCCGGTGCTGTGCTCGCTATCACCGCAACAAAGTACAGGACGAGAGAAAAACGACC	420	
Db	101141	ATCCTACCCGGTGGCTTACTTGTCTATCACCGAACAGTGTGAGGACGAGAGAAAAATGACC	101200	
Qy	421	GAACGTCTTATCTGGGCGGCAATACCGCCGCAAGAAAAAGATTACAACTTCGCGGTACAG	480	

Db	101201	GAGCGCTTATCTGGGCGGCAATACGCGCAAGAAAAAGAGTACAACCTTGTGTGTCAG	101260	
Qy	481	TGTGTCGCCATTACGATACCGGGACATTACTCAACTCAATAGCTTTCTCTGGCTGGC	540	
Db	101261	TGTGTCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCTTTCTCTGGCTGGC	101320	
Qy	541	GTGCTGCTATCAATCTCAACACTGCTTACCGATAACGAGGATGCCAGTCGACAGGT	600	
Db	101321	GTGCTGCTATCAATCTCAACAACTGCTCGTCGATGATCAAAATGCCGACTGGACAGGT	101380	
Qy	601	GAAGACGAGCCTCTGGCAACAAAAAATGAGTAGTAGTGTCTATATCAACCCAAAGTAAC	660	
Db	101381	GAAGATCAAAAGCTCTGGCAGCAAAAATGAGCAGTAGTGTCTATACCAACCCAAATAGC	101440	
Qy	661	ACTGATGCCACCGGGCTTTTATCTGACCCAGACCGATGCCAAAAGGCAAACTTACAGCGGTG	720	
Db	101441	ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAAGGCAAACTTCCAGCGCTG	101500	
Qy	721	GCTATGATGTGGCGGGCAGCTTAAAGGGAGTTGGTTAACTCAACTCAAGGTGAGCGGAA	780	
Db	101501	GCTATGATGTAGCGGGCAGCTTAAAGGCTGTGGTTAACTCAACTCAAGGTCAAGCGGAA	101560	
Qy	781	CAGGTGATTATCAAAATCGCTAACTACTCCGCGCGGGGCAAAAATTACGTGAAGAGCAC	840	
Db	101561	CAAGTGATTATCAATCGCTGACCTACTCTGCGCGCGGCAAAAATTACGTGAAGAGCAC	101620	
Qy	841	GSTAACGGGATTGTCTACTGAATACAGTACGAAACCGGAAACCCAAACGGCTTATCGGCATT	900	
Db	101621	GSTAACGGGTTTATCACCCGAATACAGCTATGAACAGAAACCCAAACGGCTTATGGTATC	101680	
Qy	901	ACCACCTGGCGTCCATCAGACGCAAGGTGTGCAAGACCTAGCGTATCAATATGACCCA	960	
Db	101681	ACTACCGCGCTCGCTCAGATACCAAGGTGTGCAAGACTTACGCTATCAATATGATCCG	101740	
Qy	961	GTAGGCAATGTCAATTAATCCGTAAATGATGCGAAGCCACTCGCTTTTGGCGCAATCAG	1020	
Db	101741	GTAGGCAATGTGATCAATATCCGTAAAGATGCGAAGCCACCGCTTTTGGCGCAATCAG	101800	
Qy	1021	AAAGTAGCCCCGGAGAAATAGTATATCTACGATTCCTCTGTATCAGCTTATCAGCGCAC	1080	
Db	101801	AAAGTGTCCCGGAGAAATAGTATATCTAGCACTCCCTGTACAGCTTATCAGTGTACT	101860	
Qy	1081	GGCGCGAAATGGCCAAATTCGGTCAGCAAAACCAACCACTTCCCTCCCTCGCTACCT	1140	
Db	101861	GGCGGTGAATGGCCAAATTAGGTACGCAAAAATTAATCAACTGCCCTCCCTCGCTACCT	101920	
Qy	1141	TCGTCAACAATATCTACTACTACTACTCGCAGCTACAGCTATGATCAGCTGGTAAAT	1200	
Db	101921	TCGCAACAATATCTACTACTACTACTCGCCGCTACAGTTATGATCAGCGGTAAAT	101980	
Qy	1201	CTGACGCAAAATTCGGCAGCTCGCCAGCTTACCAGAAACAACTACACCGTGGCTATCACC	1260	
Db	101981	CTGACGCAAAATTCGGCAGCTTACCTCGGCTACCCAAATAACTACACCGCTATCACC	102040	
Qy	1261	CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320	
Db	102041	ATCTCGAATCGCAGTAACCGCGCGTCTCAGTACGCTGACAAACAGATCCAAATCAAGTG	102100	
Qy	1321	GATACCTTGTGTGATCGCGTGGTCACCAACCCAGTTTATACCCGCGACAGACTTATC	1380	
Db	102101	GATACCTTGTGTGATCGCGTGGTCACCAACCCAGTTTATACCCGCTGAGACTGTGTC	102160	
Qy	1381	TGACACACGAGGAGGTAAAGCAGGTTAATAATGGCCCGGAAATAGTGGTACCGC	1440	
Db	102161	TGACATACGAGGAGGTAAAGCAGGTCAATAACGGTTTCAGGAATTAATGGTACCGA	102220	
Qy	1441	TACGACAGCAACGGCATGAGACAACTGAAAGTGAAGTGAAACAGCCAAACCCCAAGATATACG	1500	
Db	102221	TACGGCAGCAACGGAATGAGACAACTGAAAGTGAAGTGAAACAGCCAAACCCCAAGATATACG	102280	
Qy	1501	CAGCAACAGCGGTATCTATTTGCGGAGCTGAGCTACGCAACCCCAAGCAAGCC	1560	
Db	102281	CAGCAGCAGCGGTAAATCTATCTGCGCGGCTGGAACTAGGCACAAACCCCAAGCAAGCC	102340	

Qy	1561	ACAAACAAGAGTTACACGTTTATCACACTCGGTGAAGCGGTTCGGCACAGGTACGG	1620
Db	102341	ACAACAACAGAAAGTTACAGTGATCACACTAGTGAAGCGGTTCGGCACAGGTACGG	102400
Qy	1621	GTGTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCAACATAATCAACTACGTTACAGC	1680
Db	102401	GTGCTGCACTGGGAGAGCGGTAAACACAGAGATATCAACACAATCAGCTACGTTACAGC	102460
Qy	1681	TACGATTAATCTGATCGGCTCAGGCAGCTTGAACCTGGACCAACCAAGACAAATTTATCAGC	1740
Db	102461	TACGATAATCTGATCGGCTCAGGCAGCTTGAACCTGGACCAACCAAGGCGAGTTATTAGT	102520
Qy	1741	GAGGAAGAGTATTATCCATTTTGGCGGACACGCGTGTGGCGCAGCAAAACAGCCAAACAGAA	1800
Db	102521	GAGGAAGAGTATTATCCATTCGGCGGACACCGATGTGGCGGCGCAATAGCCAAACAGAA	102580
Qy	1801	GCCAGCTATAAAACGATTTCGCTATTTCGGCAAGAAACGAGATGCCACGGGTTGTATTAT	1860
Db	102581	GCCAACTATAAACTATTTCGCTATTTCAGGCCAAAGAACGGGATACCAACGGGCTGTATTAT	102640
Qy	1861	TACGGTTATCGTTATTACCAACCGTGGCGGGCAGATGTTTAAGCGGCGACCCGGCAGGA	1920
Db	102641	TACGGTTACCGCTATTATCAACCGTGGCGGGCAGATGTTTAAGCGGCGATCCGGCAGGA	102700
Qy	1921	ACCATGATGGCTGGAATCTATACCGATGCTAAGAAATAATCTGTGAGTTTACAAGAT	1980
Db	102701	ACCATGATGGCTGGAATCTATACCGATGCTAAGAAATAATCTCAAGTAAGTTTCAGCAT	102760
Qy	1981	GAATAATGATTAGCGCCAGAAAAGGAAATATATACCAAGAGGTAAATTTCTTTGATGAA	2040
Db	102761	GAATAATGATTAGCACCAAGAGGAAATATATCTAAAGAGGTGAATTTCTTTGATGAA	102820
Qy	2041	TTAAATTTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCAAATGGAAACGAAAGAGAGC	2100
Db	102821	TTAAATTTCAAATTTGGCAGCCAAAGTTTCAATGTTGTCAAATGGAAACGAAAGAGAGT	102880
Qy	2101	AGTTATACAAAATAAATCATCTGAAGTGGTTCGTGCGTGATTCGGATCCGTCGGGT	2160
Db	102881	AGTTATACAAAATAAATCATCTGAAGTGGTTCGTGCGTGATTCGGATCCGTCGGGT	102940
Qy	2161	TATTTGCTAAGCCAGAGAGTTACTAAAGGTATAGAAAAAGTCAAATCATATATAGC	2220
Db	102941	TATTTGCTAAGCCAGAGAGTTACTAAAGGTATAGAAAAAGTCAAATCATATATAGC	103000
Qy	2221	CGACTTGAAGAAAACAGCTCCCTTTTCAGAAAAATCAAAAAAGATCTTTCTTTAGGATCT	2280
Db	103001	CGGCTCGAAGAAAACAGATCCCTTTTCAGAAAAATCAAAAAAGATCTTTCTTTGGATCT	103060
Qy	2281	GAATATCCGGTTATATGCGAAGAACCATACAAGATACGATATCAGATATGCCGAGAG	2340
Db	103061	GAATATCCGGTTATATGCGAAGAACCATACAAGATACGATATCAGATATACGAGAGG	103120
Qy	2341	CATAAATAGAAAGTAATCACCTGATTTTATTAGAAACCGATTTCTTTGCGTTAATG	2400
Db	103121	CATAGGTATAGAAAGTAATCATCCGATTTTATGACGCAACGATTTCTTTGCTTTAATG	103180
Qy	2401	GATAAAAGTGAAGAAAATGATTTTCGGTGAAGAAAAATTTATGCGGCAATGGAGGTT	2460
Db	103181	GATAAAAGTGAAGAAAATGATTTTCGGTGAAGAAAAATTTATGCGGCAATAGAGGTT	103240
Qy	2461	AAGGTTTATCATGTTTAAAAATAAACAATCAGATTTACATGTCACATGCTATGCGC	2520
Db	103241	AAGGTTTATCATGTTTAAAAATAAACAATCAGATTTACATGTCACATGCTATGCGCT	103300
Qy	2521	CATCCTATAGCAATTGAGTAATGAAGAAAGAGCGCTGTTGCAAGAAACAGAACCCGCT	2580
Db	103301	CATCCTATAGCAATTGAGTAATGAAGAGAGCGCTGTTGCAAGAAACAGAACCCGCT	103360
Qy	2581	ATTGCAATAGATAGAGATATAATTTCAAAGGTGTGGCAAAATTCCTGACATGAAGCA	2640
Db	103361	ATTGCAATAAATAGAGATATAATTTCAAAGGCGTTGGTAAATTTCTTGGCAATGAAGCA	103420

Qy	2641	ATTAAAAAATCATTTGAAGGACATAAAAATTAATAGGATATCAACAGAGGCTATTATATT	2700
Db	103421	ATTAAAAAATCATTTGAAGGCGCAGAGATCAATAAAAATATCAACAGAGGCTATTATATT	103480
Qy	2701	CGCTCTCGCGCTATCCCTGAGATTTTAGGAATCGCGGAGAACTTCA	2745
Db	103481	CGCTCTCGCGCTATCTCGTAAGAATTTAGGAATCGCGGAGAGCTTCA	103525
RESULT 5			
ACF67367_24			
Continuation (25 of 57) of ACF67367 from base 2400001 (Photorhabdus luminescens nucleotide)			
WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367			
WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000
WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000
WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	564894

Query Match

84.8%; Score 2329; DB 10; Length 110000;

Best Local Similarity 90.5%; Pred. No. 0; Matches 2485; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

Qy	1	ATGAGCAGTTTACAAATCTGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Db	781	ATGAGCAGTTTATCGTTCTGAAATTGACAAAAAAACCACTTAAATCAGTGTATTGGATAAC	840
Qy	61	AGGAATTAATGATGACGTACTTTAGAAATATCTAGCAGCTCAAGGTGACGAAAACAGTGAT	120
Db	841	AGGAGGTTAAATGATGACGTACTTTAGAAATATCTAGTACTCAAGCTGATGAAAACAGTGAT	900
Qy	121	GAATTAATTAAGTTCTATGATGATCAATATTCCGGGATTTTCAGGTGTAAGAAACACCGATCCT	180
Db	901	GAATTTGATCACTCTATGATGATCAATATTCAAGGATTTTGAAGTAAAGATGACTGATCCT	960
Qy	181	CGTAAAAATAAAAACAGAGCGGCCCAAAATTTCAATTCGTGCTTTTAAATCTTTGCCGCTCA	240
Db	961	CGTAAAGAAATAAATACAGAGCGGCCCAAAATTTCAATTCGTGCTTTTAAATCTCGCGGTCAG	1020
Qy	241	GTTTTACGTGAAGAAAGTTGATGCGCGTGGACATTAACCTCAATGATATTGAAAGT	300
Db	1021	GTTCTACGTGAAGAAAGGTTGATGCGCGTGGACATTAACCTCAATGATATTGAAAGT	1080
Qy	301	CGCCCGGTGTTGATCAATCAATGCAACCGGTGTCGCCAACCACATCGTTATGAAGATAAC	360
Db	1081	CGCCCGGTATTAAACCATCAATGCAACCGGTGTCGCCAAGACTATCACTACGAAGATAAC	1140
Qy	361	ACCTTTCCCGTCTGCTGCTGCTATCACCGAAACAGTACAGCGAGAGAGAAAACGACC	420
Db	1141	ATCCTACCGGTGCTGCTGCTATCACCGAAACAGTACAGCGAGAGAGAAAATGACC	1200
Qy	421	GAAAGTCTTATCTGGGCGCGCAATACGCCGCAAGAAAAGATTACAACTCTGCGCGTACG	480
Db	1201	GAGCGCTTATCTGGGCGCGCAATACGCCGCAAGAAAAGATTACAACTCTGCGTACG	1260
Qy	481	TGTGTCCGCAATTACGATACCGCGGACCTTACTCACTCAATAGCCCTTCTCTGGCTGGC	540
Db	1261	TGTGTCCGCAATTACGATACCGCGGACCTTACTCACTCAATAGCCCTTCTCTGGCTGGC	1320
Qy	541	GTGCTGCTATCAAACTCTCAAACTGCTTACCGATTAACCGATGCGGACCTGGAAGGT	600
Db	1321	GTGCTGCTATCAAACTCTCAAACTGCTTACCGATTAACCGATGCGGACCTGGAAGGT	1380
Qy	601	GAAAGCAGAGCTCTGGCAACAAAACTGAGTAGTGATCTATATACCCAAAGTAAC	660
Db	1381	GAAAGTCAAAAGCTCTGGCAGCAAAATCTGAGCAGTGATGCTATACCAACCCAAATAGC	1440
Qy	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	720
Db	1441	ACTGATGCCACCGGGCTTTACTGATCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	1500
Qy	721	GCCTATGATGTGGCGGGCAGCTAAAGGGAGTTGGTTAACTCAAAAGGTCAAGCGGAA	780
Db	1501	GCCTATGATGTAGCGGGCAGCTAAAGGGAGTTGGTTAACTCAAAAGGTCAAGCGGAA	1560
Qy	781	CAGGTGATTAATCAAACTGCTAACTACTCGCGCGCGGCAAAAATTTACGTGAAGAGCAC	840
Db	1561	CAAGTGATTAATCAAACTGCTAACTACTCGCGCGCGGCAAAAATTTACGTGAAGAGCAC	1620
Qy	841	GGTAACGGGATTTGCTACTGATGATCAGCTAGCAACCGGAAACCCAAACCGGCTTATCGGCATT	900
Db	1621	GGTAACGGGATTTGCTACTGATGATCAGCTAGCAACCGGAAACCCAAACCGGCTTATCGGCATT	1680
Qy	901	ACCACTCGCGCTCCATCAGAGCCCAAGGTGTCAGACCTACGCTATCAATATGACCCA	960
Db	1681	ACTACCGCGCTCGTCAAGATACCAAGGTGTCAGACCTACGCTATCAATATGATCCG	1740
Qy	961	GTAGGCAATGCTAATTAATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	1741	GTAGGCAATGCTAATTAATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1800
Qy	1021	AAAGTAGCCCGGAGAAATAGCTATACCTACGATTTCCCTGATCAGCTTATCAGCGCAC	1080
Db			

Db	1801	AAAGTGTCCCGGAGAAATAGCTATATCTTAGACTCCCTGTACAGCTTATCAGTGTCTACT	1860
Qy	1081	GGCGCGAAATGGCCAAATATCGGTACGAAAAACAACTTCCCTCCCTCGCGTACCT	1140
Db	1861	GGCGGTGAATGGCCAAATATAGGTACGAAAAATACTCAACTGCCCTCCCTCGCGTACCT	1920
Qy	1141	TCGACAAACAAATACCTTACACTAATATATCCGAGCTACAGCTATGATCAGAGTGTAAAT	1200
Db	1921	TCGACAAACAAATACCTTACACTAATATATCTCGCGCTACAGTTTATCAGCGGTAAAT	1980
Qy	1201	CTGACCAAAATTCGGCAGCTCGCCAGCTACCCAGAAACAACTTACACCGTGGGTATCACC	1260
Db	1981	CTGACCAAAATTCGGCAGCTCGCCAGCTACCCAGAAATTAATTAACCCCGGTATCACC	2040
Qy	1261	CTCTAAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCAACCAATCCAAATCAAGTG	1320
Db	2041	ATCTCGAATCGCAGTAAACCGCGCGTCTCAGTACGCTGACAAACAGATCCAAATCAAGTG	2100
Qy	1321	GATACGTTGTTGATGCGCGTGTACCAAAACCAAGTTTATTAACCCCGGACAGACTTATC	1380
Db	2101	GATACGTTTATTTGATGCGCGTGTACCAAAACCAAGTTTATTAACCCCGTACAGACTGGTC	2160
Qy	1381	TGGACACACGAGGAGAGTTAAAGCAGGTTTAAATGGCCCGGAAATGAGTGTGTACCGC	1440
Db	2161	TGGACATCAGAGGAGAGTTAAAGCAGGTCATTAACGGTTCAGGAAATGATGGTACCGA	2220
Qy	1441	TACGACAGCAACCGCATGAGACAACTGAAAGTGAGTGAACAGCCAAACCCAGCAATCTACG	1500
Db	2221	TACGGCAGCAACCGAATGAGACAACTGAAAGTGAGTGAACAGCCAAACCCAGCAATCTACG	2280
Qy	1501	CAGCAACAGCGGTAACTTATTTGCCGGGACTGAGCTACGCAACCCAGCAGCAAGCC	1560
Db	2281	CAGCAGCAGCGGTAACTTATTTGCCGGGCTGGAACCTACGCAACCCAGCAGCAAGCC	2340
Qy	1561	ACAAACAAACGAGAGTTACAGTTTACACTCGGTGAAGCGGTGCGGCACAGGTACGG	1620
Db	2341	ACAAACAAACGAGAGTTACAGTTTACACTAGGTGAAGCGGTGCGGCACAGGTACGG	2400
Qy	1621	GTGTTGCACTGGGAGAGCGGTAAAGCCAGAGAGTGTCAACAATAATCAACTACCTTACAGC	1680
Db	2401	GTGTTGCACTGGGAGAGCGGTAAAGCCAGAGAGTGTCAACAATAATCAACTACCTTACAGC	2460
Qy	1681	TACGATTAATCTGATCGGCTCCAGCAGCTTGAACCTGGAACAAACAGGACAAATTTATCAGC	1740
Db	2461	TACGATTAATCTGATCGGCTCCAGCAGCTTGAACCTGGAACAAACAGGACAAATTTATAGT	2520
Qy	1741	GAGGAGAGATTTATCCATTTTCGCGGACAGCGCTGTGGGCGCAACAGCAGCCAAACAGAA	1800
Db	2521	GAGGAGAGATTTATCCATTTTCGCGGACAGCGATGTGGGCGCAACATAGCCAAACAGAA	2580
Qy	1801	GCAGCTATAAAACGATTCGCTATTTCGGCAAGAAACGAGATGCCACCGGTTGTATTAT	1860
Db	2581	GCCAACTATAAACTATTTCGCTATTTCAGGCAAGAAACGGGATACCAACCGGCTGTATTAT	2640
Qy	1861	TACGTTATCGTTATTAACAAACCGTGGGCGGAGATGTTTAAAGCGGACCCCGCAGGA	1920
Db	2641	TACGTTATCGCTTATTAACAAACCGTGGGCGGAGATGTTTAAAGCGGATCCCGCAGGA	2700
Qy	1921	ACCATTTGATGGGTGATCTATACCGAATGTTTAAAGAAATAATCTCTGTGATTTACAGAT	1980
Db	2701	ACCATTTGATGGGTGATCTATACCGAATGTTTAAAGAAATAATCTCTGTGATTTGAGAGAT	2760
Qy	1981	GAAAATGGATTTAGCGCCAGAAAAGGAAATATATCAAAAGAGGTAATTTCTTTGTATGAA	2040
Db	2761	GAAAATGGATTTAGCACCAGAAAAGGAAATATATCTTAAAGAGGTGAATTTCTTTGTATGAA	2820
Qy	2041	TTAAAATTAATTTGCGAGCCAAAAGTTTCAATGTTGTCAATTTGAAATGGAACAGAAAGAGC	2100
Db	2821	TTAAAATTAATTTGCGAGCCAAAATTTCAATGTTGTCAATTTGAAATGGAACAGAAAGAGT	2880
Qy	2101	AGTTATCAAAAATAAATCAATTTGAAAGTGGTTCGTTGCGGTGATTTCCGATCCGTCGGGT	2160
Db	2881	AGTTATCAAAAATAAATCAATTTGAAAGTGGTTCGTTGCGGTGATTTCCGATCCGTCGGGT	2940

Qy	2161	TATTTGCTAAGCCACGAAGAGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATAGC	2220
Db	2941	TATTTGCTAAGCCACGAAGAGTTACTAAAGGTATAGAAAAAGTCAAAATCATATATAGC	3000
Qy	2221	CGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTAGGATCT	2280
Db	3001	CGGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTGGGATCT	3060
Qy	2281	GAATATATCCGGTTATATGGCAGAAACCATACAGATACGATATCAGATATATGCCGAAGAG	2340
Db	3061	GAATATATCCGGTTATATGGCAGAAACCATACAGATACGATATCAGATATATACGAAGGG	3120
Qy	2341	CATAAATATAGAGTAATCACCCGATTTTATTTCAGAAACCGGATTTCTTTGGCGTTAATG	2400
Db	3121	CATAGGTATAGAGCAATCATCCGATTTTATGCGCAACAGATTTCTTTTGTCTTAAATG	3180
Qy	2401	GATAAAAAGTGAAAAAATGATTATTCGGGTGAAAAAGAAAAATTTATGGCGCAATGGAGGTT	2460
Db	3181	GATAAAGTGAAAAAATGATTATTCGGGTGAAAAAGAAAAATTTATGGCGCAATAGAGGTT	3240
Qy	2461	AAGTTTTATCATGATTTAAAAAATAAACAATCAGAAATTAATGTCAACTATGCAATTTGGCC	2520
Db	3241	AAGTTTTATCATGATTTAAAAAATAAACAATCAGAAATTAATGTCAACTATGCACTGGCT	3300
Qy	2521	CATCCCTATACGCAATTCAGTAATGAAGAAAGAGCGCTGTTGCAAGAAACAGAACCCGCT	2580
Db	3301	CATCCCTATACGCAATTCAGTAATGAAGAAAGAGCGCTGTTGCAAGAAACAGAACCCGCT	3360
Qy	2581	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTGGCAAATTCCTGACAATGAAAGCA	2640
Db	3361	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTGGTAATTTCTGGCAATGAAAGCA	3420
Qy	2641	ATTAAAAATCATTTGAAAGGACATAAATTAATAGGATATCAACAGAGGCTATTAAATTT	2700
Db	3421	ATTAAAAATCATTTGAAAGGCGCAGAGATCAATAAAATATCAACAGAGGCTATTAAATTT	3480
Qy	2701	CGCTCTCGGGCTATCGCTGAGAAATTTAGGAATGCGGAGAACTTCA 2745	
Db	3481	CGCTCTCGGGCTATCGCTGAGAAATTTAGGAATGCGGAGAGCTTCA 3525	
RESULT 6			
ACF65386_4/c			
Continuation (5 of 7) of ACF65386 from base 400001 (Photorhabdus luminescens nucleotide			
Best Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386			
WP	Fragment Name	Begin	End
WP	ACF65386_0	1	110000
WP	ACF65386_1	100001	210000
WP	ACF65386_2	200001	310000
WP	ACF65386_3	300001	410000
WP	ACF65386_4	400001	510000
WP	ACF65386_5	500001	610000
WP	ACF65386_6	600001	700779
Query Match 84.8%; Score 2329; DB 10; Length 110000;			
Best Local Similarity 90.5%; Pred. No. 0;			
Matches 2485; Conservative 0; Mismatches 260; Indels 0; Gaps 0;			
Qy	1	ATGAGCAGTTACAAATTCGTGCAATTGACCAAAAGAGCCCTCGATTAAGGTATTAGATAAC	60
Db	97845	ATGAGCAGTTATCGTTCTGAAATTTGACAAAAAACCACCAATTAACAGTGTATTGGATAAC	97786
Qy	61	AGGAAATTAATGTACGTACTTTTGAATATCTAGCACTCAAGCTGACGAAAAACAGTGAT	120
Db	97785	AGGAGTTAAATGTACGTACTTTTGAATATCTAGCACTCAAGCTGATGAAAAACAGTGAT	97726
Qy	121	GAATTAATTCGTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCGATCCT	180
Db	97725	GAATTTGATCACACTCTAGTGTCAATATTAAGGATTTGAGGTAAAAAAGTACTGATCCT	97666
Qy	181	CGTAAAAATAAAAAACAGAGGGGCCAAATTTTCATTCGTGTCTTTAAATCTTTGCCGGTCAA	240

Db	97665	CGTAAAGATAAAAAATCAGAGCGCGCCGAATTTCTTCGGGTCTTTTAATCTTCGGGGTCTAG	97606
Qy	241	GTTTTACGTGAAGAAAGTGTTCGATCCGGTTCGAGCTATTACCTCTCAATGATATTGAAGT	300
Db	97605	GTTCACGTGAAGAGGGTTGATCCGGTGCNACTATCATCTCAACGATTTGAAGT	97546
Qy	301	CGCCCGGTGTGATCATCAATGCAACCCGGTGTCCGCCAAACCATCGTTTATGAAGATAAC	360
Db	97545	CGCCCGGTATTAAACCATCAATGCAACCGGTGTCCGCCAAAGATCATCACTACGAAGATAAC	97486
Qy	361	ACCTTCCCGGTCTGCTGCTATACCGAAACAGTACAGCAGGAGAGAAAAACGACC	420
Db	97485	ATCTTACCCGGTCTGCTTACTTGTCTATCACGAAACAGTGCAGCAGAGAAAAATGACC	97426
Qy	421	GAAGCTTTATCTGGGCGCGCAATACGCGCAAGAAAAAGATTACAACCTTCGCGCGTCTAG	480
Db	97425	GAGCGCTTATCTGGGCGCGCAATACGCGCAAGAAAAAGATTACAACCTTGTGCTGCTAG	97366
Qy	481	TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGGTGGC	540
Db	97365	TGTGTCCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCCTTTCTCTGGTGGC	97306
Qy	541	GTGCTGTATCAAACTCTCAAACTGCTTACCGATAACAGGATGCGGACTGACAGGT	600
Db	97305	GTGCTGTATCAAACTCTCAAACTGCTTCTGCTGATGATCAAAATGCCGACTGACAGGT	97246
Qy	601	GAAGACAGAGCCTCTGGCAACAAAACTGAGTGTGATGTCTATATCACCCAAAGATAAC	660
Db	97245	GAAGATCAAGCCTCTGGCAGCAAAACTGAGCAGTGTCTATACCCAAATATAGC	97186
Qy	661	ACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	720
Db	97185	ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	97126
Qy	721	GCCTATGATGTGCGCGGAGCTTAAAGGGAGTTGGTTAACTCACTCAAGGTTCAGGCGGAA	780
Db	97125	GCCTATGATGTGCGCGGAGCTTAAAGGGTGTGTGTTTAACTCACTCAAGGTTCAGGCGGAA	97066
Qy	781	CAGTGTATTAATAATCGCTTAACCTACTCGCGCGCGGCAAAATTTACGTGAAGAGCAC	840
Db	97065	CAAAGTATTAATAATCGCTGACCTACTCTGCGCGCGGCAAAATTTACGTGAAGAGCAC	97006
Qy	841	GGTAAACGGGATTTCTACTGAATACAGTACGAAACCGGAAACCCCAACGGCTTTATCGGCATT	900
Db	97005	GGTAAACGGGTTATCACCGAATACAGTATGAACAGAAACCCCAACGGCTTTATGGTATC	96946
Qy	901	ACACCTCGCGCTCCATCAGACGCGAGGTGTTGCAAGACCTACGCTATCAATATGACCCA	960
Db	96945	ACTACCGCGCTCCGTGAGATACCAAGGTGTTGCAAGACTTACGCTATCAATATGATCCG	96886
Qy	961	GTAGGCAATGTCATTAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Db	96885	GTAGGCAATGTGATCAATATCCGTAAAGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG	96826
Qy	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTACGATTTCCCTGTATCAGCTTATCAGCGCACCC	1080
Db	96825	AAAGTGTCCCGGAGAAATAGCTATACCTACTGCTGACGCTTATCAGGCTTATCAGTGTACT	96766
Qy	1081	GGGCGGAAATGGCCAATATCGGTGAGCAAAAACAAACCACTTCCCTCCCTGCGCTACCT	1140
Db	96765	GGGCGTGAATGGCCAATATAGGTGAGCAAAAATTAATCAACTGCGCTCCCTGCGCTACCT	96706
Qy	1141	TCTGACAAACAAATACCTACACTACTACTCTCGAGCTACAGCTATGATCAAGTGTGTAAT	1200
Db	96705	TCCGACAAACAAATACCTACACTACTACTCTCGCGCTTACAGTTATGATCAAGCGGTAAAT	96646
Qy	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTTACCCAGAACCAACTACACCGTGGCTATCACC	1260
Db	96645	CTGACGCAAAATTCGGCACAGTTTCACTCGGCTTACCCAAATAACTACACCCGCTATCACC	96586
Qy	1261	CTCTCAAAACCGAGCAATTCGGGGTGTCTCAGTACGCTACCAACCGATTCCAATCAAGTG	1320
Db	96585	ATCTCGAATCGCAGTAAACCGCGGCTTCTCAGTACGCTGACCAAGATCCCAATCAAGTG	96526

CC Paenibacillus sp. and others for insecticidal thiaminase genes and
CC proteins for controlling insects, particularly lepidopterans. The current
CC sequence is that of the Photobacillus strain W14 tccc5 toxin complex DNA
CC of the invention.
XX
SQ Sequence 2817 BP; 902 A; 700 C; 614 G; 601 T; 0 U; 0 Other;
Query Match 52.5%; Score 1442.2; DB 12; Length 2817;
Best Local Similarity 82.9%; Pred. No. 0;
Matches 1664; Conservative 0; Mismatches 328; Indels 15; Gaps 1;
QY 21 AATGTACCAAAAGACCCCTCGATTAGGTATTAGATAACAGGAAATTTAAATGTAGCTAC 80
DB 21 ACTTTATCACCATACGCTACCGTACGTTTTCAGATAACCGTGGACTAGCTATCGGTAA 80
QY 81 TTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGATGAATTAATTTACGTTCTATGA 140
DB 81 TATTAGTTTTTACCGCACTACCGCAGAAAGCAATACCGATACCGGTATTATACCGGCCATCA 140
QY 141 GTTCAATATTCGGGGATTTTCAGGTAAAGACCGATCCTCGTA-----A 185
DB 141 ATATAATGCGGGGATTTTGAACCAAGATTTGATCCTCGGCTGTATGACGCCAAACA 200
QY 186 AAATAAAAAACAGAGCGGCCCAAAATTTTCAATTCGTGTCTTTAAATCTTGGCGGTCAAGTTTT 245
DB 201 GACTAACACGCTGTACACCGAATTTTATCTGGCGACATAATTTTGACCGGCAATATCCT 260
QY 246 ACGTGAAGAAAGTTGTGATCGCGTGGATCTATTTACCTCAATGATATTTGAAGTGCCTCC 305
DB 261 GCGAAACAGAGAGCGTGTGATCGCGTGGACGATTTACCTCAACGATATTGAAGCGCGCCC 320
QY 306 GGTGTTGATCATCAATGCAACCGGTGTCGCCAAACCACTCGTTATGAAGATTAACCCCT 365
DB 321 GGTGTTGATCATCAATGCAACCGGTGTCGCCAAACCACTCGTTATGAAGATTAACCCCT 380
QY 366 TCCCGGTGCTGCTGCTATACCGAAACAAAGTACAGGAGAGAGAAAACGACCGAAGC 425
DB 381 GCCCGGTGCTGCTGCTATCAGCGAACAAAGGACAGGACGAGAGAAAACGACCGAGCG 440
QY 426 TCTTATCTGGGCGCGCAATACGCGCAAGAAAAGATTAACAACCTCGCGGTGATGTGT 485
DB 441 CCTTATCTGGGCGCGCAATACGCGCAAGAAAAGACCAACCTTCGCGGTCAGTGCGT 500
QY 486 CCGCATTTAGCATACCGGGGACTTACTCACTCAATAGCTTTCTCTGGCTGCGGTGCT 545
DB 501 CCGCATTTAGCATACCGGGGACTTACTCACTCAATAGCTTTCTCTGGCTGCGGTGCT 560
QY 546 GCTATCACAATCTCAACCAACTGCTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 605
DB 561 TCTATCACAATCTCAACCAACTGCTTACCGATAACAGGATGCCGACTGGACAGGTGAAGA 620
QY 606 CAGAGCCTCTGGCAACAAACAACTGATGTAGTGTCTATATCAACCAAGATTAACACTGA 665
DB 621 CCAGAGCCTCTGGCAACAAACAACTGATGTAGTGTCTATATCAACCAAGATTAACACTGA 680
QY 666 TGCACCGGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTGGCCTA 725
DB 681 TGCACCGGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTGGCCTA 740
QY 726 TGATGTGCGCGGGCAGCTAAAGGGAGTTGGTTAACTCACTCAAAAGGTGAGGCGGAACAGGT 785
DB 741 TGATGTGCGCGGGCAGCTAAAGGGAGTTGGTTAACTCACTCAAAAGGTGAGGCGGAACAGGT 800
QY 786 GATTATCAAAATCGGTAACTTACTCCGCGCGCGCAAAAATTTACGTGAAGACGCGTAA 845
DB 801 GATTATCAAAATCGGTAACTTACTCCGCGCGCGCAAAAATTTACGTGAAGACGCGTAA 860
QY 846 CGGATTTGCTCACTCAATACAGTACGACCGGAACCGGCTTATCGGCTATCCAC 905
DB 861 CGGATTTGCTCACTCAATACAGTACGACCGGAACCGGCTTATCGGCTATCCAC 920
QY 906 TCGCGGTCCATCAGACGCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG 965

DB 921 TCGCGCTCCATCAGACGCCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG 980
QY 966 CAATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAGAAAGT 1025
DB 981 CAATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAGAAAGT 1040
QY 1026 AGCCCCGAGAAATAGCTATACCTACGATTCCTGTATCAGTCTTATCAGCGCCACCGGGCG 1085
DB 1041 AGCCCCGAGAAATAGCTATACCTACGATTCCTGTATCAGTCTTATCAGCGCCACCGGGCG 1100
QY 1086 CGAAATGGCCAAATATCGGTGACGAAACAAACAACTTCCCTCCCTGCGCTACCTTCTGA 1145
DB 1101 CGAGATGGCCAAATATCGGTGACGAAAGCAACAACTTCCCTCTCCGCGCTACCTTCTGA 1160
QY 1146 CAACAAATCTACACTAACCTATCTCGCAGCTACAGCTATGATCAAGTGGTAACTCTGAC 1205
DB 1161 TACAAATCTACACCACTATCTCGCACTTATCTATGACCGTGGCGGCAATTTGAC 1220
QY 1206 GCAAAATTCGGCCAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCAACCTCTC 1265
DB 1221 GAAATTCAGCATAGTTTACACGCGCGCAAAATTAACACGGAATATAACGGTTTC 1280
QY 1266 AAACCCAGCAATCGGGGTGTTCTCAGTACGCTAACCCAGATCCAAATCAAGTGTATAC 1325
DB 1281 AAATCGCAGCAACCGCGCGTACTCAGCACTTGACCGCAGATCCAACCTCAAGTCGATGC 1340
QY 1326 GTTGTGATGCGGTGTCACCAACACAGTTTATTTACCGGACAGACACTTATCTGGAC 1385
DB 1341 CTTATTTGATGCGGGAGGCCATCAACACAGCTTGTATTCGGCCAAAGTTCTAACTTTGGAC 1400
QY 1386 ACCACGAGGAGAGTTTAAAGCAGGTTTAAATATGCGCCCGGAAATGAGTGTGCTACGCTACGA 1445
DB 1401 ACGCGAGCGCAATTTGAACCAAGCCAAACAATAGCGCAGGAAATGAGTGTATCGTACGA 1460
QY 1446 CAGCAACCGCATGAGACAACTGAAAGTGTGAAAGCCAAACCCAGAAATCTACGCGACGA 1505
DB 1461 TAGCAACCGCATACCGCAGCTAAAGTGAATGAACAAACAACTCAGAAATATCCCGCAACA 1520
QY 1506 ACAACGGGTAACTTATTTCCCGGACTGGAGCTACGCAACAACCCAGACCAACCCCAAC 1565
DB 1521 ACAACGGGTAACTTATTTCCCGGGCTTGAATATCGTACAAACCCAGACCAACCCCAAC 1580
QY 1566 AACGGAAGAGTTTACAGCTTATCACTCGGTGAAAGCGGTGCGGCAACAGTACGGGTGTT 1625
DB 1581 AACGGAAGAGTTTACAGCTTATCACTCGTAAAGCGCGCGCAAGTCCGAGTATT 1640
QY 1626 GCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAAATATCACTACGTTTACAGCTACGA 1685
DB 1641 GCATTTGGGAGAGCGGTAAACCCAGAGATATTTAATAAATCAGCTTCTGTTACAGCTACGA 1700
QY 1686 TAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATATTCAGCGAGGA 1745
DB 1701 TAATCTTATTTGGCTCCAGCCAACTTCAATAGATAGGACGGAACAAATATTCAGTGNAGA 1760
QY 1746 AGAGTATTTATCCATTTTGGCGGGAACGCTGTGGGACGAAACAGCCAAACAGAAAGCCAG 1805
DB 1761 AGATATTTATCCATTTTGGTGTACAGCGCTGTGGCGGCAAGGAATCAAAACCGAAGCCAG 1820
QY 1806 CTATAAAACGATTCGCTATTTCCCGCAAAAGAACAGATGCCACCGGGTGTATTTATACGG 1865
DB 1821 CTATAAAACGATTCGCTATTTCTGTTAAAGAGCGGGATGTTTACCGGGCTGTATTTATATGG 1880
QY 1866 TTATCGTTATTTACCAACCGTGGCGGCGAGATGTTTAAAGCGCGGACCCCGCAGCAACCAT 1925
DB 1881 CTACCGTTATTTACCAACCGTGGCGGCGAGATGTTTAAAGTGCAGACCCCGCAGCAACCAT 1940
QY 1926 TGATGGCTGAATCTATACCGAAATGGTAAGAAATTAATCTGTGTGAGTTTACAAGATGAAA 1985
DB 1941 TGATGGCTGAATTTATATCGCATGTTGAGAAATATACCCGGTGCAGCAATTTGATGTTCA 2000
QY 1986 TGGATTAGCCCAAGAAAAGGGGAAATA 2012
DB 2001 GGGATTATCACCAGCAACAGAAACAGA 2027

PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

PS Claim 2; SEQ ID NO 7901; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded
CC proteins from *Photobacterium luminescens*. The isolated sequences are
CC sources of probes and primers for detecting the genome of *P. luminescens*
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than *P. luminescens* and are able to alter
CC response or sensitivity to toxins and antibiotics produced by *P.*
CC *luminescens*. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which *P.*
CC *luminescens* is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated *P. luminescens* genes

XX SQ Sequence 2817 BP; 922 A; 682 C; 588 G; 625 T; 0 U; 0 Other;

Query Match	48.1%;	Score 1321.4;	DB 10;	Length 2817;
Best Local Similarity	78.7%;	Pred. No. 0;		
Mismatches	1596;	Conservative	0;	Mismatches 416; Indels 15; Gaps 1;
Qy	1	ATGAGCGATTACAAATCTCGAATTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60	
Db	1	ATGAAAAACATTGACCCCTAAACCTTTATCACCATAACGCGGACCCGTCAGTGTTCACGATAAC	60	
Qy	61	AGGAAATTAATGTTACCTACTTTAGATAATCTACGCACTCAAGCTGACGAAACAGTGAT	120	
Db	61	CGTGGACTCGGTATCCCGTAAATATTAGTATTTTACCGCGCTACCGGGAAGCAATATCCGAT	120	
Qy	121	GAATTAATATGTTCTATGAGTTCAATATTCCGGGATTTTTCAGGTAAAAAGCACCGATCCT	180	
Db	121	CCGGTATTACTCGCCATCAATATAATGCGGGGGATATTGACCAAAAGCATTGATCCT	180	
Qy	181	CGTA-----AAATAAAACACAGAGCGGCGCAATTTTCATTCGTGCTTT	225	
Db	181	CGCTGTATGATGCTAAGCAGACTAACAAACCGCCGTACAAACCGAATTTTATCTGCGCAT	240	
Qy	226	AATCTTCGCGTCAAGTTTACGTGAAGAAGTGTGATGCGCGTACGACTATTACCCCTC	285	
Db	241	AATTTGACCGCAATATCTCGCAACAGAGCGTGTGATGCTGGCCGCAATATTACCCCTC	300	
Qy	286	AATGATATTGAAGTCGCGCGTGTGATCATCAATGCAACCGGTGTCGCGCAAAACCAT	345	
Db	301	AACGATATTGAGTCTCGCGGTATTGACCATCAGCGCAACCGGTGTCGCGCAAAATCAC	360	
Qy	346	CGTTATGAAGATAACACCTTCCCGTGTGCTGCTATCACCGAACAAGTACAGGCA	405	
Db	361	CTTTATGAAGATAACACCTTACCCGTCGCTACTCGCAATCACCGAACAAGCACAGACA	420	
Qy	406	GGAGAGAAACGACCGAAGCTTTATCTGGGCGGCAATACGCGCAAGAAAGATTAC	465	
Db	421	GAAGAGAAACAAACCGAGCGTCTTATCTGGGCGGCAATACGCGCAAGAAAGATTAC	480	
Qy	466	AACCTTCGCGTCAAGTGTGCTCGGCATTTACGATACCGCGGACTTACTCAACTCAATAGC	525	
Db	481	AACCTTGTGTGATGATACCGGTCAATACGATACCGCGGACTCGCTCAACTCAACAGC	540	
Qy	526	CTTTCTCTGGTGGCGGTGCTGATCAAACTCAAACTCAAACTCAAACTCAAACTCAAACT	585	
Db	541	CTTGGCTGACCGGCGGCTTTTATCAAACTCAAACTCAAACTCAAACTCAAACTCAAACT	600	
Qy	586	GCCGACTGGACAGGTGAAGACCAAGCCTCTGGCAACAAAACACTGAGTAGTGATCTAT	645	

Db	601	GCCTGCTGACAGGTGAAGACCAAGACCTCTGCGACAAAACCTGAGTAGTGATCTAT	660	
Qy	646	ATCACCAAAAGTAAACATGATGCCACCGGGCTTTACTGACCCAGACCGATGCAAGGC	705	
Db	661	ACCACCAAAATAAAACCGATGCCACCGGGTTTACTTTACCAGACCGATGCTAAAGGC	720	
Qy	706	ACATTTCAGGGCTGCGCTATGATGGCGGCGAGCTAAAGGGAGTTGGTTAAACATC	765	
Db	721	ACATTTCAGGGCGAAGCCTATGATGGCGGGTACGCTAAAGGGAGCTGGCTTAACATTA	780	
Qy	766	AAAGGTTCAGCGGAAACAGCGTGATTAACAATCGCTAAACCTACTCCCGCGCGGCAAAA	825	
Db	781	AAAGGTTCAGCGGAAACAGCGTGATTAACAATCGCTAAACCTACTCCCGCGCGGCAAAA	840	
Qy	826	TTACGTGAAGAGACACGGTAAACGGGATGTCACTGAATACAGCTACGAAACCGGAAACCAA	885	
Db	841	TTACGTGAAGAGACACGGTAAACGGGATGTCACTGAATACAGCTACGAAACCGGAAACCAA	900	
Qy	886	CGGCTTATCGGCATTAACCACTCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGC	945	
Db	901	CGGCTTATCGGCATTAACCACTCGCGTCCATCAGACGCGCAAGGTGTTGCAAGACCTACGC	960	
Qy	946	TATCAATATGACACCGTAGGCAATGCTAATATATCCGTAATGATCGGAAGCACTCGC	1005	
Db	961	TATCAATATGACACCGTAGGCAATGCTAATATATCCGTAATGATCGGAAGCACTCGC	1020	
Qy	1006	TTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAG	1065	
Db	1021	TTTTGGGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAG	1080	
Qy	1066	CTTATCAGCGCACCGGGCGGCAATGCGCAATATCGGTGCGCAACCAACCACTTCCC	1125	
Db	1081	CTTATCAGCGCACCGGGCGGCAATGCGCAATATAGGTGCGCAACCAACCACTTCCC	1140	
Qy	1126	TCCCTTCGCTACTCTGACCAACAACTACACTAACTATATCTCGCAGCTACAGCTAT	1185	
Db	1141	TCCCTTCGCTACTCTGACCAACAACTACACTAACTATATCTCGCAGCTACAGCTAT	1200	
Qy	1186	GATCAGAGTGTATCTGACGCAAAATTCGGCAAGCTCGCCAGCTACCCAGAACACTAC	1245	
Db	1201	GACGTTGGCGCAATTTGATGAAATTCAGCATAGTTTCACTGCCAGCAAAATACTAC	1260	
Qy	1246	ACGCTGCTATCACCTCTCAACCGCAGCAATCGGGTGTCTCTAGTACGCTAACCAAC	1305	
Db	1261	ACGCAAAATATAACCGTTCTAATTAAGCAACCGTCCGCTATTAAGTACACTGACCGAA	1320	
Qy	1306	GATCCAAATCAAGTGGATACGTTTGTGATGCGCGTGGTCCACCAACCACTTTATTACC	1365	
Db	1321	GATCCAAACCAAGTTGATGCTTATTTGATTCGGAGGCCATCAACCACTTTATTATCC	1380	
Qy	1366	GGACAGACCTTATCTGGACACACAGAGAGAGTTAAAGCAGGTTTAATATGCGCCGGGA	1425	
Db	1381	GGTCAAGTTCTAATATATGACACCGCGAGCGCAATGAAACCAAGTCAACAGTAGCGGGA	1440	
Qy	1426	AATGAGTGTACCGCTACGACGACGCGCATGAGCACTGAAGAGTGAAGTGAAGACGCA	1485	
Db	1441	AATGAGTGTATCACACGATAGCAACCGGCAACAGCAGCTAAAGTGAATGAACAAACA	1500	
Qy	1486	ACCAGAAATACTACGACGCAACCAACCGGTAACTTATTTGCGGGGACTGGAGTACGACA	1545	
Db	1501	ACTCAGATATCGGCAACAGCAAGAGTCACTTATCTCGCGGGCTAGAACTACGACA	1560	
Qy	1546	ACCAGAGCAACCGCACAACAAACGGAAGTTACAGCTTATCAGCTCGGTGAAGCCGGT	1605	
Db	1561	ACCAGAGCAACCGCACAACAAACGGAAGTTACAGCTTATCAGCTCGGTGAAGCCGGT	1620	
Qy	1606	CGGCAACAGTACGGGTGTTGCACTGGGAGCGGTAAAGCCAGAAAGTGAAGTGAAGTAA	1665	
Db	1621	CGGCAACAGTACGGGTGTTGCACTGGGAGCGGTAAAGCCAGAAAGTGAAGTGAAGTAA	1680	
Qy	1666	CAACTAGCTTACAGCTACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGCAACCAA	1725	

Db	1681	CAACTTCGTTACAGTACGATAATCTTATTCGGTTCCAGCCCACTTGAATTAGATAGCGAA	1740
Qy	1726	GGACAAATATTACGAGGAGAGTATTATTCATTTTGGCGGGACAGCGCTGTGGCGAGCA	1785
Db	1741	GGACAAATATTACGAGGAGAGTATTATTCATTTTGGCGGTACAGCTCTGTGGCGAGCA	1800
Qy	1786	ACAGCCAAACAGAGCCAGCTATAAAACGATTTCGCTATTTCGGCAAAAGAACAGATGCC	1845
Db	1801	AGGAATCAAAACCAAGCCAGCTATAAAACCATTCGTTATTTCAGGTAAAGAGCGGGATGCT	1860
Qy	1846	ACCGGGTTGTTATTATTCAGGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGC	1905
Db	1861	ACCGGGCTGTATTATTACGGCTACCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGT	1920
Qy	1906	CGGACCCCGCAGAGAACCAATTGATGGCTGAATCTATACCGAATGTTAAGAAATATTCCT	1965
Db	1921	CGGACCCCGCGGAACCAATTGATGGCTGAATTTTATATCGCATGGTGGAGAAATATCCG	1980
Qy	1966	GTGAGTTTACAGATGAAATGGAATTAGCGCCAGAAAAGGGAATA	2012
Db	1981	GTGACACAATTTGATGTTTCAGGGATTATCTCCGGCTAACAGAACAGA	2027
RESULT 11			
ACF65386_5/c			
Continuation (6 of 7) of ACF65386 from base 500001 (Photorhabdus luminescens nucleotide			
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386			
WP	Fragment Name	Begin	End
WP	ACF65386_0	1	110000
WP	ACF65386_1	100001	210000
WP	ACF65386_2	200001	310000
WP	ACF65386_3	300001	410000
WP	ACF65386_4	400001	510000
WP	ACF65386_5	500001	610000
WP	ACF65386_6	600001	700779
Query Match			
Best Local Similarity 48.1%; Score 1321.4; DB 10; Length 110000;			
Matches 1596; Conservative 0; Mismatches 416; Indels 15; Gaps 1;			
Qy	1	ATGAGGATTTACATTTCTGCAATTTGACCAAAAGACCCCTCGATTAAAGTTATTAGATAAC	60
Db	15073	ATGAAAAACATTTGACCTAACTTTTATCACCATACGCGGACCGTGTTCACGATAAC	15014
Qy	61	AGGAAATTTAATGTACGTACTTTAGAAATATCTAGCACTCAAGCTGACGAAACACAGTGAT	120
Db	15013	CGTGGACTCGTATCCGTATATATTAGTTTTCACGGGCTACCGCAGAGCAATACCGAT	14954
Qy	121	GAATTAATTAGTTCTATAGTTTCAATPATTCGGGATTTTCAGGTAAAGACACCGATCCT	180
Db	14953	CCGGTATTACTCGCCATCAATATAATGCGGGGGATATTGTAACCAAGCATTTGATCCT	14894
Qy	181	CGTA-----AAATAAACACAGCGCGGCCAAATTTTCATTCGTGTCCTT	225
Db	14893	CGCTGTATGATGTAAGCAGACTTAACACCGCGTACACCGAATTTTATTCGGCAGCAT	14834
Qy	226	AATCTTCGCGTCAAGTTTACGTGAAGAAAGTTGTGATCGCGTCCGACTATTACCCCTC	285
Db	14833	AATTTGACCGGCAATATCTTCGGACAGAGCGTGTGATGCTGCGCGAACAATTTACCCCTC	14774
Qy	286	AATGATATTGAAGTCCCGCGGTGTTGATCATCAATGCAACCGGTGTCGCCAAACCAT	345
Db	14773	AACGATATTGAAGTCCCGCGGTATTGACCATCAGCGCAACCGGTGTCGCCAAATTCAC	14714
Qy	346	CGTTATGAAGATTAACACCTTCCGGTGTGCTGTGCTATCACCGAAGATACGGCA	405
Db	14713	CTTTATGAAGATTAACACCTTACCGGTGTGCTGTGCTATCACCGAAGATACGGCA	14654
Qy	406	GGAGAGAAACGACCGAAGCTTTATCTGGCGGCAATACCGCGCAAGAAAGATTAC	465
Db	14653	GAAGAGAAACACCGAGCGCTTTATCTGGCGGCAATACCGCGCAAGAAAGATTAC	14594
Qy	466	AACCTCGCGGTGAGTGTGTCGGCCATTACGATACCGCGGACTTACTCAACTCAATAGC	525

Db	14593	AACCTTGTGGTCAGTGTATCCCGTCAATTACGATACCGCGGACTCGTCAACTCAACAGC	14534
Qy	526	CTTTCTCTCGCTGGCGTGTGCTATCACAATCTCAAACAATCTGTTACCGATAACCAAGAT	585
Db	14533	CTTGCCCTTCAGCGCGCGCTTTTATCACAATCTCAAACAACCGCTCGTCGATAACCAAGAT	14474
Qy	586	GCGGACTGACAGGTGAGACCGAGCCCTCTGGCAACAAAACCTAGTAGTAGTGTCTAT	645
Db	14473	GCGGACTGACAGGTGAGACCGAGCCCTCTGGCAACAAAACCTAGTAGTAGTGTCTAT	14414
Qy	646	ATCACCCAAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCAAAAGGC	705
Db	14413	ACCACCCAAATATAAACCGATGCCACCGGGCTTTACTTACCAGACCGATGCTTAAAGGC	14354
Qy	706	AACATTCAGCGGTGCGCTTATGATGTGGCGGGCAGCTAAAAGGGAGTTGGTTTAAACATC	765
Db	14353	AACATTCAGCGGCAAGCCTTATGATGTGGCGGGTACGCTAAAAGGGAGCTGGCTTAAACATTA	14294
Qy	766	AAAGTCAAGCGGACACAGGTGATTATCAAAATCGCTAACTTACCTGCGCGCGCGGCAAAA	825
Db	14293	AAAGTCAAGCGGACACAGGTGATTATCAAAATCGCTTACTTCCGCGCGCGGCAAAA	14234
Qy	826	TTAGGTGAGACGACCGTAAACGGATTGTCACTGAAATACAGCTACGAACCGGAAACCCAA	885
Db	14233	TTAGCGGAAGAGACCGTAAACGGATTATTAACGAATACAGCTATGAACCGGAATCTAG	14174
Qy	886	CGGCTTATCGGCATTACCACTCGCCCTCCATCAGAGCGCAAGGTGTTGCAAGACCTACGC	945
Db	14173	CGGCTTATCGGCATTACCACTCGCCCTCCATCAGAGCGCAAGGTGTTGCAAGACCTACGC	14114
Qy	946	TATCAATATGACCCAGTAGGCAATGTCTTAATATCCGTAATATATGCGGAAGCACTCGC	1005
Db	14113	TATCAATATGACCCAGTAGGCAATGTCTTAATATCCGTAATATATGCGGAAGCACTCGC	14054
Qy	1006	TTTGGCGCAATCNGAAGTAGCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAG	1065
Db	14053	TTTGGCGCAATCNGAAGTAGCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAG	13994
Qy	1066	CTTATCAGCGCCACCGGGCGGAAATGGGCAATATCGGTGAGCAAAACCAACCACTTCCC	1125
Db	13993	CTTATCAGTGCCACCGGAGTGAATGGCCNAATATAGGTGAGCCNAATACCCACTCCCC	13934
Qy	1126	TCCCTCGCTACCTTCTGACAAACAATACCTACATACTTAATCTCGCAGCTACAGTAT	1185
Db	13933	TCCCTCGCTACCTTCTGATTAACAACCTTAACTTACACCGCACCTATAGTTAT	13874
Qy	1186	GATCAGAGTGTATCTGAGCGCAATTCGGCAGCTCGCCAGCTACCGAGACNACTAC	1245
Db	13873	GACCGTGGCGGCAATTTGATGAAATTCAGCATAGTTTCACTCCACGCAAAATAACTAC	13814
Qy	1246	ACCGTGGCTATCACCTCTCAAACCGCAGCAATCGGGGTGTTCTCAGTAGCTAACCAAC	1305
Db	13813	ACGACGAATATAACGGTTTCTAATACGCAACCGTGGCGTATTAAGTACACTGACCGAA	13754
Qy	1306	GATCCAAATCAAGTGGATAGTTGTTGATGCGCGGTGTCACCAAAACCACTTATTAACC	1365
Db	13753	GATCCAAACCAAGTTGATGCTTTATTTGATTGCGGAGGCCATCAAAACCACTTATTAACC	13694
Qy	1366	GGAACAGACTTATCTGGACACCAACGAGGAGGTAAAGCAGGTTAATATGSCCGGGA	1425
Db	13693	GGTCAAGTTCTAATATATGGACACCGCGAGGCGAAATGAAACAACTCAACAGTAGCGGGA	13634
Qy	1426	AATGAGTGTGTACCGCTACGACACGCGCATGAGCAACTGAAAGTGTAGTGAACGCCA	1485
Db	13633	AATGAGTGTGTATCACTACGATACGCGCACGACAGCTAAAGTGAATGAACACAA	13574
Qy	1486	ACCAGAAATATACGACGCAACCAACGGGTAACTTATTTGCGGGACTTGGAGTACGACA	1545
Db	13573	ACTCAGATATCGGCAACAGCAAGATCACTTATCTGCGGGGTAGAACTACGACA	13514
Qy	1546	ACCAGAGCAACCGCAACCAACGGAAGGTACAGCTTATCACTCGGTGAAGCGGT	1605

Db 13513 ACCCAACATGCGAGTACTACACGGAATATTGTCAGGTATTCACATCTCGGTAAAGCTGGT 13454
 Qy 1606 CGGCAAGTACGGGTGTTGCACTGGAGAGCGGTAAAGCAGAGATGTCACAAATAAT 1665
 Db 13453 CGTGGCAAGTCCGGGTATTACATTGGGAGAGCGGAAACCCGGAAGATATCAACAAAT 13394
 Qy 1666 CAATCTAGTTACAGCTACGATAATCTGATCGGCTCCAGCGAGCTTGAACCTGGACAAACAA 1725
 Db 13393 CAATCTGTTACAGCTACGATAATCTTATCGGTTCCAGCCAACTTGAATTAGATAGCGAA 13334
 Qy 1726 GGACAAATTTACGAGGAGAGATATTATTCATTTGGCGGACAGCGCTGTGGGACGA 1785
 Db 13333 GGACAAATTTACGAGGAGAGATATTATTCATTTGGCGGTACAGCTGTGGGACGA 13274
 Qy 1786 AACAGCCAAACAGAGCCAGCTATAAAACGATTCGCTATTCGCGCAAGAACAGAGATGCC 1845
 Db 13273 AGGAATCAACCGAAGCCAGCTATATAAACCATTCGTTATTTCAGGTAAAGACGGGATGCT 13214
 Qy 1846 ACCGGGTTGATTATTACGGTTATCGTTATTACCAACCGTGGGCGGCAGATGTTAAGC 1905
 Db 13213 ACCGGGTTGATTATTACGGTTATCGGTTATTACCAACCGTGGGCGGCAGATGTTAAGT 13154
 Qy 1906 GCGACCCGCGGAGAACCATTTGATGGCTGAATCTATACCGAATGGTAAGAAATTAATCCT 1965
 Db 13153 GCGACCCGCGGAGAACCATTTGATGGCTGAATTTATATCGATGGTGAGAAATTAATCCG 13094
 Qy 1966 GTGAGTTTACAGATGAATGGATTAGCGCCAGCAAGAAAGGAAATA 2012
 Db 13093 GTGACAAATTTGATTTTCAGGGATTATCTCCGCTAACAGAACAGA 13047

RESULT 12

AC70848
 ID AC70848 standard; DNA; 2811 BP.
 XX
 AC AC70848;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Photorhabdus luminescens nucleotide sequence #9315.
 XX
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough; gene; db.
 XX
 OS Photorhabdus luminescens.
 XX
 PN W0200294867-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 07-FEB-2002; 2002WO-IB003040.
 XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;
 XX
 DR WPI; 2003-148459/14.
 XX
 PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 9315; 1205pp; French.
 XX
 CC The invention relates to the isolation of genes and their encoded
 CC proteins from Photorhabdus luminescens. The isolated sequences are
 CC sources of probes and primers for detecting the genome of P. luminescens
 CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than P. luminescens and are able to alter
 CC response or sensitivity to toxins and antibiotics produced by P.
 CC luminescens. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens genes
 XX
 SQ Sequence 2811 BP; 929 A; 660 C; 631 G; 591 T; 0 U; 0 Other;
 Query Match 36.9%; Score 1013.2; DB 10; Length 2811;
 Best Local Similarity 70.5%; Pred. No. 3.2e-272;
 Matches 1415; Conservative 0; Mismatches 573; Indels 18; Gaps 4;
 Qy 1 ATGAGCAGATTACAAATTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC 60
 Db 1 ATGATTCGTTACAAATTCGCAATTTACCGAAATACCCCATCTCTCAGCGTACGAGATAAT 60
 Qy 61 AGAAATTAATGTACGTACTTTAGAAATATCTACGCACCTCAAGCTACAGAA---ACAGT 117
 Db 61 CGAGGGTTAAATATACATACGCTGGAATATCTCGGACTCAAGCTGATGAAGCAATAGC 120
 Qy 118 GATGAATTAATACGTTCTTATGATTTCAATATTCGCGGATTTCCAGGTAAAGACACCGAT 177
 Db 121 AACGAAATTGATCACTCGCTATCAATTTAATACTACGGAATTTCAAGTAAAGACACAGAC 180
 Qy 178 CCTCGTAAATAAATAAACCAGACGCGCCAAATTTCAATCTGCTCTTTTAATCTTGCCTG 237
 Db 181 CGAGTAGATATAAACCAGAGTGGTTCNAATCTCACTGATCTTTAGTCTCGCTGGG 240
 Qy 238 CAAGTTTTACGTGAAGAAAGTGTGATGCGGTGCGACTATTAATACCTCAATGATATTGAA 297
 Db 241 AATACACTGCGTGAAGAAAGTATCGATGCTGGCGAAGATTACCTTTGAACGATATCGAA 300
 Qy 298 AGTGGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCAACCACCATCTGTGAAGAT 357
 Db 301 GGAAGCCCGAGTACTGACTATCAATGCAATCGGCGCTGTCAGACCCCACTCATATGAAGT 360
 Qy 358 AACACCCCTTCCCGTCTGCTCGCTATCACCGAAACAAGTACAGGAGGAGAGAAACG 417
 Db 361 AATACCTTGGCCGCGCTGCTGGCTGTACCGAGTTATACAAAGAGACGAGAAACCC 420
 Qy 418 ACCGAACGCTTTATCTGGCGGCAATACGCCGCAAGAAAGATTACAACCTCGCGCGT 477
 Db 421 ACGAGCGCTTTATTTGGGCAACAATACAGATGCGAGAGAAACACCAAGATCTCGCGCGG 480
 Qy 478 CAGTGTGTCGCCATTTAGATACGCGGGAATTTACTCAACTCAATAGCTTTCTCTGGCT 537
 Db 481 CAATGTATACGCCATTTATGATCTCGCGGGCTGGTCAACTGGGAAAGTTTGTCTCTTAACA 540
 Qy 538 GCGTGTGCTATCACAAATCTCAACAACTGCTTACCAGATAACCCAGGATGCGGACTGGACA 597
 Db 541 GGATCGGTTTTATCACAGTCTGCTCAATTAATAGCCGACGATCAGGAAGCTGATTGGCGC 600
 Qy 598 GGTGAAGACGAGCGCTCTCGCAACAAATACTAGTATGATGCTTATATCACCCAAAGT 657
 Db 601 GGTGATGATGAATAATAGCTGGCGTACAAACTGAATGGCAACATATTCAGACTCAACAT 660
 Qy 658 AACACTGATGCCCGGGGCTTTACTGACCCAGACCGATGCCAAGGCAACATTCACGGG 717
 Db 661 AAAATGATGCCATTTGTTGCTGCTAACTCAAAATCGACCGCAAGGGAATATGCAACGG 720
 Qy 718 CTGSCCTATGATGTGGCGGCGCAGCTAAAGGGAGTTGGTTAACTCACTCAAGGTCAGGCG 777

Db	721	CTGCGCTATGATGTGCGGGCCAACTGAAAGGTAGTGGTTAAACACTTAAAGGCGCAAGCC	780
Qy	778	GAACAGGTGATTATCAAACTGCTAACTACTCTCGCGCCGCGGCAAAATTTACGTGAAGAG	837
Db	781	GAATAAGTTATTGTACAGTCTATTACTGGTCAGCAGCCGGAATAAAATTTACGAAAGAG	840
Qy	838	CACGGTAACGGGATTGTCACTGAATACAGCTACGAACCGGAACCCACAGCGCTTATCGGC	897
Db	841	CACGGTAATGGCGTTATTACGGAATATACCTATGAACACAGAGACCCAAACGATTAAATTAAC	900
Qy	898	ATTACCACTCGCGCTCCATCAG---CGCCNAGGTGTGCAAGACCTACGCTATCAATAT	954
Db	901	ATTACAAACCGCGCAACTAGAGATAGTACAAAACCACTACAAGATTTTACGTTATGATAT	960
Qy	955	GACCAGTAGGCAATGTCATTAAATATCCGTAAATGATCGGAAGCCACTCGCTTTTGGCGC	1014
Db	961	GATCCCGTGGCAATGTATCAATTTTCGTATGATGCAAGCAACCCGATTTCTGGCGT	1020
Qy	1015	AATCAGAAAGTAGCCCCGGGAAATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGC	1074
Db	1021	AATCAGAAAAATAGTACCGGAAATGCTATATTCCTATGATTTCTGTACCAACTCATCCAA	1080
Qy	1075	GCCACCGGCGCGAAATGGCCAAATATCGGTTCAGCAAAAACCAACCTCCCTC-----C	1128
Db	1081	GCAACCGGCGCGAAATGGCTTAACATTTGGTTCAGCAAGGAAGCCAGCTCCCTCTCTTAATT	1140
Qy	1129	CCTGCGGTACTCTCTGCAACAATATCCTACACTAACTATATCTGCAGCTACAGCTATGAT	1188
Db	1141	ACCCTCTTCTACCGATGACATACCTTTATCTHACTATATTTGCTATTATCCTTAGCAC	1200
Qy	1189	CACAGTGGTAACTTGACGCCAAATTCGGCACAGCTCGCCAGCTACCCAGAAACAACATACACC	1248
Db	1201	GATAGCGCAACTGTACACAAAATCCAGCACAGTCTCGGCAAGTAACTAACTACACC	1260
Qy	1249	GTGCTATACCTCTCAAACCGCAGCAATTCGGGGTGTTCCTCAGTAGCTTAAACCCGAT	1308
Db	1261	ACAAATATCACCAATTTCAAAACCGTAATAACCGCGGTGTCTCTCAGTACCTTCACCAACGAC	1320
Qy	1309	CCAATCAAGTGGATAGTGTGTTTGATGCGGTGTCCACAAACCAAGTTTATACCGGA	1368
Db	1321	CCCAATCTGTTGATACATTTCTTTGATGCAAGTGGTTCATCAACCACTGTCTCTCAGG	1380
Qy	1369	CAGACCTTATCTGGACACCAAGGAGAGTTAAAGCAGGTTAA-----TAATGGCCCG	1422
Db	1381	CAATCCTTAAACTGGACACCAAGCGGAGAACTACAACAAGTGAACCAAGTGGTAAATACC	1440
Qy	1423	GGAAATCAGTGGTACCGCTAGCAGACAAACGCAATGAGACAACATGAAGTGAAGTGAACAG	1482
Db	1441	GCGCGTAGTGGTACCACTATGACAGTGAACGCGGCTACTGMAAATAAAGCAACAG	1500
Qy	1483	CCAAACCAGAAATACTACGCAACCAACGGGTATCTATTTGCGGGAACCTGGAAGCTACGC	1542
Db	1501	CAAAATCCAAATACCAACGACAGCAACAGTCACTTATCGCAGGGTTGGAATATAC	1560
Qy	1543	ACAAACCCAGCAACCGCCACAAACAAACGGAAGAGTTACACGTTATCACTCGGTGAAGCC	1602
Db	1561	ACCACAAGCGGCAACCAATATCACCGAAGACTTTACAGTTATTCTGTGAGCAAGCA	1620
Qy	1603	GGTCCGCAACAGGTACGGGTGTTGCACTGGGAGAGCGGTAAAGCCAGAAAGTGTCAACAT	1662
Db	1621	GGAAAGCAAAAGTACGCGTACTACCTGGGAAAAAGGCCAAACCCCGGCATAAATAAC	1680
Qy	1663	AATCAACTAGTTACGTAACGTAATACTCATCGGCTCCAGCCAGCTTGAACTGGACAAC	1722
Db	1681	GATCAAGTTCAGATATAGCTACGATTAATCTTACACAGACGCAATTTAGAACTGGATATG	1740
Qy	1723	CAAGGCAAAATTTATCAGCAGGAAGAGTATTATCCATTTGCGGGAACAGCGCTGTGGCA	1782
Db	1741	CACGGAAATGATCAGTTGGGAAGATATTACCCCTATGTTGGCACCGCAGTATGGCA	1800
Qy	1783	GCAACAGCCAAACAGAAAGCCAGCTATAAAACGATTCGCTATTTCCGCAAGAACGAGAT	1842

[illegible]

QY	241	GTTTTACGTGAAGAAAGTGTGATGCGCGTCCGAGCTATTACCTCAATGATATGAAAGT	300
Db	15411	ATTTTGTGACAGAAACGTCGATGCTGTCGCACTGTCACCTTGAATGATATGAAGGC	15470
QY	301	CGCCCGGTGTGATCATCAATCAACCGGTGTCGGCCAAACCATCGTTATGAAGATAAC	360
Db	15471	CGTCCGCTACTGACGTAACTGCAACAGGTGTATCAAAACCCGCAATATGAACGTCT	15530
QY	361	ACCCTTCCCGGTGCTGCTCGCTATCACCGAAACAAGTAC- ---AGCGAGGAGAGAAACG	417
Db	15531	TCCCTACCCGCTGCTGTGTGTTGTTACCGAACAATACCAGAAACATCCCGTATC	15590
QY	418	ACCGAAGCTTTATCTGCGCGCGGCAATACGCCCGAAGAAAGATTAACACCTCGCGGT	477
Db	15591	ACCGAAGCGCTGATTTGGGTGGCAATAGCGAAGACGAGAGAAACCATATCTTGCAGC	15650
QY	478	CAGTGTGCGCCATTAACGATACCGCGGAGTACTCAACTCAATAGCCTTCTCTGGCT	537
Db	15651	CAGTGGTGGCCACTATGACACCGCGGGAGTCACCGATTAGAGAGTTTGTCACTGACC	15710
QY	538	GGCGTGTGCTATCACAATCTCAACAACTGCTTACCGATAACAGGATGCCGACTGGACA	597
Db	15711	GGTACTGTTTTATCTCAATCCAGCCAACTATTGAGCGACACTCAAGAGCTAGCTGGACA	15770
QY	598	GGTGAAGACAGAGCCTCTGGCAACAAAACCTGAGTAGTGATGCTATATCAACCCAAAGT	657
Db	15771	GGTGAATAAGAAACCGTCTGGCAAAACATGCTGGCTGATGACATCTACACAACCCCTGAGC	15830
QY	658	AACACTGATGCCACCGGGCTTTACTGACCCAGACAGATGCCAAAGCCACATTCAGCGG	717
Db	15831	GCCTTTGATGCCACCGGCTTTACTCACTACAGCCGATGCGAAAGGGAACATTCAGAGG	15890
QY	718	CTGCGCTATGATGTGGCGCGGAGCTTAAAGGAGTGTGTTAACTCAACAGTTCAGGCG	777
Db	15891	CTAACCTATGATGTGGCGCGGAGCTTAAAGGAGTGTGTTAACTTAAAGACCAACCG	15950
QY	778	GACAGGTGATTAATAAATCGCTAACTACTCCGCGCGCGGCAAAATTAACGTGAAGAG	837
Db	15951	GAAACAAGTGATTAATCACTGACCTTACCTGACCTATTTCGCGCGCGGCAAAATTAACGCGAGGA	16010
QY	838	CAGGTAAACGGATTTGCTACTGATATACAGTACGATAGCAACCGGAAACCCAGCGTTACGGC	897
Db	16011	CACGGCAATGGTGTATCACCGAATACAGTTATGAACCGGAAACCCCAACAGCTTATCGGT	16070
QY	898	ATTACCACTCGCGTCCATCAGACGCAAGGTGTGCAAGACCTACGCTATCAATATGAC	957
Db	16071	ACCAAAACCCACCGTCCGTCAAGTGCACAAAGTGTGCAAGATCTACGTTATGATATGAC	16130
QY	958	CCAGTAGGCAATGTCAATTAATATCCGTAATGATGCGGAAAGCCACTCGCTTTTCGCGCAAT	1017
Db	16131	CCGCTAGGCAATGTCAATCAGTATCCGTAATGATGCGGAAAGCCACTCGCTTTTCGCGCAAT	16190
QY	1018	CAGAAAGTAGCCCGGAGATAGCTATACCTACGATTCCTGCTATCAGCTTATCAGGCGC	1077
Db	16191	CAGAAAGTAGCCCGGAGAAACCTTATACCTACGACTCTTGTATCAGCTTATCAGGCGCA	16250
QY	1078	ACCGGCGCAAAATGGCCAAATATCGGTACGCAAAAACCAACCACTTCCCTCCCTGGGCTA	1137
Db	16251	ACCGGCGCGAGATGGGGAATATAGTACGCAAAAGTACCAACTTCCCTCCCTCACCCCTA	16310
QY	1138	CCTTCTGACAAACATACCTACATACTATCTCGCAGCTACAGCTATGATACAGTGT	1197
Db	16311	CCTTCTGATAACAAACCTTACCAACCTATACCCGTAATATGACTTATGACCGTGGCGGC	16370
QY	1198	AACTGACGCAAAATTCGGGACAGCTCGCAGCTACCCAGAAACAACTACACCGTGGCTATC	1257
Db	16371	AAATTTGACTAAATATCCAGCACAGTTTCAACCGGCGCAAAACCACTACCAACCAACATC	16430
QY	1258	ACCCTCTCAAAACCGCAGCAATTCGGGGTGTCTCAGTACGCTAACCCAGCTCAAAATCAA	1317
Db	16431	ACGGTTTCTAACCGGAGCAATTCGGCAGTACTCAGCAGCTCTGACCGAGATCCGGCGCA	16490
QY	1318	GTGGATACGTTGTTGATGCGCGTGGTCAACAAACCAAGTTTATATCCCGGACAGACACTT	1377

Search completed: December 13, 2005, 19:53:52
Job time : 1499 secs

This Page Blank (upside down)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 19:08:12 ; Search time 13299 Seconds
(without alignments)
11732.858 Million cell updates/sec

Title: US-10-647-956A-5
Perfect score: 2745
Sequence: 1 atgagcagttacaattctgc.....taggaatgcggagaacttca 2745

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_ste.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2745	100.0	2745	6	AR427909 Sequence
2	2653.8	96.7	127816	1	AF346500 Photorhab
3	2329	84.8	349519	1	EX571862 Photorhab
C	1440.6	52.5	2817	6	CQ824622 Sequence
5	1440.6	52.5	2817	6	CQ854091 Sequence
6	1013.2	36.9	349907	1	EX571874 Photorhab
7	1012.4	36.9	37948	6	AR166758 Sequence
8	1012.4	36.9	37948	6	BD136648 Insectici
9	1004.6	36.6	2883	6	CQ824618 Sequence
10	1004.6	36.6	2883	6	CQ854080 Sequence
11	972.4	35.4	349107	1	EX571873 Photorhab
12	962	35.0	3132	6	CQ854059 Sequence
13	962	35.0	3132	6	AR285426 Sequence
14	962	35.0	11518	1	AF047028 Photorhab
15	962	35.0	25655	1	AF346499 Photorhab
16	957.2	34.9	2850	6	CQ824620 Sequence
C	930	33.9	349107	1	EX571873 Photorhab
18	730.8	26.6	2889	6	CQ854084 Sequence

19	730.8	26.6	2947	6	CQ854087 Sequence
20	730.8	26.6	7508	6	CQ854088 Sequence
21	691.2	25.2	37544	6	AX027489 Sequence
22	666	24.3	3048	6	CQ854049 Sequence
23	666	24.3	3048	6	CQ854926 Sequence
C	666	24.3	39005	6	CQ854040 Sequence
24	666	24.3	39005	6	CQ854017 Sequence
C	666	24.3	39005	6	CQ854917 Sequence
25	664.4	24.2	3048	1	AY538173 Xenorhabd
26	629.4	22.9	18937	6	AX092884 Sequence
27	629.4	22.9	18937	6	AX092884 Sequence
C	614.2	22.4	11663	1	AF135182 Serratia
28	614.2	22.4	11663	1	AF135182 Serratia
C	614.2	22.4	11663	1	AF135182 Serratia
29	614.2	22.4	38457	1	AE013804 Xenorhabd
30	614.2	22.4	38457	1	AE013804 Xenorhabd
C	614.2	22.4	38457	1	AE013804 Xenorhabd
31	614.2	22.4	291326	1	AE017135 Yersinia
32	614.2	22.4	291326	1	AE017135 Yersinia
33	611	22.3	110000	1	AE017135 Yersinia
34	609.8	22.2	2937	1	AY220493 Yersinia
35	599	21.8	38258	6	AY220493 Yersinia
36	586.2	21.4	13244	1	AE013619 Yersinia
37	586.2	21.4	229338	1	AE017142 Yersinia
C	586.2	21.4	229338	1	AE017142 Yersinia
38	586.2	21.4	235050	1	AE017142 Yersinia
C	586.2	21.4	235050	1	AE017142 Yersinia
39	583	21.2	110000	1	AE017142 Yersinia
C	583	21.2	110000	1	AE017142 Yersinia
40	583	21.2	110000	1	AE017142 Yersinia
41	579.2	21.1	110000	1	AE017142 Yersinia
C	579.2	21.1	110000	1	AE017142 Yersinia
42	568.6	20.7	291326	1	AE017135 Yersinia
C	568.6	20.7	291326	1	AE017135 Yersinia
43	568.6	20.7	313050	1	AE017135 Yersinia
44	501.4	18.3	20157	1	AY647257 Yersinia
45	368.4	13.4	2793	6	CQ854075 Sequence

ALIGNMENTS

RESULT 1
AR427909
LOCUS AR427909 2745 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6639129.
ACCESSION AR427909
VERSION AR427909.1 GI:40186940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2745)
AUTHORS ffrench-Constant,R.H., Bowen,D.J., Rocheleau,T.A. and Waterfield,N.R.
TITLE DNA sequences from photorhabdus luminescens
JOURNAL Patent: US 6639129-A 5 28-OCT-2003;
Wisconsin Alumni Research Foundation and University of Bath;
Madison, WI

FEATURES
source
1..2745
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2745; DB 6; Length 2745;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAGTTACATTTCTGCAATTCACCAAAAGACCCCTCGATTAAAGTATTAGATAAC 60
DB 1 ATGAGCAGTTACATTTCTGCAATTCACCAAAAGACCCCTCGATTAAAGTATTAGATAAC 60
QY 61 AGGAATTAATGTCAGTCTTCTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT 120
DB 61 AGGAATTAATGTCAGTCTTCTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT 120
QY 121 GAATTAATACGTTCTTATGAGTTCAATATTCGGGGATTTTCAGGTAAAAAGACCGATCCT 180
DB 121 GAATTAATACGTTCTTATGAGTTCAATATTCGGGGATTTTCAGGTAAAAAGACCGATCCT 180
QY 181 CGTAAAAATAAACACAGCGGCCCAATTCATTCGTTGCTCTTTAATCTTGGCGGTCAA 240

Db 181 CGTAAAAATAAAACACAGAGCGGCCCAAATTTTCATTCGTGCTTTTAATCTTCCGGGTCAA 240
Qy 241 GTTTTACGTGAAGAAAGTGTGATGCGCGTGGACTATTACCTCAATGATATTGAAGT 300
Db 241 GTTTTACGTGAAGAAAGTGTGATGCGCGTGGACTATTACCTCAATGATATTGAAGT 300
Qy 301 CGCCCGGTGTGATCATCAATGCAACCGGTGTCCGCCAAACCATCTGTTATGAAGATAAC 360
Db 301 CGCCCGGTGTGATCATCAATGCAACCGGTGTCCGCCAAACCATCTGTTATGAAGATAAC 360
Qy 361 ACCCTTCCCGTGTCTGCTGCTATCACCGCAACAGTA CAGG CAGAGAGAAACGACC 420
Db 361 ACCCTTCCCGTGTCTGCTGCTATCACCGCAACAGTA CAGG CAGAGAGAAACGACC 420
Qy 421 GAACGTCTTATCTGGCGCGGCATACCGCCGAGAAAAGTTACRACCTCGCGGTGAC 480
Db 421 GAACGTCTTATCTGGCGCGGCAATACCGCCGAGAAAAGTTACRACCTCGCGGTGAC 480
Qy 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAAATAGCCTTTCTTGGCTGGC 540
Db 481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAAATAGCCTTTCTTGGCTGGC 540
Qy 541 GTGTGTCTATCAAACTCTCAACACTGCTTACCGATTAAC CAGGATGCCGACTGACAGGT 600
Db 541 GTGTGTCTATCAAACTCTCAACACTGCTTACCGATTAAC CAGGATGCCGACTGACAGGT 600
Qy 601 GAAGAC CAGAGCTCTGGCACAAAAC TGAAGTGTGATGCTATATCACCCAAAGTAAC 660
Db 601 GAAGAC CAGAGCTCTGGCACAAAAC TGAAGTGTGATGCTATATCACCCAAAGTAAC 660
Qy 661 ACTGATGCCACCGGGGCTTACTGACCCAGACCGATGCCAAAAGGCAACATTTCAGCGGCTG 720
Db 661 ACTGATGCCACCGGGGCTTACTGACCCAGACCGATGCCAAAAGGCAACATTTCAGCGGCTG 720
Qy 721 GCCTATGATGTGGCCGGGAGCTAAAAGGGAGTTGGTTAACTCAAAGGTTCAGCGGGA 780
Db 721 GCCTATGATGTGGCCGGGAGCTAAAAGGGAGTTGGTTAACTCAAAGGTTCAGCGGGA 780
Qy 781 CAGGTGATTATCAAACTCGTAACTACTCCGCCCGCGGGCAAAAATTACGTGAAGACAC 840
Db 781 CAGGTGATTATCAAACTCGTAACTACTCCGCCCGCGGGCAAAAATTACGTGAAGACAC 840
Qy 841 GGTAAACGGGATGTGCACTGAATACAGCTACGAAACCGGAAACCCAAACCGCTTATCGGCAAT 900
Db 841 GGTAAACGGGATGTGCACTGAATACAGCTACGAAACCGGAAACCCAAACCGCTTATCGGCAAT 900
Qy 901 ACCACTCGCGCTCCATCAGACGCCAAGGTGTGCAAGACCTTACGCTATCAATATGACCCA 960
Db 901 ACCACTCGCGCTCCATCAGACGCCAAGGTGTGCAAGACCTTACGCTATCAATATGACCCA 960
Qy 961 GTAGGCAATGCTAATATATCCGTAATGATGCGGAGGCCACTCGCTTTTGGCGCAATCAG 1020
Db 961 GTAGGCAATGCTAATATATCCGTAATGATGCGGAGGCCACTCGCTTTTGGCGCAATCAG 1020
Qy 1021 AAAGTAGCCCGGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
Db 1021 AAAGTAGCCCGGAGAAATAGCTATACCTTACGATTCCTGTATCAGCTTATCAGCGCCACC 1080
Qy 1081 GGGCGGAAATGGGCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTGCGCTACCT 1140
Db 1081 GGGCGGAAATGGGCAATATCGGTGAGCAAAACCAACCACTTCCCTCCCTGCGCTACCT 1140
Qy 1141 TCTGACAACTACTTACCTAATCTACTCTGAGCTACAGCTATGATCAGTGGTAAT 1200
Db 1141 TCTGACAACTACTTACCTAATCTACTCTGAGCTACAGCTATGATCAGTGGTAAT 1200
Qy 1201 CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACCGTGGCTATCAC 1260
Db 1201 CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACCGTGGCTATCAC 1260
Qy 1261 CTCTCAAAACCGCAGCAATTCGGGTGTTCTCAGTACGCTAACCCAGATCCAAATCAAGTG 1320
Db 1261 CTCTCAAAACCGCAGCAATTCGGGTGTTCTCAGTACGCTAACCCAGATCCAAATCAAGTG 1320

Qy 1321 GATACGTTGTTTGTATGTCGGTGGTCAACAAAC CAGTTTATTATCCCGGACAGACACTTATC 1380
Db 1321 GATACGTTGTTTGTATGTCGGTGGTCAACAAAC CAGTTTATTATCCCGGACAGACACTTATC 1380
Qy 1381 TGGACACCAACGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGGAAATAGTGTGATCCGC 1440
Db 1381 TGGACACCAACGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGGAAATAGTGTGATCCGC 1440
Qy 1441 TACGACAGCAACCGCATGAGACAACTGAAAGTGAAGTGAACAGCCACCAAGATATCTACG 1500
Db 1441 TACGACAGCAACCGCATGAGACAACTGAAAGTGAAGTGAACAGCCACCAAGATATCTACG 1500
Qy 1501 CAGCAACACCGGTAAATCTATTTGCGGACTGGAGCTAGCGACACAAACCCAGAGCAACGCC 1560
Db 1501 CAGCAACACCGGTAAATCTATTTGCGGACTGGAGCTAGCGACACCAACCCAGAGCAACGCC 1560
Qy 1561 ACAACAAACGGAAGTTTACAGTTTATCACCTCGGTGAAGCCGGTCCGACAGGTACGG 1620
Db 1561 ACAACAAACGGAAGTTTACAGTTTATCACCTCGGTGAAGCCGGTCCGACAGGTACGG 1620
Qy 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGGTAAAGCAGGTAAAGCAGGTAAAGCAGGTAAAG 1680
Db 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGGTAAAGCAGGTAAAGCAGGTAAAGCAGGTAAAG 1680
Qy 1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAGC 1740
Db 1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAGC 1740
Qy 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGCGCTGTGGCAGCAAAACAGCCAAACAGAA 1800
Db 1741 GAGGAAGAGTATTATCCATTTGGCGGACAGCGCTGTGGCAGCAAAACAGCCAAACAGAA 1800
Qy 1801 GCCAGCTATAAAACGATTCGCTATTCGGCAAAAGACGAGATGCCACCGGGTGTATTAT 1860
Db 1801 GCCAGCTATAAAACGATTCGCTATTCGGCAAAAGACGAGATGCCACCGGGTGTATTAT 1860
Qy 1861 TACGTTATCGTTTATTACCAACCGTGGCGGACAGATGGTTAAGCGGACCCCGGACGGA 1920
Db 1861 TACGTTATCGTTTATTACCAACCGTGGCGGACAGATGGTTAAGCGGACCCCGGACGGA 1920
Qy 1921 ACCATTGATGGGTGAATCTATACCGAATGGTAAGAAATTAATCTGTGAGTTTACAAGAT 1980
Db 1921 ACCATTGATGGGTGAATCTATACCGAATGGTAAGAAATTAATCTGTGAGTTTACAAGAT 1980
Qy 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA 2040
Db 1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATATCAAGAGAGGTAAATTTCTTTGATGAA 2040
Qy 2041 TTAATAATTCAAATTTGGCAGCAAAAGTTTACATGTTGTCAAATGGAAACGAGAAAGAGC 2100
Db 2041 TTAATAATTCAAATTTGGCAGCAAAAGTTTACATGTTGTCAAATGGAAACGAGAAAGAGC 2100
Qy 2101 AGTTATACAAAAATTAATCAATTTGAAAGTGGTTTCTGTTCCGATTCGATCCGCTCGGGT 2160
Db 2101 AGTTATACAAAAATTAATCAATTTGAAAGTGGTTTCTGTTCCGATTCGATCCGCTCGGGT 2160
Qy 2161 TATTTGCTAAGCCACGAGAGTTACTTAAAGGTTATAGAAAAAAGTCAAAATCATATATAGC 2220
Db 2161 TATTTGCTAAGCCACGAGAGTTACTTAAAGGTTATAGAAAAAAGTCAAAATCATATATAGC 2220
Qy 2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Db 2221 CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
Qy 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340
Qy 2341 CATAAATATAGAAGTAAATCACCTGATTTTATTCAGAAAAACGATTTCTTTGGGTTAATG 2400
Db 2341 CATAAATATAGAAGTAAATCACCTGATTTTATTCAGAAAAACGATTTCTTTGGGTTAATG 2400

QY 2401 GATAAAGTCAAAAAATGATTATTCGGTGAAGAAAAATTTATCGGCAATGGAGGTT 2460
Db |||||||
QY 2401 GATAAAGTCAAAAAATGATTATTCGGTGAAGAAAAATTTATCGGCAATGGAGGTT 2460
Db |||||||
QY 2461 AAGGTTTATCATGATTAAAAATAAACAATCAGAATTACATGTCACATTCGATTCGGCC 2520
Db |||||||
QY 2461 AAGGTTTATCATGATTAAAAATAAACAATCAGAATTACATGTCACATTCGATTCGGCC 2520
Db |||||||
QY 2521 CATCCCTATACGCAATGAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 2580
Db |||||||
QY 2521 CATCCCTATACGCAATGAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 2580
Db |||||||
QY 2581 ATTGCAATAGATAGAGAATAATAATTTCAAGAGTGTGGCAAAATTCCTGACAATGAAAGCA 2640
Db |||||||
QY 2581 ATTGCAATAGATAGAGAATAATAATTTCAAGAGTGTGGCAAAATTCCTGACAATGAAAGCA 2640
Db |||||||
QY 2641 ATTAAAAAATCATTGAAAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Db |||||||
QY 2641 ATTAAAAAATCATTGAAAGACATAAAATTAATAGGATATCAACAGAGGCTATTATATT 2700
Db |||||||
QY 2701 CGCTCTCGGCTATCGCTGAGAATTTAGGAATCGGAGAACTTCA 2745
Db |||||||
QY 2701 CGCTCTCGGCTATCGCTGAGAATTTAGGAATCGGAGAACTTCA 2745
Db |||||||

RESULT 2
AF346500
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 toxin complex pathogenicity
island 1, partial sequence.
ACCESSION
AF346500 AY144119
VERSION
AF346500.2 GI:27479637
KEYWORDS
SOURCE
Photorhabdus luminescens
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 127816)
AUTHORS
Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and
ffrench-Constant,R.H.
TITLE
The tc genes of Photorhabdus: a growing family
JOURNAL
Trends Microbiol. 9 (4), 185-191 (2001)
PUBMED
11286884
REFERENCE
2 (bases 1 to 127816)
AUTHORS
Waterfield,N.R., Daborn,P.J. and ffrench-Constant,R.H.
TITLE
Genomic islands in Photorhabdus
JOURNAL
Trends Microbiol. 10 (12), 541-545 (2002)
PUBMED
12564983
REFERENCE
3 (bases 1 to 127816)
AUTHORS
ffrench-Constant,R.H., Bowen,D.J. and Waterfield,N.R.
TITLE
Direct Submission
JOURNAL
Submitted (19-JAN-2001) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
REFERENCE
4 (bases 1 to 127816)
AUTHORS
Waterfield,N.R. and ffrench-Constant,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2002) Biology and Biochemistry, University of
Bath, Claverton Down, Bath BA2 7AY, UK
REMARK
Sequence update by submitter
COMMENT
On Jan 3, 2003 this sequence version replaced gi:16416925.
FEATURES
Location/Qualifiers
source
1..127816
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
<1..406
/gene="orf1"
<1..406
/gene="orf1"
/codon_start=2
/transl_table=11
/product="Orf1"

gene
CDS

/protein_id="AAO17167.1"
/db_xref="GI:27479640"
/translation="VLCSPAYIEASEKILI1PENLASHNCLIIYLSLSSSPRRMFMHQN
DKVVDLKGTYVNNGLAKQAALSGHGVLLPELLVDELQSGELVRLLPSEWADT
QALYAIQPHKERSIKARAFIDFLVNALDET"
695..1432
/gene="orf2"
695..1432
/gene="orf2"
/codon_start=1
/transl_table=11
/product="Orf2"
/protein_id="AAO17168.1"
/db_xref="GI:27479641"
/translation="MNSAISASENLVSLYDGRQPTVGIEINKILFSGVVRVSTAP
IEEAKPIELVSKTALTEGESEKILSFLHRGELLEQIRLAGRQPEAHRGGLGIS
EIGVAPYKVDKMAISVEARKTVLEKFKGLHVNSESDGMGIDEVMTVVAGGPTWFF
RLPAGELAKLSIGRVETGDPARLSVGLGMHAGFLDAKDGLLVAFHAGPKHPVMRYD
ESVDGTEMLGTPWIDFGSDIPKLVK"
1769..2752
/gene="orf3"
1769..2752
/gene="orf3"
/note="similar to putative Serratia heptosylIII
transferase WaaQ in GenBank Accession Number AAD28803"
/codon_start=1
/transl_table=11
/product="Orf3"
/protein_id="AAO17169.1"
/db_xref="GI:27479642"
/translation="MKIALLRRNGLDLICTOPLIKYQYTPPIAIIHFLBSNNEL
ADYLCEITTHIIPKGNKYITLTGALKWRKLHFDIAISAKTPMKLNLFLMLGAK
KRYAVTQSHQHEKILNPTCPQHIHQSLKILKTFDSEINKLSLSELLPKISSQYL
LPKQHGSPITLFSVNNRQSSCITHERIALIAQKIRNHPDVPVFIIISLIRHDSHAE
KLAMTGDQAOIVECQSLHSFLSLNSTDLIIVDGGICHLAAALDKLVALYGVTKP
ENWAPLASENQCTLYDPQVNNIPLIEDIYQAVFKLSPEKTLILLESSCR"
3949..4473
/gene="phf5"
3949..4473
/gene="phf5"
/note="similar to Salmonella enterica serovar Typhi Stga
probable fimbrial subunit protein found in GenBank
Accession Number CAD03135"
/codon_start=1
/transl_table=11
/product="Phf5"
/protein_id="AAO17170.1"
/db_xref="GI:27479643"
/translation="MKNFILASLVAVLGFISFSALSVDGTIKFRGTIEQTCTVKG
TSGKDIAVNFNVHKSJLDGKAGFSDPKSFVTNLTGCPDLKGFVYKDDTKTSDGN
YFKILSSSTAKNIAIALYKSGSSTPIKPGDSIKIPGVAGDTSPNLESKLVTAAVTVA
GSFTRDINFITISVP"
4531..5199
/gene="phfC"
4531..5199
/gene="phfC"
/note="similar to hypothetical 257 kD fimbrial chaperrone
of Escherichia coli K-12 found in GenBank Accession Number
C65104"
/codon_start=1
/transl_table=11
/product="PhfC"
/protein_id="AAO17171.1"
/db_xref="GI:27479644"
/translation="MFRILISFLAIFTQATIGTGLTLYNGSKEATISITNS
DTERPYLVOSWDNDNSQNVFVITPLPKMSKESHQIRVSYIGNHLPADRESIF
LNNVAIPAVEKNDNSKMITIKKILYRPSGLSDNDANDAINLEASRNANGVOL
TNPTAYVNLNEMKINGTLIPRPGFIPPFSHKVFSAQNGIKNVTLTAINDYGGTTEER
QTNF"
5233..7730
/gene="phfD"
5233..7730
/gene="phfD"

gene
CDS

gene
CDS

gene
CDS

/note="PhfD-like; type I fimbrial usher Photorhabdus
luminescens NC19 found in GenBank Accession Number
AAK16068"
/codon_start=1
/transl_table=11
/product="phfB"
/protein_id="AAO17172.1"
/db_xref="GI:27479645"
/translation="MKKILSPALMICCLSLPAVAELFYDINALQLSDEKENINLSL
AKTDSHPGYKNNVYVKKDIQVKSIFNCGEKLCPELSILLKEIGVIGTSPFEL
ASLAEQIISQPKYIKQAGAEIDLALMLNPPQAMQSIQIGDIPQWDDGLPM
FFNYHLTGKNNQSEONVNLNRSFNLGFWIRHNSYNHTGTTSPWEMLSLKY
AERDIRPLRSLVIGTSQDMVDFSTENGKILMSQMLPDSQQQFA PVVRGIAMT
HARVEHQKNIYIQTFVPPGAREITDIYPSNLNGDLEISIEYENGVRKFTOPPAAS
PLMRSCQKIFANIGRFGSGKQSKRRFIQTEAIGLWDSITTIYGGVIVSSDIQSHA
LGHLNUGKIYAGSVIDVNTAATHPNGEKSGSQYIRYSKGFETNTVTLAGRYN
TNGYFSFDANNYSYNNYTNHNFQITDNNRNSAPKNNRMOITMGQSLGYSLSAQW
QDYWDKTSKNQSYMSYNTNIRDISLSLSYNYHNRNINNDQVFNISIPLDKWL
PSNNHSADVDSYNTNGSSOHSMTLSGLLEQONLNTYISQNSYSEKSEKESGN
AASLYRGSYNSVGYTIDHRKNQRVNYGLEGAIIAHYPGVTLAQNISSESGSALIR
APGATNAKVNNTSISTDRGTYVVPYISQIRENMLSLDNTFGDDVDIDNPTTKVIP
TKALTLADLADYSIRVGRHVFILQHHGKKLPFGTVITGPNGVNGVNEKEGVFLSGVSD
7758..8738
/gene="phfA"
7758..8738
/gene="phfA"
/note="PhfA-like; fimbrial adhesin Photorhabdus luminescens
NC19 found in GenBank Accession Number AAK16069"
/codon_start=1
/transl_table=11
/product="phfA"
/protein_id="AAO17173.1"
/db_xref="GI:27479646"
/translation="MRNKLIIALLLTFLNVTKSIASCLSKNFKAILNLVDINEII
NSRNHNAYILIAQYGMELASKIDIKADSAIANCDSDATILFKTAPNRSANPNPD
SGLIKTNANNIYFVVKYLGSKSNPENKILSLKDIGEVQVLYVDGDLTPGDKLKKGL
ISSLTVDNKLRIKIDKENVIENTSMTSTPYRKLVLGRHKISDPNGKQAKSRP
SFYISIECKGNILPTIYFSGETIAEVDPKDKDSVIRLUNKYSGSREAGVGVMIIHKGV
FVAMRKPIYTVPSGRIGVYISPLSAHYIYQDDTTITGTGTANASVQFTIEYK"
9016..10026
/gene="phfB"
9016..10026
/gene="phfB"
/note="PhfB-like; fimbrial adhesin Photorhabdus
luminescens NC19 found in GenBank Accession Number
AAK16070"
/codon_start=1
/transl_table=11
/product="phfB"
/protein_id="AAO17174.1"
/db_xref="GI:27479647"
/translation="MKSYLRLIISAVLLFSINKYAAACISESTTSSTGVYFDLNSLKL
NLNTSNTKSIHVAFSAEQLASSMGLNIDPIFCDDNGYLVFGESYVPSMAGNTEHG
KTLTGIDNLVLFVASTGNLNMKPYTMDGRSYIYVPPKKKIWKDIDGIDIVDY
KEGAKISGRSLHAGIISLQTSNGIRLITIRNTRHYHTAGGCWALSGDQNTPEHDYV
SSSTFGKGTAGHADFNIGTIECTRIEPTITFSARTINGAPESIQLGNKQNPNTAG
VGVOILYMGTPVPVIGKPFVVGHSRNRNRYNLPFTARYIQDDRTITAGKANATAHTVQ
YE"
10072..10815
/gene="nrgA"
10072..10815
/gene="nrgA"
/note="NrgA-like; similar to EntD 4'-phosphopantetheinyl
transferase Photorhabdus luminescens NC19 found in GenBank
Accession Number AAK16071"
/codon_start=1
/transl_table=11
/product="nrgA"
/protein_id="AAO17175.1"
/db_xref="GI:27479648"
/translation="MEQTVIHTNQAPLPEYDNGFITQIEYGVVNNPQVHFQWTRFEL
SHYHDELFNQLNLPFPATLAKAVKKRAEYLAARYCAREQLLAQLGQPEFNLSGNDRA

PIWEGICGSVSHSTHCAIVLAAPOTHNRLIGVDVEAIVDRQNMDEITRMI VNDREIQ
LLKXCHLPLEQAFTAFSVKESLYKALYPOVKRFPGFEAAEITALSLENNEITLMLRE
TLTHYPTGTIFRGQFIYIPQSHILTVIQ"
/genes="hpcR"
complement (10892..11338)
/genes="hpcR"
complement (10892..11338)
/note="HpcR-like; regulator of homoprotocatechuate

Query Match 96.7%; Score 2653.8; DB 1; Length 127816;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2688; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy	1	ATCAGCAGTTACAAATTCGCAATTGTCACAAATGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Db	98698	ATCAGCAGTTACAAATTCGCAATTGTCACAAATGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	98757
Qy	61	AGGAAATTAATTAATGACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT	120
Db	98758	AGGAAATTAATTAATGACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT	98817
Qy	121	GAATTAATTAATGACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT	180
Db	98818	GAATTAATTAATGACGTACTTTAGAAATATCTACGCACCTCAAGCTGACGAAAAACAGTGAT	98877
Qy	181	CGTAAATAATAAAACACAGAGCGGCCCAAAATTCATTCTGTCCTTTAATCTTGC CGGTCAA	240
Db	98878	CGTAAATAATAAAACACAGAGCGGCCCAAAATTCATTCTGTCCTTTAATCTTGC CGGTCAA	98937
Qy	241	GTTTACGTGAAGAAAGTGTGATGCGGTCGGAATATTACCCCTCAATGATATTGAAAGT	300
Db	98938	GTTTACGTGAAGAAAGTGTGATGCGGTCGGAATATTACCCCTCAATGATATTGAAAGT	98997
Qy	301	CGCCCGGTGTGATCATCAATGCAACCGGTGTCCGCAAAACCATCGTTATGAAGATAAC	360
Db	98998	CGCCCGGTGTGATCATCAATGCAACCGGTGTCCGCAAAACCATCGTTATGAAGATAAC	99057
Qy	361	ACCTTCCCGGTGTGATCGCTATCACCAGCAAGTACAGCAGGAGAGAGAAACAGACC	420
Db	99058	ACCTTCCCGGTGTGATCGCTATCACCAGCAAGTACAGCAGGAGAGAGAAACAGACC	99117
Qy	421	GAAAGTCTTATCTGGGCGGCAATACGCCGCAAGAAAGATTTACACCTCGCGGTGAG	480
Db	99118	GAAAGTCTTATCTGGGCGGCAATACGCCGCAAGAAAGATTTACACCTCGCGGTGAG	99177
Qy	481	TGTGTCCGCAATTAACGATACCGGGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGC	540
Db	99178	TGTGTCCGCAATTAACGATACCGGGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGC	99237
Qy	541	GTCTGTCTATCACAATCTCAACCACTGCTTACCGATAACAGGATGCGACTGGACAGGT	600
Db	99238	GTCTGTCTATCACAATCTCAGCACTACTCGTCAATGATTAATAATGCTGACTGGACAGGT	99297
Qy	601	GAAGACACAGACCTCTGGCAACAAAACTGAGTAGTGATCTATATACCCCAAGATAAC	660
Db	99298	GAAGACCAAGCTCTGGCAGCAAAACTGAGCAGTGATCTCTATACCCCAAAAAATAA	99357
Qy	661	ACTGATGCCACCGGGGCTTTACTGACCCAGACGATGCCAAAGGCAACATTCAGCGGCTG	720
Db	99358	GCCGATGCCACCGGGGCTTTATTGACCCAGACGATGCCAAAGGCAACATTCAGCGGCTG	99417
Qy	721	GCCTATGATCTGGCGGAGCTAAAGGAGTTGGTTAAACACTCAAGAGGTTCAGCGCGGAA	780
Db	99418	GCCTATGATCTGGCGGAGCTAAAGGAGTTGGTTAAACACTCAAGAGGTTCAGCGCGGAA	99477
Qy	781	CAGTGATTAATCAAAATCGCTAAACCTACTCCCGCGCGGCAAAATTAATTCGTGAAGACAC	840
Db	99478	CAAGTGATTAATCAAAATCGCTAAACCTACTCCCGCGCGGCAAAATTAATTCGTGAAGACAC	99537
Qy	841	GGTAAACCGGATTTGCTCACTGAATACAGCTACGAACCGGAAACCCAAACCGCTTTCGGCAT	900
Db	99538	GGTAAACCGGATTTGCTCACTGAATACAGCTATGAACCGGAAACCCAAACCGCTTTCGGCAT	99597

Db 59363 ACAAACAAGAGGTTACACGTGATCACACTAGGTGAAGCGGTCCGCGACACAGGTCCGG 59304

Qy 1621 GTGTTGCACTGGGAGAGCGGTAAAGCAGAGATGTCACCAATAATCAACTACGTTACAGC 1680

Db 59303 GTGCTGCACTGGGAGAGCGGTAAAGCAGAGATGTCACCAATAATCAACTACGTTACAGC 59244

Qy 1681 TACGATAATCTGATCGGCTCCAGCGAGCTTGAACCTGGACACCAAGGACAAATTTATCAGC 1740

Db 59243 TACGATAATCTGATCGGCTCCAGCGAGCTTGAACCTGGACACCAAGGACAAATTTATGAT 59184

Qy 1741 GAGGAAGATTTATTCATTTGCGGAGACAGCGCTGTGGGAGCAAAACAGCCAAACAGAA 1800

Db 59183 GAGGAAGATTTATTCATTTCCGCGGACACAGCATGTGGGAGCAAAACAGCCAAACAGAA 59124

Qy 1801 GCCAGCTATAAAACGATTCGCTATTCCGCGCAAAACAGAGATGCCACCGGCTGTATTAT 1860

Db 59123 GCCAACTATAAACTATTTCGCTATTTCAGGCAAAACAGCGGATATCAACCGGCTGTATTAT 59064

Qy 1861 TACGGTTATCTGTTATTACCAACCGTGGCGGCGAGATGTTAAGCGGAGCCCGGACAGGA 1920

Db 59063 TACGGTTACCGCTATTATCAACCGTGGCGGCGAGATGTTAAGCGGAGTCCGCGACGA 59004

Qy 1921 ACCATTGATGGCTGAATCTATACCGAATGTAAGAAATTAATCTCTGTAGTTTACAAGAT 1980

Db 59003 ACCATTGATGGCTGAATCTATACCGAATGTAAGAAATTAATCTCAGTAAGTTTCAGGAT 58944

Qy 1981 GAAATGATTTAGCGCCAGAAAAGGGAATATACCAAGAGGTAAATTTCTTTGATGAA 2040

Db 58943 GAAATGATTTAGCACCAAGAAAGGAAATATATCTAAAGAGGTGAATTTCTTTGATGAA 58884

Qy 2041 TTAATAATCAAAATGGGACCCAAAAGTTTCAATGTTGTCAATGTAAGGAAAGGAAAGAGAGC 2100

Db 58884 TTAATAATCAAAATGGGACCCAAAATTTCAATGTTGTCAATGTAAGGAAAGGAAAGGAAAGT 58824

Qy 2101 AGTTATACAAAATAAATCAATGAAAGTGTTCGTTGCGTGATTCGATCCGTCGGGT 2160

Db 58823 AGTTATACAAAATAAATCAATGAAAGTGTTCGTTGCGTGATTCGATCCGTCGGGT 58764

Qy 2161 TATTGCTAAGCCAGAGAGTTACTAAAGGTTATAGAAAAGTCAAAATCATATATAGC 2220

Db 58763 TATTGCTAAGCCAGAGAGTTACTAAAGGTTATAGAAAAGTCAAAATCATATATAGC 58704

Qy 2221 CGACTTGAAGAAAACAGCTCCCTTTTCAAAAAATCAAAAAAGCAATCTTTCTTTAGGATCT 2280

Db 58703 CGGCTCGAAGAAAACAGATCCCTTTTCAAAAAATCAAAAAAGCAATCTTTCTTTAGGATCT 58644

Qy 2281 GAAATATCCGTTTATATGCGAAGAACCAATACAGATACGATATCAGAAATATGCGGAAGAG 2340

Db 58643 GAAATATCCGTTTATATGCGAAGAACCAATACAGATACGATATCAGAAATATACAGAAAGG 58584

Qy 2341 CATAAATATAGAAATATCACCTGATTTTATTTCAGAAAACGATTTCTTTGCGTTAATG 2400

Db 58583 CATAGGTTATAGAAATATCATCCGATTTTATGCAAGCAAGATTTCTTTGCTTTAATG 58524

Qy 2401 GATAAAGTGAAAAAATGATTTTCCGCTGAAAGAAAAATTTATGCGGCAATGAGGTT 2460

Db 58523 GATAAAGTGAAAAAATGATTTTCCGCTGAAAGAAAAATTTATGCGGCAATGAGGTT 58464

Qy 2461 AAGGTTTATCATGATTTAAAAAATAAACAATCAGAAATTTACATGCAACTATGCAATGGCC 2520

Db 58463 AAGGTTTATCATGATTTAAAAAATAAACAATCAGAAATTTACATGCAACTATGCAACTGGCT 58404

Qy 2521 CATCCCTATACCAATTCAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 2580

Db 58403 CATCCCTATACCAATTCAGTAATGAAGAAAGCGCTGTTGCAAGAAACAGAACCCGCT 58344

Qy 2581 ATTGCAATAGATAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGACAAATGAAAGCA 2640

Db 58343 ATTGCAATAGATAGAAATATAATTTCAAAGGTGTTGGCAAAATTCCTGCAATGAAAGCA 58284

Qy 2641 ATTAATAAATCATTTGAAAGGACATAAAATTAATAGGATATCAACAGAGGCTATTAAATAT 2700

Db 58283 ATTAATAAATCATTTGAAAGGACAGAGATCAATAAAATATCAACAGAGGCTATTAAATAT 58224

Qy 2701 CGCTCTCGGCTATCGCTGAGAAATTTAGCAATGCGGAGAACTTCA 2745

Db 58223 CGCTCTCGGCTATCGCTAAGAATTTAGGAATGCGGAGAGCTTCA 58179

RESULT 4

LOCUS CQ824622 2817 bp DNA linear PAT 21-JUN-2004

DEFINITION Sequence 15 from Patent WO2004044217.

ACCESSION CQ824622

VERSION CQ824622.1 GI:49021703

KEYWORDS

SOURCE

ORGANISM

Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

REFERENCE

1

French-Constant, R.H. and Waterfield, N.R.

Dna sequences from tcd genomic region of photorhabdus luminescens

Patent: WO 2004044217-A 15 27-MAY-2004;

UNIVERSITY OF BATH (GB)

FEATURES

Location/Qualifiers

1..2817

/organism="Photorhabdus luminescens"

/mol_type="unassigned DNA"

/db_xref="taxon:29488"

1..2817

/note="unnamed protein product"

/codon_start=1

/transl_table=11

/protein_id="CAG38452.1"

/db_xref="GI:49021704"

/translation="MENIDPKLVHHTPTVSHDNRGLAIRNISFHRHTTAEATDTRIT

RHYNAGGLNQSIDPRLDADAKQTNNAVOPNFWRNLGNLRTESVDAGRTITLND

IEGRVLTINAAGQRHNYEDNTLPRLLAISEQCAAEKTERLIERLINAGTQEQKDH

NLAGOCVRHYDTAGLTQLNSALATGLVLSQSQQLLTDNQDADTDQSLQWQKLSKD

VYITQNTDALTGALLTQTDAGNIQRLAYDVGQLKGSWLTLLKGQAEQVLIKSLTYS

AGOKLEEHGNGIVTBSYVEPETRIGITTRRPSDAKVLQDLRYQDPVGVNISRN

DEATFWRNQKVAPENSVTYDSLYOLISATGEMANIGQSNQLSPALPSDNNTYT

NYRTVYDRGGNLTQIQQSSPAQNNYTTDITVNSRNPVLTSTADPTVDALFD

AGHQSTLSUGQVLTWTPRGLQKQANSAGNEWIRYDSNGIRQLKVEQQTQNI PQQ

DVYLPGLSIRITNNATTEELHVTILGKAGRAQVRVLHWSGKEDINNQLRYSY

NNLIGSQLQSDGQIIIEEYVYFPGTALWAARNPTQFDOGLSPANTBEAIIQK

YGVRYVQWAGRWLADPAGTIDGLNLYRVNRNPNPTQFDOGLSPANTBEAIIQK

GSFTGMEAVYKKWAKPQTKRORATAAOTQEAEHESLTNNPSVDISPIKNYTTDSQ

INAAIRENRTIPAVESIDATLSLQDRQMRVTVMTYVDNSTPSPHSPQEGNSINV

GDIVDNALYSTSAHRGFLNFVHKKETSETRYVVMKAFNLNAGVNVPAASHNAGEBQ

VFKVDLNDSRKSLAEKILRVSGPQSGQAEILLPRETQFEVSMKHQGRDTYVLLQDI

NQSAATHRVNRVTYTGNTGKSSAN"

ORIGIN

Query Match 52.5%; Score 1440.6; DB 6; Length 2817;

Best Local Similarity 82.9%; Pred. No. 0;

Matches 1663; Conservative 0; Mismatches 329; Indels 15; Gaps 1;

Qy 21 AATTGACCAAAAGACCCCTCGATTAGGTATTAGATAACAGGAAAATTAATGTACCGTAC 80

Db 21 ACTTTATCACCATACGCTACCGTACGTGTTTCAGGATAACCGTGAGTAGTATCCGTAA 80

Qy 81 TTTAGAAATATCTACGCACTCAAGCTACGAAAAACAGTGATGAATTAATTCAGTTCTATGA 140

Db 81 TATTAGTTTTTCCGCGACTACCCGAGAAACAAATACCGATACCGGTATTATCCCGCCATCA 140

Qy 141 GTTCAATATTTCGCGGATTTTCAGGTAAAGAACCGGATCCCTCGTA-----A 185

Db 141 ATATAAATCCGCGGATATTGAAACCAAGCATTCGCTCGCTGTATGACGCCAAACA 200

Qy 186 AATAAAAAACACAGCGCGCCAAATTTTCATTTCGTGCTCTTTAATCTTCCGCTCAAGTTTT 245

Db 201 GACTAACACGCTGTACACCGGAATTTTATCTGCGGACATAATTTGACCGGCAATATCCT 260

Qy 246 ACGTGAAGAAAGTGTGTGATCCGCTCGGACTATTTACCCCTCAATGATATTGAAGTCGCC 305

Db 261 GCGAACAGAGCGTCGATGCCGTCGGA CGATTACCCCTCAACGATATTGAGGCCGCC 320
Qy 306 GGTGTTGATCATCAATGCAACCGGTGTCGCGCAAAACCATCGTTTATGAAGATAACACCCCT 365
Db 321 GGTGTTGACCATCAATGACGCGGTGTCGCGCAAAACCATCGCTTACGAAGATAACACCCCT 380
Qy 366 TCCCGGTGCTGCTGCTATCACCGGAACAAGTACAGCAGGAGAGAGAAAACGACCGAACG 425
Db 381 GCCCGGTGCGCTGCTGCTATCAGCGAACAAGGACAGGCGAAGAGAGAAAACGACCGAGCG 440
Qy 426 TCTTATCTGGCGCGCAATACGCGCAAGAAAAGATTTACAACCTCGCGGTGCTGCTGCT 485
Db 441 CCTTATCTGGCGCGCAATACGCGCAAGAAAAGAACCAACCTTCCCGGTGCTGCTGCT 500
Qy 486 CCGCATTATACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGCTGCGGTGCT 545
Db 501 CCGCATTATACGATACCGCGGACTTACTCAACTCAACAGCCTTGCCTGACCGCGCGCT 560
Qy 546 GCTATCACAATCTCAACACTGCTTACCGATAACAGGATGCCGACTGGACAGTGAAGA 605
Db 561 TCTATCA CAATCTCAACAACTGCTTACCGATAACAGGATGCCGACTGGACAGTGAAGA 620
Qy 606 CCAGAGCCTCTGGCAACAAAACCTGAGTAGTGCTATATCAACCCAAAAGTAACTGA 665
Db 621 CCAGAGCCTCTGGCAACAAAACCTGAGTAGTGCTATATCAACCCAAAAGTAACTGA 680
Qy 666 TGCCACCGCGGCTTACTGACCCAGACCGATGCGCAAGGCAAACTTCAAGCGGCTGGCCTA 725
Db 681 TGCCACCGCGGCTTACTGACCCAGACCGATGCGCAAGGCAAACTTCAAGCGGCTGGCCTA 740
Qy 726 TGATGTGGCGGAGCTAAAGGAGTTGGTTAACTCAACTCAAAAGTCAAGCGGAAACAGGT 785
Db 741 TGATGTGGCGGAGCTAAAGGAGTTGGTTAACTCAAAAGTCAAGCGGAAACAGGT 800
Qy 786 GATTATCAATCGTAACTACTCCGCGCGCGGCAAAAATTAAGTCAAGAGCACGGTAA 845
Db 801 GATTATCAATCGTAACTACTCCGCGCGCGGCAAAAATTAAGTCAAGAGCACGGTAA 860
Qy 846 CCGGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGGCTTATCGGCATTACCA 905
Db 861 CCGGATTGTCACTGAATACAGCTACGAAACCGGAAACCCAAACGGCTTATCGGCATTACCA 920
Qy 906 TCGCGGTCCATCAGACGCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG 965
Db 921 TCGCGGTCCATCAGACGCCAAGGTGTTGCAAGACCTACGCTATCAATATGACCCAGTAGG 980
Qy 966 CAATGTCATTAAATATCGTAAATGATCGGGAAGCGACTCGCTTTTGGGCAATCAGAAAGT 1025
Db 981 CAATGTCATTAAATATCGTAAATGATCGGGAAGCGACTCGCTTTTGGGCAATCAGAAAGT 1040
Qy 1026 AGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACCGGGCG 1085
Db 1041 AGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAGCTTATCAGCGCCACCGGGCG 1100
Qy 1086 CGAAATGGCCAAATATCGGTGAGCAAAACCAACCTTCCCTCCCTGCGTACTCTGTA 1145
Db 1101 CGAGATGGCCAAATATCGGTGAGCAAAACCAACCTTCCCTCTCCGCGCTACTCTGTA 1160
Qy 1146 CAACAATACCTACACTAATATATCTGACGCTACAGCTATGATCAAGTGTATCTGAC 1205
Db 1161 TAACAATATACCTACCAACTATATCTGCACTTATCTATGACCGGTGGCGCAATTTGAC 1220
Qy 1206 GCAAAATTCGACAGCTCGCGAGTACCGGACCACTACCGGTGCTATCAACCTCTC 1265
Db 1221 GAAATTCGACAGTATGATCAGCGCGCAAAATAACTACACCGGATTAACCGTTTC 1280
Qy 1266 AAACCGCAGCAATCGGGGTGTTCTCAGTAGCTAAACACCGATCCAAATCAAGTGGATAC 1325
Db 1281 AATTCGAGCAACCGCGGTACTTCAGCACATTGACCGGAGATCCAACTCAAGTCCATGC 1340
Qy 1326 GTTGTGTTGATGCGCGGTGTCACAAACCAAGTTTATTACCGGACAGACACTTATCTGGAC 1385

Db 1341 CTTATTTGATCGGGAGCCATCAAAACCAGCTTGTATTATCGGCCAAGTCTTAACCTTGAC 1400
Qy 1386 ACCACGAGGAGAGTTAAAGCAGGTTAATATATGCCCGGGAAATGAGTGGTACCGCTACGA 1445
Db 1401 ACCGCGAGGCGAATTTGAAACCAAGCCAAATAGCGCAGGAAATGAGTGGTATCGCTACGA 1460
Qy 1446 CAGCAACGGCAGTACAGCAACTGAAAGTGAAGTGAAGCCNAACCCAGAAATACTAGCGNACA 1505
Db 1461 TAGCAACGGCAGTACCGCAGCTAAAGTGAATGAACCAAACTCAGAATATCCCGCAACA 1520
Qy 1506 ACAACGGGTAACTTATTTGCGGGACTGAGCTTACGCAAAACCCAGAGCAACCCCAAC 1565
Db 1521 ACAACGGGTAACTTATCTACCGGGCTGGAATACGTACAAACCCAGAAACAAACCCCAAC 1580
Qy 1566 AACCGAAGAGTTACACGTTTATCACTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTT 1625
Db 1581 AACAGAAGAGTTACACGTTTATCACACTCGGTAAAGCGCGCGCGCAAGTCCGAGTATT 1640
Qy 1626 GCATCGGAGAGCGGTAAAGCCAGAGATGTCAACAATATCAACTAGTTCAGCTACGTA 1685
Db 1641 GCATTCGGAGAGCGGTAAACCCAGAGATATTAATAACAATCAGCTTCGTTTACAGTACGA 1700
Qy 1686 TAACTCTGATCGCTCCAGCCAGCTTCAACTGGACACCAAGGACAAATATATCAGCCGGA 1745
Db 1701 TAACTCTTATTTGGCTCCAGCCAACTTCAATTAGATAGCAGCGGACAAATATATCAGTGA 1760
Qy 1746 AGAGTATTATCCATTTTGGCGGACAGCGCTGTGGGCGACAAACAGCAACAGAACGAC 1805
Db 1761 AGAATATTATCCATTTGTTGTTACAGCGCTGTGGGCGGCAAGGAATCAAAACCGNAGCC 1820
Qy 1806 CTATAAAACGATTCGCTTATTCGGGCAAGAACAGAGATGCCACCGGTTTGTATTATACGG 1865
Db 1821 CTATAAAACGATTCGCTTATTCGTTAAAGAGCGGATGTTACCGGCTGTATTATTATGG 1880
Qy 1866 TTATCTGTTATTAACCAACCGTGGCGGAGAGTGTAAAGCGGCGCCGCGGAGAACCAT 1925
Db 1881 CTACCGTTTATTAACCAACCGTGGCGGAGAGTGTAAAGTGTGACAGACCCGCGGAGAACCAT 1940
Qy 1926 TGATGGCTGGAATCTATACCGAATGTAAGAATATCTGTGAGTTTACAGATGAAA 1985
Db 1941 TGATGACCTGAATTTATATCGCATGTTGAGAAATAACCCGGTGACCAATTTGATGTTCA 2000
Qy 1986 TGATTTAGCGCCAGAAAAAGGGAATA 2012
Db 2001 GGGATTATCACCGGCCAACAGAACAGA 2027

RESULT 5
CQ854091
LOCUS 2817 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 57 from Patent WO2004067727.
ACCESSION CQ854091
VERSION CQ854091.1 GI:51510128
KEYWORDS
SOURCE
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS Hey, T.D., Schlieper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
Li, Z.S., Ni, W., Zhu, B., Merlo, D.J., and Apel-Birkhold, P.C.
TITLE Mixing and matching tc proteins for pest control
JOURNAL Patent: WO 2004067727-A 57 12-AUG-2004;
Dow Agrosciences LLC (US)
FEATURES
source location/Qualifiers
1..2817
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/strain="W14"
/db_xref="taxon:29488"
1..2817
exon
ORIGIN

Query Match		52.5%;	Score 1440.6;	DB 6;	Length 2817;	
Best Local Similarity		82.9%;	Pred. No. 0;			
Matches 1663;		Conservative	0;	Mismatches 329;	Indels 15;	Gaps 1;
Qy	21	AAATTGACCAAAAGACCCCTCGAATTAAGGTATTAGATAACAGGAAATTAATGATGAC	80			
Db	21	ACITTTATCACCATACGCTACCGTCAGTGTTCACGATAAACCGTGGACTAGCTATCCGTAA	80			
Qy	81	TTTAGAATATCTAGCAGCTCAGCTGACGAAACAGATGATGAATTAATTAAGTCTCTATGA	140			
Db	81	TATTTAGTTTTTACCGCACTACCGCAGAGCAATATACCGATACCCGTTATTAACCGCCATCA	140			
Qy	141	GTTCATATTTCCGGATTTTCAGGTAAAGAACACCGATCCCTCGTA-----A	185			
Db	141	ATATAATTCGGCGCGGATTTTGAACCAAGCAATTTGATTCCTCGCCTGTATGACGCCAACA	200			
Qy	186	AAATAAAAAACAGAGCGGCCCAATTTTCATTCGTGTCTTTAATCTTCGCCGTCAAGTTTT	245			
Db	201	GACTAACCAAGCTGTACCAACCGAATTTATCTGCGGACATAAATTTGACCGCAATATCCT	260			
Qy	246	ACGTGAAGAAAGTGTGATGCGCGTCCGATATTTACCTCAATGATATTGAAGTCCGCC	305			
Db	261	GCGAACACAGAGCTGATGCGGTCCGACGATTTACCTTCAACGATATTGAAGCCGCC	320			
Qy	306	GGTGTGATCATCAATGCAACCGGTGTCGCCAAAAACCATCGTTATGAGATACACCT	365			
Db	321	GGTGTGACCATCAATGACGCGGTGTCGCCAAAAACCATCGTTATGAGATACACCT	380			
Qy	366	TCCCGGTGCTGCTGCTATCACCGAAACAGTACAGCAGGAGAGAAACGACCGAACG	425			
Db	381	GCCCGGTGCTGCTGCTATCAGGAACAGGACAGGACAGAGAAACGACCGAGCG	440			
Qy	426	TCCTATCTGGCGCGGCAATACGCGCAAGAAAAAGATTACACCTCGCGGTCTAGTGT	485			
Db	441	CTTATCTGGCGCGCAATACGCGCAAGAAAAAGACCAACCTTGCCTGCTCAGTGGT	500			
Qy	486	CCGCATTTACGATACCGGGACCTTACTCACTCAATAGCCCTTCTCTGGCTGCGCTCGT	545			
Db	501	CCGCATTTACGATACCGGAGACCTCACTCACTCAACAGCCTTGCCTGACCGCGCGCGT	560			
Qy	546	GCTATCAAAATCTCAACAACTGCTTACCGATAACACAGGATCCGACTGGACAGGTGAAGA	605			
Db	561	TCATATCAAAATCTCAACAACTGCTTACCGATAACACAGGATCCGACTGGACAGGTGAAGA	620			
Qy	606	CCAGAGCTCTGGCAACAAAAAATCAGTAGTGTCTATATCAACCCAAAGTAACTAGTA	665			
Db	621	CCAGAGCTCTGGCAACAAAAAATCAGTAGTGTCTATATCAACCCAAAGTAACTAGTA	680			
Qy	666	TGCCACCGGGCTTTACTGACCCAGCGATGCCAAAGGCAACATTCAGCGGCTGGCCTA	725			
Db	691	TGCCACCGGGCTTTACTGACCCAGCGATGCCAAAGGCAACATTCAGCGGCTGGCCTA	740			
Qy	726	TGATGTGCGCGGAGCTAAAAGGAGTTGGTTAACTCAAGCTCAAGGCTCAGGCGGAACAGGT	785			
Db	741	TGATGTGCGCGGAGCTAAAAGGAGTTGGTTAACTCAAGGCTCAGGCGGAACAGGT	800			
Qy	786	GATTATCAAAATCGCTAACCTACTCCGCGCGGGCAAAAAATTCAGTAAGAGCAGGTAA	845			
Db	801	GATTATCAAAATCGCTAACCTACTCCGCGCGGGCAAAAAATTCAGTAAGAGCAGGTAA	860			
Qy	846	CGGATTTGCTACTGAATACAGTACGAACCGGAACCCAAACGGCTTATCGGCATTAACAC	905			
Db	861	CGGATTTGCTACTGAATACAGTACGAACCGGAACCCAAACGGCTTATCGGCATTAACAC	920			
Qy	906	TCCCGGTCCATCAGACGCGCAAGTGTTCGAAGACCTTACGCTATCAATATGACCCAGTAGG	965			
Db	921	TCCCGGTCCATCAGACGCGCAAGTGTTCGAAGACCTTACGCTATCAATATGACCCAGTAGG	980			
Qy	966	CAATGCTCAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATTCAGAAAGT	1025			
Db	981	CAATGCTCAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATTCAGAAAGT	1040			
Qy	1026	AGCCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGCGGCCACCGGGCG	1085			

1041	AGCCCCGGAGATAGCTATACCTACGATTCCTCTGTATCAGCTTATCAGCGGCCACCGGGCG	1100
1086	CGAAATGGCCCAATATCGGTACGCAAAACAACTTCCCTCCCTGCGCTACCTTCTGA	1145
1101	CGAGATGGCCCAATATCGGTACGCAAAAGCAACAACTTCCCTCTCCGGCGCTACCTTCTGA	1160
1146	CAACAACTACTACACTTAATCTACTCGCAGCTACAGCTATGATCAAGTGGTAATCTGAC	1205
1161	TAACATACTACACCACTTACTCGCACTTACTTATGACCGTGGCGCAATTTGAC	1220
1206	GCAAAATTCGGCAAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCACCCCTCTC	1265
1221	GAAATTCAGCATAGTTTACACAGCGCGCAAAATTAATCAACGAGATTAACCGTTTC	1280
1266	AAACCCGCAATCGGGTGTCTCAGTACGCTTAACCAACCGATCCAAATCAAGTGTATAC	1325
1281	AAATCCAGCAACCGCGCGTACTCAGCACTTGACCGCAGATCCAACTCAAGTCTGATGC	1340
1326	GTGTTTGTATGCGGTGGTCCACAAACCAAGTTTATTACCGGACAGACACTTATCTGGAC	1385
1341	CTTATTTGATGCGGAGGCCATCAACCAAGCTTGTATTCCGGCCAAGTTCTAATTTGGAC	1400
1386	ACCACGAGGAGTTTAAAGCAGGTTAATTAATGGCCCGGGAATGAGTGTGATCCGCTACGA	1445
1401	ACCGGAGCGCAATTGAAACAAAGCCAAATAGCGCAGGAAATGAGTGTGATTCGCTACGA	1460
1446	CAGCAACGGATCAGCAACTGAACTGAGTGAACAGCAACCCAGAAATTAATCAAGTGTGAT	1505
1461	TAGCAACGGCATACGCGAGCTAAAGTGAATGAACAACTCAGAAATATCCCGCAACA	1520
1506	ACAACGGTAACTATTGTCGGGACTGGAGCTTACCAACAAACCCAGAGCAACCCCAAC	1565
1521	ACAAAGGTTAATTTCTACCGGGCTGGAAATACGTACAAACCCAGCAACCCCAAC	1580
1566	AACGGAAGAGTTACAGCTTATCAGCTCGGTGAAGCGGTTCGCGCAACGATACGGGTGTT	1625
1581	AACAGAAGAGTTACAGCTTATCAGCTCGGTAAAGCGCGCGCAAGTCCGAGTATT	1640
1626	GCACTGGGAGAGCGGTAAAGCAGAGATGTCAACAAATTAATCACTAGTTTACAGCTACGA	1685
1641	GCACTGGGAGAGCGGTAAAGCAGAGATTAATAACAACTCAGCTTCTGTTTACAGCTACGA	1700
1686	TAATCTGATCGGCTCCAGCAGCTTCAACTGGCAACCAAGGACAAATTAATCAAGCAGGA	1745
1701	TAATCTTATTTGGTTCAGCCCACTTCAATTAAGTAGGACGGAACAAATTAATCAAGTGA	1760
1746	AGAGTATTATCCATTTTGGCGGACAGCGCTGTGGGACGCAACAGCCAAACAGAACCCAG	1805
1761	AGAATATTATCCATTTGGTGTACAGCGCTGTGGCGGCAAGGAATCAAAACCGAAGCCAG	1820
1806	CTATAAAACGATTCGCTATTCGCGCAAGAAAGACAGATGCCACCGGGTGTATTATTACGG	1865
1821	CTATAAAACGATTCGCTATTCGCTTAAAGACGCGGATGTTTACCGGGCTGTATTATTATGG	1880
1866	TTATCGTTATTACCAACCGTGGCGGACAGTGTAAAGCGGACCCCGCAGCAACCAT	1925
1881	CTACCGTTATTACCAACCGTGGCGGACAGTGTAGGTGACAGACCCCGCAGGAACCAT	1940
1926	TGATGGCTCAATCTATACCGAATGGTAAGAAATAATCTCTGTGAGTTTACAAGATGAAA	1985
1941	TGATGGCTCAATCTATACCGAATGGTAAGAAATAATCTCTGTGAGTTTACAAGATGAAA	2000
1986	TGATTTAGCCCAAGAAAGGGAATA	2012
2001	GGGATTATCACCGGCCAACAGAACAGA	2027

RESULT 6

BX571874

LOCUS

DEFINITION

349907 bp

DNA

linear

BCT 17-APR-2005

Photorhabdus luminescens subsp. laumondii Tt01 complete genome;

segment 16/17.

Db	28861	CCCAATCTCGTTGATACATCTTTTGATGCGAGGTGGTTCATCAAAACCAAGTCGTGTTCTCAGGG	28920
Qy	1369	CAGACACTTATCTGGACACACAGGAGAGGTTAAAGCAGGTTAA-----TAATGGCCCG	1422
Db	28921	CAATCTTAAACTGGACACACGGGAGAACTACAACAGTGAACCAAGTGGTAAATACC	28980
Qy	1423	GGAAATGAGTGGTACCGCTAGCAGCAACGCGATGAGACMACTGAAAGTGAAGTGAACAG	1482
Db	28981	GCCGCTGAGTGGTACCACATATGACAGTGAACGCGATGCGGTACTGAAATAAAGCAACAG	29040
Qy	1483	CCAACCCAGAAATACTAGCAGCAACCAACGGGTAAATCTATTTCGGGACTTGGAGTACGC	1542
Db	29041	CAAAACATCCAAATACACGACGACGACGACGACGACGACGACGACGACGACGACGACG	29100
Qy	1543	ACAACCCAGACCAACCCCAACCAACGAGAGTTCACGTTTATCACACTCGGTGAAGCC	1602
Db	29101	ACCACACAAGCGGCAACCAATATCACCGAAGACTTACAAGTTATTACTGTGACGCAAGCA	29160
Qy	1603	GGTCCGGCAGAGTACGGGTGGTGGCTGGAGAGCGGTAAGCCAGAAGATGTCAACAAT	1662
Db	29161	GGAAAAGCAAGTACGCGTACTACACTGGGAAAAAGGCCAACCCACCGCATAAATAAC	29220
Qy	1663	AATCAACTAGTTACAGTACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAAC	1722
Db	29221	GATCAAGTCAGATATAGTACGATAATCTTACACAGCAGCGAATTAGAACTGGATATG	29280
Qy	1723	CAAGGACAAATATCAGCAGGAGAGTATTATTCATTTGGCGGGACAGCGCTGTGGGCA	1782
Db	29281	CACGGAGAAATGATCAGTTGGGAAGAGTATTACCCCTATGTTGGCACCGCAGTATGGCA	29340
Qy	1783	GCAACAGCCAAACAGAGCCAGCTATAAAACGATTTCGCTATTTCCGGCAAAAGAACAGAT	1842
Db	29341	GCAAGAAATCAGATTGAAGCTGTTACAAACCAATTCGTTATTCAGTTAAAGAACCTGAT	29400
Qy	1843	GCCACCGGTTGATTTATTCAGGTTATCGTTATTAACCAACCGTGGGGCGGAGATGGTTA	1902
Db	29401	GCAACGGGACTGACTATTACGGCTACCGCTATTATCAACCGTGGGGCGGATAGATGGTTA	29460
Qy	1903	AGCGCGACCCGACGAAACATTTGATGGCTGAATCTATACCGAATGGTAAGAAATAAT	1962
Db	29461	AGCGCTGACCCGCTGGAACCGTAGATGGTCTGATTTGACCGTATGTTAGAAATAT	29520
Qy	1963	CTGTGAGTTTACAAGTGAATGG	1988
Db	29521	CCAAATACCGGCATAGATGAAGTGG	29546
RESULT 7			
AR166758			
LOCUS	37948 bp DNA linear PAT 17-OCT-2001		
DEFINITION	Sequence 11 from patent US 6281413.		
ACCESSION	AR166758		
VERSION	AR166758.1 GI:16242227		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 37948)		
AUTHORS	Kramer, V. Cary., Morgan, M. Kent., Anderson, A. Robert., Hart, H. Prim., Warren, G. W., Dunn, M. M. and Chen, J. Shong.		
TITLE	Insecticidal toxins from Photorhabdus luminescens and nucleic acid sequences coding therefor		
JOURNAL	Patent: US 6281413-A 11 28-AUG-2001;		
FEATURES	Location/Qualifiers		
source	1..37948		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
ORIGIN			
Query Match	36.9%; Score 1012.4; DB 6; Length 37948;		
Best Local Similarity	69.5%; Pred. No. 4.5e-227;		
Matches 1414; Conservative	0; Mismatches 596; Indels 24; Gaps 2;		

Qy	1	ATGAGCAGTTACAAATTTCTGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Db	15171	ATGAAAAACATCGATCCTAAACCTTTATCAAAAGACCCCTGTCGTCACATCTACGATAAC	15230
Qy	61	AGGAATTAATAGTACGTACTTTTAGAATATCTACGCACTCAAGCTCAGCAAAACAGTGAT	120
Db	15231	CGAGGTCTAACGATCGTAACATCGACTTTTACCCTGTAACCCGCAACCGCGATACCGAT	15290
Qy	121	GAATTAATTAAGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCGATCCT	180
Db	15291	ATCCGTTATTACTCGCCATCAATATGACTCCCTTGGCACCTAAGCCAAAGCACCGATCCG	15350
Qy	181	CGTAAAAATAAAAAACAGAGCGCCCAATTTCAATTCGTGCTCTTTAATCTTGGCGGTCAA	240
Db	15351	CGTCTATATGAAGCCAAAACTAACTTTCTCTGCGAGTATGATTTGACCGGTAAT	15410
Qy	241	GTTTTACGTGAAGAAGTGTGATGCGGTCGAGCTATTACCTCAATGATATTGAAAGT	300
Db	15411	ATTTTGTGTACAGAAAGCGTCTGATGCTGCGACTGTCACTTGAATGATATTGAAGGC	15470
Qy	301	CGCCCGTGTGATCATCAATGCAACCGGTCTCGCAAAACCATCGTTTATGAAGATAAC	360
Db	15471	CGTCCGCTACTGACAGTAATCTGCACAGGTGTATACAAACCCGCAATATGAACGTCT	15530
Qy	361	ACCTTCCCGGTCTGCTCGCTATCACCGAAACAGTAC---AGCGAGAGAGAAAAACG	417
Db	15531	TCCCTACCCGGTCTGTTGTCTGTTACCGAAACAAATACCAGAAAAACATCCCTATC	15590
Qy	418	ACGGAAGCTTTATCTGGGCGGCAATACGCGCAGAAAGATTTACAACTTCGCGGT	477
Db	15591	ACCGAAGCTGATTTGGGCTGGCAATACGGAAGCAGAGAAAAACCATATCTTGGCAGC	15650
Qy	478	CAGTGTCTCGGCATTAACGATACCGGGACTTACTCAACTCAATAGCCCTTCTCTGGCT	537
Db	15651	CAGTGTCTGGCACTATGACAGCGGGAGTACCCGATAGAGAGTTGTCACTGACC	15710
Qy	538	GGCGTCTGCTATCAAACTCTCAAACTGCTTACCGATAACAGATGCGGACTGAGACA	597
Db	15711	GGTACTGTTTATCTCAATCCAGCCAACTATTGAGCGCACTCAAGAAAGCTAGCTGACA	15770
Qy	598	GGTGAAGACAGAGCTCTGGCAACAAATCTGAGTAGTGTCTTATATCAACCCAAAGT	657
Db	15771	GGTGAATAATGAACCGTCTGGCAAAACATGCTGGCTGATGACATCTACAAACCTTGAGC	15830
Qy	658	AAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTTACAGCGG	717
Db	15831	GCCTTTGATGCCACCGGCTTTACTCACTCAGACCGATGCGNAAGGGAACATTCAGAGG	15890
Qy	718	CTGGCCTATGATGTGGCGGAGCTTAAAGGGAGTTGGTTAACTCAAAAGTTCAGGCG	777
Db	15891	CTAACCTATGATGTGGCGGCGAGCTAAACGGGAGCTGGTTAACTTAAAGACCAACCG	15950
Qy	778	GAAACAGTGAATTTCAATCGCTTAACCTACTCGGCGCGGCGGCAAAATTTACGTGAGAG	837
Db	15951	GAAACAGTGAATTTCAAGATCCCTGACCTATTCCGCGCGGCGGCAAAATTTACGCGAGAA	16010
Qy	838	CACGGTAAACGGGATTTGCTCACTGAATACACTAGCAACCGGAAACCCAAACGGCTTATCGGC	897
Db	16011	CACGGCAATGGTGTATTACCGAATACAGTTATGAACCGGAAACCCCAACAGCTTATCGGT	16070
Qy	898	ATTACACTCGCGCTCCATCAGACGCAAGGTGTTGCAAGACCTACGCTATCAATATGAC	957
Db	16071	ACCAAAACCCACCGTCCGTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCTG	16130
Qy	958	CCAGTAGGCAATGTCTAATTAATTCGTAATGATGCGGAAGCACTCGCTTTTGGCGCAAT	1017
Db	16131	CCGGTAGGCAATGTCTAATGATTCAGTATCCGTAATGACGCAAGAGCCACCGCTTCTGSCAAT	16190
Qy	1018	CAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTTCCTGTTATCAGCTTATCAGCGCC	1077
Db	16191	CAGAAAGTAGCCCGGAGAAACCTTATACCTACGCTCTCTGTTATCAGCTTATCAGCGCA	16250
Qy	1078	ACCGGCGGAAATGGCCAATATCGGTGAGCAAAACAAACAACTTCCCTCCCTGCGCTA	1137

Query Match		36.68;	Score 1004.6;	DB 6;	Length 2883;
Best Local Similarity		69.34;	Pred. No. 3.3e-225;	Mismatches 594;	Indels 42; Gaps 3;
Matches 1433;		Conservative 0;			
Qy	1	ATGAGCAGTTACAAATCTGCAATTTGACAAAGACCCCTCGATTAAAGGTATTAGATAAC	60		
Db	1	ATGAAACACATTGATCCAACTTTATCAAAAACCCCTACTGTCCAGGGTTACGATAC	60		
Qy	61	AGGAAATTAATGACCTACTTTAGATAATCTACGCACTCAAGCTGACGAAACAGTGAT	120		
Db	61	CGTGGTCTGATAATCCGTAAACATCGATTTTCATCGTACTACCGCAAAATGGTGATCCCGAT	120		
Qy	121	GAATTAAATAGTTCTATGATGTTCAATATTCGGGATTTTCAGGTAAAGACCCGATCCT	180		
Db	121	ACCGGTATTACCGCCCAATACATAGATATTACGCGACACCTAAATCAAGCATCGATCCG	180		
Qy	181	CGTAAATAAATAACCA-----GAGCGGCCCAAAATTTTCATTCGTGTCCTT	225		
Db	181	CGCTATATGAGCAAGCAACCAACAAATACGATCAAAACCAATTTTCTTTGGCAGTAT	240		
Qy	226	AATCTCCGGTCAAGTTTACGTGAAGAAAGTGTGATGCGGTGCGACTATTACCCCTC	285		
Db	241	GAITTGACCGGTAAATCCCTATGTACAGAGAGCAATTGATGAGGTGCGACTGTCCACCTG	300		
Qy	286	AATGATATTGAAAGTCGCGGTGTTGATCATCAATGCAACCCGCTGTCGCCAAACCAT	345		
Db	301	AATGATATTGAGGCCCTCGCTACTAAACGCTGACTCAACAGGGGTTATACAAATCGA	360		
Qy	346	CGTTATGAAGATACACCTTTCCCGTTCGTCTGCTATCACGAAACAAAGTACAGGCA	405		
Db	361	CAATATGAACCTTCTCCCTGCGCGGTGCTGTTATCTGTTGCCGAACAAACACCCGAG	420		
Qy	406	GGAGAGAAA-----ACGACCGAAACGCTTATCTGCGCGGCAATACCGCCGAAGAAAA	459		
Db	421	GAAAAACATCCCGTATACCGAAACGCTGATTTGGGCTGGCAATACCGAAGCAGAGAAA	480		
Qy	460	GATTACAACTTCGCGGTGAGTGTGCGCCATTACGATACCGGGGACTTACTCACTC	519		
Db	481	GACCATACCTTTCGCGGCCAGTGGTGGTCTACTATGACACGGCGGGAGTTACCCGGTTA	540		
Qy	520	AATAGCCTTTCTCTGGTGGCGTCTGCTATCAAACTCTCAACAACTGCTTACCGATAAC	579		
Db	541	GAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAATATTGATCGACACT	600		
Qy	580	CAGATCCGCACTGGACAGGTGAAGACAGAGCTCTTGGCAACAAAACTGAGTAGTAT	639		
Db	601	CAAGAGCAAACTGGACAGGTGATAACGAAACCGCTCTGGCAAAACATGCTGGCTGATGAC	660		
Qy	640	GTCTATATCAACCAAGTAAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCC	699		
Db	661	ATCTACAAACCTTGAGACCTTCGATGCCACCGGTCTTACTGACTCAGACCGATGCG	720		
Qy	700	AAAGGCAACATTCAGCGCTGGCTATGATGTGCGCGGAGCTTAAAGAGGAGTTGGTTA	759		
Db	721	AAAGGGAACATTCAGAGACTGGCTTATGATGTGCGCGGAGCTTAAACGGGAGCTGGCTA	780		
Qy	760	ACATCAAAAGTCAAGCGGAAACAGGTGATTATCAAAATCGCTAACCTACTCCGCGCGGG	819		
Db	781	ACATCAAAAGCCACAGCGGAACAGTGATTATCAAAATCCCTGACTACTCCGCGCGGGA	840		
Qy	820	CAAAAATTAAGTGAAGACAGGTAAACGGGATTCGCTCAATACAGCTACGACCCGGA	879		
Db	841	CAAAAATTAAGTGAAGAACAGGCAATGATTTATCACCGAATACAGTTATGAACCCGGA	900		
Qy	880	ACCAACCGGCTTATCGGATTTACCACTCGCCGCTCCATCAGACGCAAGGTGTTCAAGAC	939		
Db	901	ACCAACCGGCTATCGGATTCAAAACCCCGCTCGCTCAGACACATAAGTGCTACAGAC	960		
Qy	940	CTAGCCTATCAATATGACCCGATAGGCAATGTCAATTAATATCCGTAAATGATGCCGAAGCC	999		
Db	961	CTGCGCTATGAATATGACCCCGTAGGCAATGTCAATGATCCGATCCGTAAATGACCGCGAAGCC	1020		
Qy	1000	ACTCGCTTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTG	1059		
Db	1021	ACCGCTTTTGGCAAAATCAGAAAGTAGTCGGGAAAACACTTTATACCTACGATTCCTG	1080		
Qy	1060	TATCAGCTTATCAGCGCCACCGGGCGGAAATGGCCAATATCGGTGAGCAAAAAACAACAA	1119		
Db	1081	TATCAGCTTATCAGCGCCACCGGGCGGAAATGGGAAATATAGGTCAACAAGATCACCAA	1140		
Qy	1120	CTTCCCTCCGCTGCTCTCTCTGACAAATACCTACACTAACTATCTACTCTCGCAGTAC	1179		
Db	1141	TTTCCCTCACCCGCTCTACCTTCTGATAACAACCTTATACCAACTATACCCGCTACTAT	1200		
Qy	1180	AGCTATGATCACAGTGTGATCTGACGCAAAATTCGCGACAGCTCGCCAGCTACCCGAAC	1239		
Db	1201	ACTTATGACCGTGGCGCAATCTGACAAAATCCAGCACAGTTTACCGGGCAGCAAAAC	1260		
Qy	1240	AATACACCGTGGCTATCACCTCTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTA	1299		
Db	1261	AATACACCAACCAATATCAGGTTTCAAATTCGCGCAACCGCGCAGTACTCAGCACATTG	1320		
Qy	1300	ACCACGATCCAAATCAAGTGGATACGTTGTTGATGCCGGTGTCAACCAACAGGTTTA	1359		
Db	1321	ACGGAAGATCCGCGCAAGTAGATGCTTTGTTGATCGAGCGGACATCAGAACACCTTG	1380		
Qy	1360	TTACCCGCGCAGACACTTATCTCGACACACAGGAGAGTTAAAGCAGGTTAAATAATGGC	1419		
Db	1381	ATATCAGGACAAAACCTGAACTGGAATATCTGTTGTTGAACTGCAACAGTAACTGGTT	1440		
Qy	1420	CCGGGAAATGAG-----TGTTACCGCTACGACAGCAACCGGATG	1458		
Db	1441	AAACGGGACAAAGGCGCAATGATGATCGGGAATGTTATCGTTATAGCGGTGACGGAAGA	1500		
Qy	1459	AGAACTGAAAGTGTAGTGAAGCCAAACCCAGAAATACTACGAGCAACAAACGGGTATC	1518		
Db	1501	AGGATGTTTAAATATCAATGAACAGCGGCGAGCAACAAACCTCAACACACCTGTGACT	1560		
Qy	1519	TATTTGCGGAGCTGGAGCTACGCAACAAACAGAGCAACCCCAACAAAGAGAGTTA	1578		
Db	1561	TATTTGCGGAACTTAGAACTTCTGTTCAACAAACAGCAACGCGCCACAAACCGAAGATTG	1620		
Qy	1579	CAGCTTATCACTCGGTGAAGCCGTCGCGCACAGGTACGGGTGTTGCACTCGGAGAGC	1638		
Db	1621	CAAGTTATCACCTAGCGGAAGCGGCGCGGACAGGTACGAGTATTTACATTTGGGAGAGC	1680		
Qy	1639	GGTAAGCAGAAAGATGCAACAATTAATCAACTAGTTTACGCTACGATTAATCTGATCGGC	1698		
Db	1681	GGTAAACCGGAAGATATCGACAAATATCAGTTTCGCTTATAGTTACGATAATCTTATCGGT	1740		
Qy	1699	TCCAGCCAGCTTCAACTGGACAAACCAAGGACAAATTTATCAGCAGGAAGAGTATTATCCA	1758		
Db	1741	TCCAGTCACTTGAATTAGATAGCGAAGGACAAATTTATCAGTGAAGAAATATTATATCCC	1800		
Qy	1759	TTTGGCGGAGACGCTGTGGGAGCAAAACAGCCAAACAGAAAGCCAGCTATAAACCGATT	1818		
Db	1801	TATGGTGAACACAGCATTTATGGCGCGCCAGGAATCAGACAGAACCCAGTTATAAACTATC	1860		
Qy	1819	CGCTATTCCGCGAAAGAAACAGAGATGCCACCGGGTTGTTATTATTACGGTTATCGTTATAC	1878		
Db	1861	CGTTATTACGGAAGAGCGGGAATGCCACCGGCTATTTACTACGGCTATCGGTTATTTAC	1920		
Qy	1879	CAACCGTGGCGGAGATGTTTAAAGCGCGGACCCGCGAGAACCAATTTGATGGGCTCAAT	1938		
Db	1921	CAACCGTGGATAGGAACGGTGGTTAAGCTCCGATCCGCGAGGAACAACTCGATGGGCTCAAT	1980		
Qy	1939	CTATACCGAATGGTAAAGAAATAATCTCTGTGAGTTTACAAGATGAAATATGATTAAGCCCA	1998		
Db	1981	TTATATCGATGGTGAAGAAATAATCCAGTTACCTCTCTGATACCTCTCTGATGATTAATGCCA	2040		
Qy	1999	GAAGAAGGAAATATATACCAAGAGGTAAA	2027		
Db	2041	ACAATTGCAGAACGCAATAGCAGCACTAAA	2069		

RESULT 10	CQ854080	2883 bp	DNA	linear	PAT 23-AUG-2004
LOCUS	Sequence 46 from Patent WO2004067727.				
DEFINITION	CQ854080				
ACCESSION	CQ854080.1	GI:51510119			
VERSION					
KEYWORDS	Photorhabdus luminescens				
SOURCE	Photorhabdus luminescens				
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.				
REFERENCE	1				
AUTHORS	Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C., Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.				
TITLE	Mixing and matching tc proteins for pest control				
JOURNAL	Patent: WO 2004067727-A 46 12-AUG-2004;				
	Dow Agrosciences LLC (US)				
FEATURES	Location/Qualifiers				
source	1..2883				
	/organism="Photorhabdus luminescens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:29488"				
CDS	1..2883				
	/notes="unnamed protein product"				
	/codon_start=1				
	/transl_table=11				
	/protein_id="CAH19032.1"				
	/db_xref="GI:51510120"				
	/translation="MKNDIPKLYQKTPVSVYDNRGLIIRNIDFHTTANGDPDPRIT RHQYDIHGLHNSIQDPLREAEKQTNNTIKPNFLQYDLITGNPLCTESIDAGRTVLND IGERPLLTATVATGTQRYETSSLPGRLLSVAEQTEPKTSRITBERLIWAGNTVEASK DHNLAQCVRHYDTAGVTRLESLSLTGVSQSLLDITQEANWTDNETVMQNMLA DIYTLSTFDATGALLTQTDAGNIQRLAYDAGOLGMSWLTKLEGOTEQVVIKSLTV SAAGOKLREHNDVITEVSEYEPQRLIGIKTRPEPDKVLQDLRYEYDVGUVIS1 RDAEATRFHWQKVPENYTYDSLYQLISATGREMANICQOQSHQPPSPALPSDNT YNTYRTYIDRGKLNLTQHSNPATQNTYTNITVNSRNRVALSITLEDPAQVDAL FPAQGHNTLISQNLNMTNGEQLVLRDKGANDREWYRISGDRMLKINQ DNNLAQTVRLYLPNLELRLELQNSTATIEDLVITGEAGRAQVRVLHWESGKPEDI QNNQYRSYDNLISQLELDESGOIISEBEEYPYGATLWAARQNTVEASYKTYRSG KERDATGLYGVRYVQWIGRLSSDPAGTIDGLNLYRMVRNPNVLLTDPDGLMPTI AERIALKKNKTVDSAPSNATNVAINIRPPVAPKPSLPKASTSSQPTTHPIGAANI KPTTSGSSIVAPLSPVGNKTSISLPSASQSSSSSTINLQKKSFTLYRADNRSPF EWSKEPEFGKAWTPLDTMKARQFASIFIGQKTSNLPKETVKNISTWGAKPDKLDS N1KYTKDKSTVWVSTAINTEAGOGSGAPLHKIDMLDYEPAIDGQKLNPLPEGRITN MVPSELLDTPQIETSSIIALNHPVNDABEISFLTTIPLKNVPHKR"				
ORIGIN					
Query Match	36.6%;	Score 1004.6;	DB 6;	Length 2883;	
Best Local Similarity	69.3%;	Pred. No. 3.3e-225;			
Matches 1433;	Conservative 0;	Mismatches 594;	Indels 42;	Gaps 3;	
Qy	1	ATGAGCAGTTACAAATTCGCAATTCACAAAGACCCCTCGATTAAAGGTATTAGATAAC	60		
Db	1	ATGAAAACAACTGATCCCAAACTTTATCAAAAACCCCTACTGTGTCAGCGTTTACGATAAC	60		
Qy	61	AGGAAATTAATGTACGTACTTTAGATAATCTACGCACCTCAAGCTGACGAAAAACAGTGAT	120		
Db	61	CGTGGTCTGATACGTAACATCGATTTTCATCGTACTACCGCAATGGTGATCCCGAT	120		
Qy	121	GAATTAATTAAGTTCTATGAGTTCAATATTCGCGGATTTTCAGGTAAAAAGACCGATCCT	180		
Db	121	ACCGGTATTACCGCCCATCAACAGGATAATCACGACACCTAAATCAAAAGCATCGATCCG	180		
Qy	181	CGTAAAAATAAAACCA-----GAGGGGCCAAATTTCAATTCGTGTCCTTT	225		
Db	181	CGCTTATATGAAGCCCAAGCAAAACCAATATACGATCAAAACCAATTTTCTTTGGCAGTAT	240		
Qy	226	AATCTTCCGGTCAAGTTTTCAGTGAAGAAAGTTGTATGCCGGTCGGACTATTACCCCTC	285		
Db	241	GATTTGACCGGTAAATCCCTTATGTAACAGAGACATTTGATCGAGGTTCGCACATGTACCTTG	300		
Qy	286	AATGATATTGAAAGTCGCGCGGTGTTGATCATCAATGCAACCGGTGTCCGCCAAACCAT	345		
Db					

FEATURES		source
Qy	1420	CCGGGAATCAG-----TGGTACCGCTACGACACCAACGGCATG 1458
Db	1441	AAACGGGACAAAGGCGCCCAATGATGATCGGGAATGGTATCGTTATACGGGTGACGGAGA 1500
Qy	1459	AGACAACTGAAAGTGAAGTGAACAGACCAACCCAGCAATACTACGCAACCAACACCGGTAATC 1518
Db	1501	AGGATGTTAAANAATCAATGAACAGACAGCCAGCAACACGCTCAAAACAACACGCTGACT 1560
Qy	1519	TATTTCGGGACATGGAGCTACGCACAAACCCAGAGCAACGCCACAACACGGAAGAGTTA 1578
Db	1561	TATTTCGGCAACTTAGAACTTCGTCTAAACAACAAACAGCAGCGGCACAAACCGAAGATTG 1620
Qy	1579	CAGTTATACATCTCGGTGAAGCGGTGCGGCACAGGTACGGGTGTCACCTGGGAGGC 1638
Db	1621	CAAGTTATACCGGTAGCGGAAGCGGGCGGGCAGGTACGAGTATACATTGGGAGGC 1680
Qy	1639	GGTAAGCCAGAAGATGTCACAAATAATCAACTAGTTACAGCTACGATACGATAATCTGATCGGC 1698
Db	1681	GGTAACCGGAGATATCGACATAATCAGTTGCGTTATAGTTACGATATCTTATCGGT 1740
Qy	1699	TCAGCCAGCTTGAACTGGGACAAACCAAGGACAAATATACGCGGAGGAAGATATTATCCA 1758
Db	1741	TCCAGTCAACTTGAACTTAGATAGCGAAGGACAAATATATCAGTGAAGAAGAATATTATCCC 1800
Qy	1759	TTTGGCGGGACAGCGCTGTGGGCAGCAACAGCCAAACAGACGACGACCTATTAACCGATT 1818
Db	1801	TATGGTGAACAGACATATTGGGCGGCCAGGAATCAGACAGAAGCCAGTTATAAACATATC 1860
Qy	1819	CGCTATTCCGCGAAAGAACAGATGCCACCGGGTTGATTATTACCGGTATTCGTTATTAC 1878
Db	1861	CGTTATTACGCAAGAGCGGATGCCACCGGGCTATTATTACTACGCTATCGGTATTAC 1920
Qy	1879	CAACCGTGGCGGCGCAGATGTTAAGCGCGGACCCGCGAGAACCATATGATGGGCTGAAT 1938
Db	1921	CAACCGTGGATAGCAGCGTGGTTAAGCTCCGATCCGCGAGGAACAATCGATGGGCTGAAT 1980
Qy	1939	CTATACCGAATGGTAAGAAATAATCCTGTGAGTTTACAAGATGAATGATGATAGCCCCA 1998
Db	1981	TTATATCGGATGGTGAGGAATAATCCAGTTACCTCTCTTGATCTCGATGGAATTAATGCCA 2040
Qy	1999	GAACAAAGGGAATATATACCAAGAGGTAAA 2027
Db	2041	ACAAATTCAGAACCCATAGCAGCACTAAA 2069
RESULT 11		
BX571873		
LOCUS		
DEFINITION		349107 bp DNA linear BCT 17-APR-2005
		Photorhabdus luminescens subsp. laumondii TTO1 complete genome;
		segment 15/17.
ACCESSION		BX571873 BX470251
VERSION		BX571873.1 GI:36787441
KEYWORDS		complete genome.
SOURCE		Photorhabdus luminescens subsp. laumondii TTO1
ORGANISM		Photorhabdus luminescens subsp. laumondii TTO1
		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
		Enterobacteriaceae; Photorhabdus.
REFERENCE		1
AUTHORS		Duchaud,E., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S.,
		Bocs,S., Boursaux-Eude,C., Chandler,M., Daasa,E., Derose,R.,
		Derzelle,S., Freysinet,G., Gaudriault,S., Givaudan,A., Glaser,P.,
		Medigue,C., Lanois,A., Powell,K., Siguler,P., Wingate,V.,
		Zouine,M., Boemare,N., Danchin,A. and Kunst,F.
TITLE		Complete genome sequence of the entomopathogenic bacterium
		Photorhabdus luminescens
JOURNAL		Nat. Biotechnol. 11 (1) (2003) In press
REFERENCE		2
AUTHORS		Duchaud,E., Frangeul,L., Rusniok,C. and Kunst,F.
		Direct Submission
TITLE		Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25
JOURNAL		rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail:
		lfrangeu@pasteur.fr, fkunst@pasteur.fr

Location/Qualifiers	
1. .349107	
/organism="Photorhabdus luminescens subsp. laumondii TTO1"	
/mol_type="genomic DNA"	
/strain="TTO1"	
/db_xref="taxon:243265"	
complement (80. .3225)	
/gene="tccC1"	
/locus_tag="plu4167"	
complement (80. .3211)	
/gene="tccC1"	
/locus_tag="plu4167"	
/function="Unknown, probable insecticidal toxin"	
/note="Highly similar to insecticidal toxin"	
protein TccC of W14."	
/codon_start=1	
/transl_table=11	
/product="Insecticidal toxin complex protein TccC1"	
/protein_id="CAE16539.1"	
/db_xref="GI:36787442"	
/db_xref="GOA:O7MZV7"	
/db_xref="InterPro:IPR000408"	
/db_xref="InterPro:IPR002345"	
/db_xref="InterPro:IPR006530"	
/db_xref="UniProt/TREMBL:Q7MZV7"	
/translation="MSTPDTALYTOTPTVSNFVMDNRLGSLRIDGFHRVWIGGIDTRVT	
RQYDARGVLNHSIDPLDQAQDNSVKPNFVQYVDLAGHALRTERESVDAGRTVALND	
IEGRPVMTNATGVROTTRYEGNTLPRLLSVSEQVPDQETSQVTERFIWAENTAEK	
EYNLSGLCTRHYYDTAGVTRLMSSLAGAILSQSHQWLAEQGEANWSDDETVVQRMLA	
SEVYTTQSTNAIGALLTQDSKQIRLAYDIAGQLKGSWLTVKQREQVIVYDPSLVN	
SAAHGKLRBEHGVITEYSEYPTQRLMGITTRAEESQSEARVLQDLRYEYDPSVN	
VLSIHNDAETAFWRNQRKVEPNRYVYDLSYOLMSATREMANIGQSNQLPSPAMPV	
PADNSTYTYQRTYSYDRGGLVQIRHSSPATQNSVYTEMVSSRSNRVTLSTLTDP	
TVQDGLFAGHQKRLIPQCNLDNWRGRLQRTVPVSRNSDSSEYRYSDDGVRLLK	
VSEQGTGNTQVORTVLPGLRLITGVADKTTQNLQVITVGEAGRAQVRVLHWESGK	
PADIDNNQVRYSDYNNLSSQIELDSEGLSQSEYYPYGGTVAAAKNQTEASYKFI	
RYSGERDATGLYGYRYYPQWGRSLSDPAGTVYDGLNVYVMVRNRPITLTDHGL	
ALSPNERNATFWAFELFRKPDGMSAMRQKIGRAITAGLAIQGLAAIAAGTAGA	
ALPVLVLAAGVAGALMGVNGSLLEKGLALLVQKSTLVOGSAAGAAGASSA	
AAYGARAQGVVASAAGATGAVGSINNADRGIGGAIGSAGVGTIDTMLGTSSTLT	
HEVAAAAGGAAGMTGTQGSTNAGIHAGITGYIGSWIGFGLDVASNPAHLANYAVG	
YAAGLGAEMAIINRVIGGFLRLGLRAVSPYAAGLARQLVHFSIAFPVFEPISVLGG	
LAGIGTGLHVRVNGRDSWVSRGLSAAAGSGIDHLAGMIGNQIRGRLVLTGTGAINAIDYG	
TSAIGAARRVISL"	
complement (3220. .3225)	
/gene="tccC1"	
/locus_tag="plu4167"	
complement (3345. .8051)	
/gene="tccB1"	
/locus_tag="plu4168"	
complement (3345. .8039)	
/gene="tccB1"	
/locus_tag="plu4168"	
/function="Unknown, probable insecticidal toxin"	
/note="Highly similar to insecticidal toxin complex	
protein TccB of W14 Putative transmembrane protein."	
/codon_start=1	
/transl_table=11	
/product="Insecticidal toxin complex protein TccB1"	
/protein_id="CAE16540.1"	
/db_xref="GI:36787443"	
/db_xref="UniProt/TREMBL:Q7MZV6"	
/translation="MLSTWEKOLNESQDALVTGYMNFVASTLKGVDGPVTVEDLYE	
YLLIDPEVADEVTSRVAQIASIQQYMRVLNVSPEGRQAMELSTANERWDNDSOVA	
IWAAGAERYNAENYISPIRQEKSHYFSELETTLNQNRLDPRQVDAVLGYLNEFSA	
VSNLYVLSDGYNQDFDAIYFIRGTTTPRYRQMDLSKRQDPAGNPVTNFCW	
NDWQEITLPLSGDTVLEHTVPVFNDRLVAVWERDPAVKQKADGKNIGKTHAYSIDP	
GVKRYDDTWTAPNTTMTQQADESSETSRSLSIDESKTLTKRVNLLATTDIFSIDP	
TEETDSNPYGRMLGVFNFTCTPHQNRPAVYGYLYCDSAFNHHILRLPSKDFLFT	
YQDETNDQNCQFQAVDKKYIVTKVISGRFTEDEPTGTVGKVDLLKLGTTGAYVID	
QDGLTHIQTTNGDFVNRHIFGYNDIVDSKSGYGTWSGNGFYLDYHDGNYTTH	
NAAINYAPYAGGGGSPNGTMALEQRWNEGWAI SPLDDAHTITVQSGYIAMEGETFA	
SYVLPIDPGTMLLDWDSDKINFAISLNKLESVFTSPDWPTLTITIKNFSKIADNRKFQOE	


```
Qy 580 CAGGATCCGACTGGACAGAGTGAAGACAGAGCCCTCTGGCAACAAAACTGAGTAGTGA 639
Db 25483 CAAGAAGCGGATGGTTCGGCGATGATAAAGATCTGGGATGAAGAAATTAAGTAACGAT 25542
Qy 640 GTCTATATCAACCCAAAGTAACACTGATGCCACCGGGCTTTTACTGACCCAGACCGATGCC 699
Db 25543 GTATACACACCGAAAAACAAGACGGATGCTACCGGCACCTCTGTTGACACAAACCGATGCC 25602
Qy 700 AAAGGCAACATTGACGGCTGGCCCTATGATGTGGCCGGGACGCTAAAAGGAGTGTGTTA 759
Db 25603 AAAGGAAACATCCAGCATCTGGCCCTATAATGTAGCCGACAAATTTGAAAGGAAGCTGGCTA 25662
Qy 760 AACTCAAAAGTCAAGCGGAACAGGTGATTAATCAAAATCGCTTAACCTACTCCGCGCGGG 819
Db 25663 ACGTAAAGGCCMAAAGAGCAGATTAATCAATTAATCCCTAACCTATTGACGCGCAGGA 25722
Qy 820 CAAAAATACGTGTGAAGAGCAGGTAAACGGGATTTGCTCAATACAGCTACGAAACCGGAA 879
Db 25723 CAAAAAATACGGAAGAGCAGGTAAACGGTATCATCAACCGAATATCTTACGAGCCGGAA 25782
Qy 880 ACCCAACGGCTTATCGGCATTAACCACTCGCGTCCATCAGAGCCCAAGGTGTTGCAAGAC 939
Db 25783 ACCCAGGCACTAATGGGCATCACAAACCGCTGTTCAAATGATAGCAAGGCTTTTACAAGAC 25842
Qy 940 CTAGCTATCAATATGACCCAGTAGGCAATGCTCAATTAATATCCGTAAATGATGCGGAAGCC 999
Db 25843 TTAGCTATGAATATGATCCGGTTGGCAACATAATCAGTCTCCGTAACGATGCAAGACG 25902
Qy 1000 ACTCGCTTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTCG 1059
Db 25903 ACCCGCTTCTGGCGCAATCAGAAATGGTGCCAGAAATATCTATACCTACGATTCCTCG 25962
Qy 1060 TATCAGCTTATCAGCGCCACCGGGCGGAAATGCGCAATATCGGTACGAAACCAACAA 1119
Db 25963 TATCAGCTTATTAAGCGCAACAGGGCGGAAATGCGAAATATCGGCCAGCAGAATCAGAA 26022
Qy 1120 CTTCCTCCCTCGCTGCTACCTTCTGACAAACAAATACCTACACTACTATCTCGCAGCTAC 1179
Db 26023 CTCCCTCTCAGCAGCTCCCTTCCGATAACAACTTATACCAATTAACCCGCACTTAT 26082
Qy 1180 AGCTATGATCACAGTGGTAAATCTGACGCAAAATCGGCACAGCTCGCCAGCTACCCAGAAC 1239
Db 26083 GCCTATGACCGTGGTGCAACCTGACCCAAATCGGCATAGCTCACCCGCGAGCCAAAC 26142
Qy 1240 AACTACACCGTGGCTATCAACCTCTCAAACCGGAGCAATCGGGGTGTTCTCAGTACCGCTA 1299
Db 26143 AACTACACCAAGACATAAACCGTCTCGAAACCGCAGCAACCGCGCGTACTGAGTACCTTG 26202
Qy 1300 ACCACCGATCCAAATCAAGTGATACGTTGTTGATGCGCGTGTGTCACCAACCAAGTTTA 1359
Db 26203 ACCACTACCCGACCAAGTGGATGCAATGTTGTTGAGGAGTGTGATCGCTATGGCAACGAC 26262
Qy 1360 TTACCCGGACAGACACTTATCTGGACACACGAGGAGATTAAAGCAGGTTA----- 1411
Db 26263 CTACCCGGACAAACCTAACTGGAATGCAAGAGTGAATCTACACAGATGACACCGGTA 26322
Qy 1412 -----ATAATGGCCCGGGAATGAGTGGTACCGCTACGACAGCAAC 1452
Db 26323 AAACGGGATAACCTCACTGACCGTGACAGCAGACATAGAGTGGTATCGCTATGGCAACGAC 26382
Qy 1453 GGCATGAGACAACTGAAAGTGAGTGAACAGCCCAACCCAGATATCTACGACGACACACGG 1512
Db 26383 GGAATGCGGTGTTTAAAGAGTCAGTGAACAGCAAAATGCAAAATATCTCCAGCAACGACGA 26442
Qy 1513 GTAATCTATTGCGGGACTGGAGCTACGCAACCAACCCAGACCAACGCAACCAACGAA 1572
Db 26443 GTCGTTTACCTGTGAGGATTAAGACTAGTACACAAACAAACCGGTGATATCACGAAAGAA 26502
Qy 1573 GAGTTACAGTTATCACTCGGTGAAGCGGTGCGGCACAGGTACGGGGTGTTCATCTGG 1632
Db 26503 GAGTTGACAGATTATACCGTGGGTGAAGCGGTGCTGCGCAAGTGCAGAGTCTTACATTTGG 26562
```

```
Qy 1633 GAGAGCGGTGAAGCCAGAAGATGTCACAAATAATCAACTACGTTACAGCTACGATAATCTG 1692
Db 26563 GAAAGCGGCAAAACCGGAAACATCAACAATAATCAGGTACGTTACAGTTATGCAATCTC 26622
Qy 1693 ATCGGCTCAGCCAGCTTGAACCTGGACAACCAAGGACAAATTTATCAGCGAGGAGAGTAT 1752
Db 26623 ATTGGCTCCAGCCAGCTTGAAGCTAGATAGTGTGGGCAAAATTTATCAGTCAAGAAGATAC 26682
Qy 1753 TATCCATTTGGGGGACAGCGCTGTGGGAGCAAAACAGCCAAACAGAACGACGCTATAA 1812
Db 26683 TATCCATTTGGCGGTACAGCGCTCTGGCGCGCAAGAAACACAGAACGACGCTTACAA 26742
Qy 1813 ACGATTTCGCTATTTCGGGCAAGAAACAGAGATGCCACCGGGTTGTATTATTACCGTTATCGT 1872
Db 26743 ACGATCCGGTATTCTGTTAAAGAGCGGGATGCCACCGAGTGTATTATTACCGCTATCGG 26802
Qy 1873 TATTACAACCGTGGGGGCGAGATGTTAAGCGCGGACCCGCGCAGCAACCAATTTATGGG 1932
Db 26803 TATTATCAGCCGTGGGTGGGAAGATGGCTAAGTGTCTGATCCAGCAGCAACGATAGTGG 26862
Qy 1933 CTGAATCTATACCGAATGGTAAAGAAATAATCTCTGTGAGTTTACAAGATGAAATGGATTA 1992
Db 26863 CTAAATTTTATATCGGATGGTCAAGAAATAATCCCATTTCTTATCAGCAATAACGGATTA 26922
Qy 1993 GCGCCAGAAAAAGGAAATATATACCAAGAGGTAAAT 2028
Db 26923 CATCCAAATAGTAATAACAATGGACTAGAACGAAT 26958
Qy 205 CCAAAATTCATTCGTGCTTTTAATCTTCCGCGTCAAGTTTTACGTGAAGAAAGTGTGAT 264
Db 220 CCTAAATTTTCTGCGGACGATGATCTGGCCGGTCTATGCCCGGTGATGCGGACAGAGTGTGAT 279
Qy 265 GCGGTGCGACTATTACCTCAATGATATTGAAAGTCGCCCGGTGTTGATCATCAATGCA 324
Db 280 GCTGCTGCTATCTGTGCATTGAATGATATTGAAGGTGCTTCGGTAATGAACAATGAATGCG 339
Qy 325 ACCGTTGTCGCGCAAAACCAATCGTTATGAAGATAAACACCTCTCCCGTCTGCTGCTGCT 384
Db 340 ACCGTTGTTCTGTCAGACCCGTCCTATGAAGGCAACACCTTGGCCGCTCGCTGTTATCT 399
Qy 385 ATCACCAGAAACAGT-----ACAGGCGAGGAGAGAAACGACCAACGCTTATCTGGGCC 438
Db 400 GTGAGCGAGCAAGTTTTCAACCAAGAGAGTGTCTAAAGTGACAGAGCGCTTTATCTGGCT 459
```

LOCUS CQ854059 3132 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 25 from Patent WO2004067727.
ACCESSION CQ854059
VERSION CQ854059.1 GI:51510104
KEYWORDS
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

REFERENCE 1
AUTHORS Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.
TITLE Mixing and matching tc proteins for pest control
JOURNAL Patent: WO 2004067727-A, 25 12-AUG-2004;
Dow Agrosciences LLC (US)
FEATURES
Location/Qualifiers
1..3132
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/db_xref="taxon:29488"
1..3132

exon
ORIGIN

Query Match 35.0%; Score 962; DB 6; Length 3132;
Best Local Similarity 72.2%; Pred. No. 3, 4e-215;
Matches 1323; Conservative 0; Mismatches 470; Indels 39; Gaps 4;

439 GGCAATACCGCGGAGAAAGATTACAACTCGCGGTGAGTGTGTGTCGCCCAATTAGCAT 498
460 GGGAAATACAACTCGGAGAAAGAGTATAACCTCTCCGGTCTGTGTATACGCCCACTAGCAC 519
499 ACCGCGGAGCTTACTCAACTCAATAGCTTTCTCTGCTGGCGTCTGTGCTATCACAACTCT 558
520 ACAGCGGAGTACCCGGTTGATGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 579
559 CAACAACTGCTTACCGATACCCAGGATGCGGACTGGAAGAGTGAAGAGTGAAGAGTGAAGAGT 618
580 CACCAATTGCTGCGGAGGCGAGGAGCTAACTGGAGCGGTGACGACGAAATCTGTCTGG 639
619 CAACAACTGAGTGTGATGTCTATATACCCCAAGATTAACACTGATGCGCAACCGGGGCT 678
640 CAGGGAATGCTGCGGAGTGAAGTCTTATACGACCAAAAGTACCCTAATGCGCATCGGGGCT 699
679 TTAAGTACCCAGACCGATGCGGAGGCAATCACTCAGCGGTGCGCTATGATGTCGGCGGG 738
700 TTAAGTACCCAGACCGATGCGGAGGCAATCACTCAGCGGTGCGCTATGATGTCGGCGGT 759
739 CAGCTAAAGCGGAGTGTGTTAACTCACTCAAAAGTTCAGCGGAGTGAATGTTATCAAACTG 798
760 CAGTAAAGCGGAGTGTGTTAACTCACTCAAAAGTTCAGCGGAGTGAATGTTATCAAACTG 819
799 CTAACTTACTCGCGCGCGGCAAAATTAAGTGAAGAGCAACCGGTAAACCGGATGTCACCT 858
820 CTGAGCTGTGTCAGCGGAGTCAATAATTCGCTGAAGAGCAACCGGTAAACCGGATGTCACCT 879
859 GAATACAGCTACGAACCGGAGGCAACCGGCTTATCGGCAATACCACTCGCC----- 910
880 GAGTACAGTATGAGCGGAGGCACTCAACGCTGATAGGTATACCAACCGCGGTGCGGAA 939
911 -----GTCCATCAGACGCGGAGGTTGTGCAAGACTACGCTATCAATATGACCCAGTAGGC 966
940 GGGAGTCAATCAGGAGCGCAGATTTGCAGGATCTAGCTATAGGTATGATGATGATGATGATG 999
967 AATGTCAATTAATTCGGTAATGATGCGGAGGCACTCGCTTTTGGCGCAATCAGAAAGTA 1026
1000 AATGTTATCAGTATCCATAATGATGCGGAGGCACTCGCTTTTGGCGCAATCAGAAAGTG 1059
1027 GCGCGGAGATAGCTATACCTAGTATCCCTGATCAGCTTATCAGCTTATCAGCGCACCGGCGC 1086
1060 GAGCGGAGATAGCTATGATGTTATGATTTCTGATCAGCTTATGATGATGATGATGATGATG 1119
1087 GAAATGCGCAATATCGGTACGCAAAACCAACCACTTCCCTCCCTG-----CGCTACCT 1140
1120 GAAATGCGTAAATTCGGTACGCAAAAGCAACCACTTCCCTCACCCTTATACCTGTCTCT 1179
1141 TCTGACAACTAATACCTACCTAATATCTGAGCTTACAGCTTATGATCAGTGGTAAAT 1200
1180 ACTGACGACGACTTATACCAATTTACCTTCGTACCTTATCTTATGACCGTGGCGGTAAT 1239
1201 CTGACGCAATTTGGGACGACTCGGAGTACCCAGCAACCACTACAGCTGGGTATCACC 1260
1240 TTGGTTCAATTCGACACAGCTTCCCGGAGCTCAAAATAGTTATACACACAGATATCACC 1299
1261 CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTACCAACCGATCCAAATCAAGTG 1320
1300 GTTTCAGCCGCAATACCGGGGGGTATGAGTACATTAACGACAGATCCACCCGAGTG 1359
1321 GATACGTTGTTGATGCGGTGTCACCAACCACTTTATTCACCGGACAGACACTTATC 1380
1360 GATGCGCTATTTGATTCGCGCGGTCTACAGAGATGTTAATACCGGGGCAAAATCTGGAT 1419
1381 TGACACACGAGGAGGTTAAAGCAGGT-----TAAATATGCGCGCGGA 1425
1420 TGGAAATATTCGGGGTGAATTCGCAACGAGTCACACCGGTGAGCGGTGAAATATGAGTGAC 1479
1426 AATGAGTGTGACGCTACGACACAGCGGATCAGACCACTGAAGTGTGAGTGAACGCCA 1485
1480 AGTGAATGGTATCGCTATAGCAGTGTGGCATCGGCTGCTAAAGTGTGAGTGAACAGCAG 1539

1486 ACCGAATACTACGAGCAACCGGGTAATCTATTTCGCGGACTGGAGCTACGCACA 1545
1540 ACGGCAACAGTACTCAAGTACAAACCGGGTGACTTATCTGCGGGATTTAGAGCTACGGACA 1599
1546 ACCGAGCAACCGCCACCAACCGGAAGAGTTACAGCTTATCACACTCGGTGAAGCGGCT 1605
1600 ACTGGGGTTGCAGATAAACACCGGAAGATTTCGAGGTGATACGGTGAAGCGGCT 1659
1606 CCGCACAAGTACGGGTGTTGCACTCGGAGAGCGGTAAAGCCAGAAGATGTCAAACAATAT 1665
1660 CCGCACAAGTAAAGGGTATTGCACCTGGAAAGTGTAAAGCCAGACAGATATTGACAAAT 1719
1666 CAACTACGTTACAGCTACGATCTGATCGGCTCCAGCCAGCTTGAACCTGGACACCA 1725
1720 CAGGTGCGTACAGCTACGATTAATCTGCTTGGCTCCAGCCAGCTTGAACCTGSAATAGCAA 1779
1726 GGAACAAATATCAGCCAGGAAGAGTATTATCAATTTGGGGGACAGCGCTGTGGGCAGCA 1785
1780 GGGCAGATTCTCAGTCAGGAAGAGTATTATCCGTATGGCGGTACGGGATATGGGCGGCG 1839
1786 AACAGCCAAACAGAACCCAGCTATAAAACGATTTCGCTATTTCGGCAAAAGAACAGATGCC 1845
1840 AGAAATCAGACAGAACCCAGCTACAAATTTATTCGTTACTCCGGTAAAGAGCGGATGCC 1899
1846 ACCGGGTTGATTTATTTACGGTTATCGTTATTACCAACCGTGGCGGCGCAGATGGTTAAGC 1905
1900 ACTGGATTGTTATTTATTTACGGCTACCGTTATTATCAACCTTGGGTGCGATGGTTGAT 1959
1906 GCGGACCCGCGAGAACCAATGATGGCTGGAATCTATACGAATGTTAAGAAATATATCT 1965
1960 GCTGATCCGCGGGAACCGTGGATGGCTGGAATTTGTACGAATGTTGAGGAATATACCCC 2019
1966 GTGAGTTTACAAGATGAAAATGGATTAGCGCC 1997
2020 ATCAGATTGCTGACCATGACGATGACGATGACACC 2051

RESULT 13
AR285426
LOCUS AR285426
DEFINITION Sequence 60 from patent US 6528484.
ACCESSION AR285426
VERSION AR285426.1 GI:29722605
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3132)
AUTHORS Ensign,J.C., Bowen,D.J., Petell,J., Fatig,R., Schoonover,S.,
ffrench-Constant,R.H., Rocheleau,T.A., Blackburn,M.B., Hey,T.D.,
Merlo,D.J., Orr,G.L., Roberts,J.L., Strickland,J.A., Guo,L.,
Ciche,T.A. and Sukhapinda,K.
TITLE Insecticidal protein toxins from Photorhabdus
JOURNAL Patent: US 6528484-A 04-MAR-2003;
FEATURES Wisconsin Alumni Research Foundation; Madison, WI
source Location/Qualifiers
1..3132
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 35.0%; Score 962; DB 6; Length 3132;
Best Local Similarity 72.2%; Pred. No. 3,4e-215;
Matches 1323; Conservative 0; Mismatches 470; Indels 39; Gaps 4;

205 CCMAATTTTCATGCTGCTTTAATCTTCGCGGTCAAGTTTACGTGAAGAAAGTGTGAT 264
220 CCTAATTTTGTCTGGCAGCATGATCTGGCGGTCATGCCCTCGGACAGAGTGTGAT 279
265 GCGGTGCGACATTTACCTCAATGATATTGAAGTCGCCGCTGTTGATCATCAATGCA 324
280 GCTGGTCTGATGTTGATGATGATTTGAAGGTCGTTGAGGATGATGATGATGATGCG 339


```
/db_xref="taxon:29488"
1. .2898
/genes="tcca"
1. .2898
/genes="tcca"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tcca"
/protein_id="AAC38628.1"
/db_xref="GI:3265042"
/translation="MNLASPLISRTSEIHNLPGLTDLGYTSVDFVDMRPERETRE
HRADLRSRSEKMYDLAVGAHQVHLHFRNSISEAQFGRSPFSVSGDYANQFLDA
NTGKWDKAPSGSPENDAPVAYLTHYIQLALSOENKNGATYIMNTLAERPDDIGALLIN
DRAINIVPQLQAGKPTITVPQKDSPLAADIILSQALSAIAQMQQHDLEFSALLL
AQSGLTQIDITLPQTLDPQNFATAGKSLDTTASALTQLQIMASQFSPEQKII
TETVGQDFQYLDVNSLTVNFSMDTMTDRTSLTPQVPELMCLSTCVGSGTVKSDN
VSGSDTTPPEAFAGFIHAGKPEAITLSRSGAEAHFALTNNLTDKLDNRNRTVRL
QKWLNPYEDIDLLVTSMDAETGNALSNDNTLRMLGVFKHYQAKYGVSAKQFAGH
LRVAFAPITPFDQVFNSTFTVDINDQFVYTLTTGGDGAUVKXISTALG
LNHRQELLADNIRAQGNVTOSTLNCNLFVVSFAFYRLANLARTLGINPESFCALVDR
LDAGTGVNQAGKPTITVPQKDSPLAADIILSQALSAIAQMQQHDLEFSALLL
LSDNPISTQGTDDOLNFIQVNMNLGTSFVGAATLSRSGAPLVDNTHAIOWFALLS
AGNSPLIDVGLVGTIOGVATVNTQSLSDDEKKAITLTLNLOVQKQGVVA
VSLLAQTLNVQSPLPALLRWSCQTYQMLSATWALKDAVKAADIIPADYLRQREVV
RSLLTQQFTPLSPAMVOTLLDYPFAGSAETVTDISLWMLYTLSCSYDLLQMGEG
GTEDVLYLRTNATTPLSQSDAAQTATLLGMEYNELQAAWSVLGGIAKTPQLDA
LRLQQAQNTGLGVTTQQQGYLLSRSDSYTLWQSTGQALVAGVSHVSGSN"
2992. .7689
/genes="tccb"
2992. .7689
/genes="tccb"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tccb"
/protein_id="AAC38629.1"
/db_xref="GI:3265043"
/translation="MLSTMEKQLNESQDALVTGYMNFVAPTLKGVSGQFVTVEDLYE
YLLIDPEADEVETSRVAQAIASIQYMTLRVLNMGSEPGRAQMEPSTANEWRDNDQYA
IWAAGAEVSNYINDEKFDQAIYFPIGRTTKPYRYWRMDLSKNRQDPAQNPVTPNCW
NMQEITLPLSGDVTLEHTVRPVFYNDRLVYAVVERDPAVQKADGKNIKTHAYNIK
FGYKRDYDTPATLTLTQQGSESTORSLLEDQSSSTLRLQVNLATLTFDSIDP
TEETSDNPFYGRMLGVFVFEQGDGANKRKNPVGYLYCDSAFNRHRLPLSKNLF
STYRDGQNSLQFPAVDKYYITKVVGTGADDEPNTGWSKVDLKGQGTGAYYI
DODGLTLHTQTTNGDFINRHTFGYNDLVDSKSGYGTWSGNEGYLDYHDGYYTF
HNAIINYPSGVGSGVPNGTWALEORINEGWAIPLLDTLHTVTKGSIYIWEGETP
TGYNLIIPGTVLLDFDKINFAIGLUNKLESVTFSDWTLTIKNEFKIANDRKFYQ
EINAEATDGRNLFRYSTQTFGLTSGATYSTYTLSEADFSTDPDKNYLQVNLNVMD
HYDRPSGKKGASWSKFWNVYVALQDSKAPDAIPRLSVRYDSKRLGVLYLDFWTSLL
PAKTRLNTFTVRLIEKANGLDLSLDYTLQADPSLEADLVTDGKSEPMDFNGSLY
FWELFPHLPVLVATRFANEQSPAPKSLHYIFDPAMKNKPHNAPAYMNVRLPVEGNS
DLSRLHDSIDPDTQAYAPHYIYQKAVFIAYVSNLIAQGMWYRQLTRGLQFQARYY
NLAEULGRPVSLSSTWTPQTLDTLAAQKAVLRDFEHLQANSUTALPALPGRNVY
YKLADNGYFNEPLNMLSHMDTLARLYNRHNLTVDPKPLSLPLYPAAVPDVPALL
AQRAQSGTITNGYSGAMLYVPYRFSAMLPYRAYSVGTLTLSFQNLISLERSACQ
EELAQOQLDMSSYATLQOALDGLAADLALLAQATAQQRHDHYTYLQNNISSA
EOLVMDTOTSAQSLISSSTQVOTASGALKVIPNI FGLADGSGRYEGVTEAIIAIGMAA
QNTSVASERLATENYRRREWEQIYQQAQSEVDALQKOLDALAVREKAQTSLOQ
AKAQQVQITRMLTYLTFRTQATLYOWLQSMALYIQAIDAVVALCLSAQACWQVEL
GDYATFIQTGWNDHYRQLQGETLQNLHQMEAYLVRHERRLNIVRTSLKSLG
DDGFGKLTGKGVDFPLSEKLFNDYFPHYLRQIKTVSVTLPLVGPYQNVKATLTQT
SSSILLAADINVKRLNDPTGEGDATHIVNLRASQOVALSSGINADGSAFELRLDE
RYLSFPGTGAVSKWTLNFRPSVDEHIDDKTLKADENQMAALLANMDVDLVQVHYTACDG
GASFANQVKTLIS"
7820. .10951
/genes="tccc"
7820. .10951
/genes="tccc"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tccc"
/protein_id="AAC38630.1"
```

```
/db_xref="GI:3265044"
/translation="MSPSETTLYTQTPVTVLDRGLSIRDIGFHRIVIGCGDTRVT
RHOYDARGHLNYSIDRLYDAQADNSVKNPFWQHDLAGHALRITSVDAGRTVALND
IEGRSVMTNATGVTRTYEGNTLPGRLLSVSEQVFNQESAKVTERFTWAGNTTSEK
EYNLSGLCIRHYDTAGVTRLMSQSLAGMLSQHLLAEQGASWGSDDETVMQGMILA
SEVYTTQSTTNAIGALLTQDAKGNIRLAYDIAGQLKGSMLTVKGSQBOVIKYSLSW
SAAGHLREEHNGVUVTEYSYEPETORLIGITTRAEQSQSGARVLQDLRYKYDPVGN
VLSIHDAEATFRWNRQKVEPNRIVYDLSYLQMSATREMANIQGQSQNPSPVIVP
PDDSTYTNLYRTYTDGRGNLVQIRHSPATONSYYTDDITVSSRNRVAVLSLTITDDP
RDVALFDGSGHQHKLIPQGNLDWNI RGELOQVTPVPSRENDSSEWRYSDGMRLLK
VSEQNTGNSVQVRYTLPGLERTTGADKTTEDLOVITVGEAGRAQVRVLHWESGK
PTDINNQVRSYDNLGSSOLELSEGOILSOEEVYPYGGTAIWAARNQTEASYKFI
RYSKERDATGLYYGYRYQPMVGRWLSADPAGTVDGLNLYMVNRNPILTLDHGL
AEPNRNRNTFWFASLFRKPDGMSMRQCKI GRALAGLIAIGCLAATIAANTAGA
AIPVLTVGAAGVAGIGALMGVNSLLEKALLARLVQKSTLVGSAAGAASASSA
AAYGAAQCGVSAAGAVTGAVGWINNADRGIGAGIAGSAVGTITMLGTASTLT
HEVGAAAGAACGMITGTQGSTAGIAGITTYGYSWIGFGLDVASNPDHGLANAVG
YAAGIAEAMVNRIMGGFLSRLGRVVSYPYAGLAROLVHFSVAPVPEPIFVSLGG
LVGGTGTGLHRVWGRESMISRALSGSIDHVAGMIGNQIRGRVLTITTTGIANAIIDY
TSVAGAAKRVFSL"
complement(11117. .11518)
/genes="tccz"
complement(11117. .11518)
/genes="tccz"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tccz"
/protein_id="AAC38631.1"
/db_xref="GI:3265045"
/translation="MKNLFVIMLLSVITGCSGKSTSNROTAEELKFAFSGGNFI
LTHACTDKIDYLPDEGNDQIEIALKNDKQCFAPHPDALINKNIGTQMAISPKGTHLA
TATIQTPLNPSFRMGVKKQKQBAISMNALKN"
Query Match 35.0%; Score 962; DB 1; Length 11518;
Best Local Similarity 72.2%; Pred. No. 3.3e-215;
Matches 1323; Conservative 0; Mismatches 470; Indels 39; Gaps 4;
ORIGIN
QY 205 CCAATTTTCATTCGTCTCTTAATCTGCGCGTCAAGTTTTCAGTGAAGAAGTGTGTAT 264
Db 8039 CTTAATTTTGTCTGGCAGCATGATCTGCGCGTCAATGCGCTGGCAGACAGAGTGTGAT 8098
QY 265 GCGGTGCGACTATTACCTCAATGATTTGAAAGTGGCGCGTGTGTGATCATCATGCA 324
Db 8099 GCTGGTGTCTGTTGTCATTTGAATGATTTGAAGTGTGTTGCGTAAACAATGAATGCG 8158
QY 325 ACCGTGTGCGGCARAAACCATCGTTATGAAGATAACACCTTCCCGTGTCTGTGCTCGCT 384
Db 8159 ACCGTGTGCTGCAGACCCGTCGTTATGAAGGCAACACCTTGGCCCGTGCCTTGTATCT 8218
QY 385 ATCACCGAACAAAGT-----ACAGGCAGGAGAGAAACACGACCGAAGCTCTTATCTGGGCC 438
Db 8219 GTGAGCGAGCAAGTTTCAACCAAGAGAGTGTCTAAAGTGACAGAGCGCTTATCTGGCT 8278
QY 439 GGAATACCGCGCAGAAAAAGATTACAACCTGCGCGGTGAGTGTCTCGCCATTACGAT 498
Db 8279 GGAATACAACTCGGAGAAAGATATAACCTCTCGCGTCTGTGTATATACGCCACTACGAC 8338
QY 499 ACCGCGGACTTACTCAACTCAATGACCTTCTCTGCGTGGCGTGTGTATCACAATCT 558
Db 8339 ACAGCGGAGTGACCCGGTGTGATGAGTCACTCACTGCGGCGCCCATGCTATCCCAATCT 8398
QY 559 CAACAACTGCTTACCCATAACACAGGATCGCAGATGAGAGAGTGAAGACAGAGAGCTCTGG 618
Db 8399 CACCAATCTGCGGGAAGGCGCAGGAGCTTAAGTGAGCGGTGACCGAAGAACTGTCTGG 8458
QY 619 CAACAAAACTGAGTAGTGTATGTCTATATCACCACAAAGTAACTGATGCGCACCGGGCT 678
Db 8459 CAGGGAATGCTGCAAGTGAAGTCTATACGACACAAAGTACCACTAATGCGCATCGGGCT 8518
QY 679 TTACTGACCCAGACCGATGCCAAGGCAACATTCAGCGGCTGCGCTTATGATGTCGCGGG 738
Db 8519 TTACTGACCCAAACCGATGCGAAGGCAATATTTCAGCGCTGTGCTTATGACATTTGCCGT 8578
```



```
QY 739 CAGCTAAAGGGAGTTGGTTAAACACTCAAGAGTCAGGCGGAACAGAGTGATTATCAAAATCG 798
Db 8579 CAGTTAAAGGGAGTTGGTTGACGGTGAAGAGCGCAGAGTGACAGAGTGATGTTAAGTCC 8638
QY 799 CTAACCTACTCCGCGCGCGGCAAAATTAACGTGAAGAGCACGGTAACCGGATGTCACAT 858
Db 8639 CTGAGCTGGTCAGCGCAGAGTCATAAATTCGGTGAAGAGCACGGTAACCGGCGGTTAAG 8698
QY 859 GAATACAGCTACGAAACCGGAAACCCAAACCGGTTATCGGCATTAACACTCCGCC----- 910
Db 8699 GAGTACAGTTATGAGCGGAAACCTCAACGCTGATAGTAGTATCACCAACCGCGCGTGCCGAA 8758
QY 911 -----GTCCATCAGACGCCAGAGTGTTCAGAGCTACCGCTATCAATATGACCCAGTAGGC 966
Db 8759 GGGAGTCAATCAGAGGCCAGATATTCAGATCTACGCTATAGTATGATCCGGTGGG 8818
QY 967 AATGTCAATTAATATCCGTAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAGAAAGTA 1026
Db 8819 AATGTTATCAGTATCCATATGATGCCGAAGCTACCGCTTTTGGCGTATCAGAAAGTG 8878
QY 1027 GCCCGGAGATAGCTATACCTACGATTCCTGTATCAGCTTATCAGGCTATCAGCGGCGC 1086
Db 8879 GAGCGGAGAAATCGCTATGTTATGATCTCTGTATCAGCTTATGAGTGGCAGACGGCGT 8938
QY 1087 GAAATGGCCAATATCGCTCAGCAAAACCAACCACTCCCTCCCTG-----CGCTACCT 1140
Db 8939 GAAATGGCTAATATCGCTCAGCAAAAGCAACCACTCCCTCACCCTGTTATACCTGTTCT 8998
QY 1141 TCTGACAACTAATCTACACTAATATCTCGAGCTACAGCTATGATCATCAGTGGTAAT 1200
Db 8999 ACTGACAGACGACTTATACCAATTAATCTCGTACCTTACTTATGACCGTGGCGGTAAT 9058
QY 1201 CTGACGCAAAATTCGGCAAGCTCCGCCAGCTACCCAGAACTACCACTACCGTGGCTATCAC 1260
Db 9059 TTGGTTCAATTCGCACAGCTTACCCGCGACTCAAAATAGTTACACACAGATATCAC 9118
QY 1261 CTCTCAACCGCAGCAATCGGGTGTCTCAGTAGCTTAACCCAGCTCAAACTCAAGTG 1320
Db 9119 GTTTCAGCGCGCAGTACCGGGCGGTATTTGAGTACATTAACGACAGATCAACCCGAGTG 9178
QY 1321 GATACGTTGTTGATGCGGTGTGTCAACCAACAGTTTATTTACCGGACAGACACTTATC 1380
Db 9179 GATCGGCTATTTGATTCGGCGGTCATCAGAGATGTTAATACCGGGCGCAAACTCTGAT 9238
QY 1381 TGGACACAAGAGAGTTAAAGAGGT-----TATAATGCGCCCGGA 1425
Db 9239 TGGAAATATTCGGGTGAATTCGAACGAGTCAACCGGTGAGCGGTGAAATATGACGTGAC 9298
QY 1426 AATGAGTGGTACCTACGACAGCAACGGCATGAGCAACTGAAGTCAGTGAACAGCCA 1485
Db 9299 AGTGAATGGTATCGCTATAGCAGTATGGCATGCGGCTGCTTAAAGTAGTGAACAGCAG 9358
QY 1486 ACCCAGAACTACGACAGCAACACGGGTAATCTATTTCCGCGGACTGGAGCTACGCACA 1545
Db 9359 ACCGGCAACAGTACTCAAGTACACAGGCTGACTTATCTGCGCGGATAGAGCTACGCACA 9418
QY 1546 ACCCAGAGCAACGCCAACCAACCGGAAGAGTTACACGTTATCACTCGGTGAAGCGCGT 1605
Db 9419 ACTGGGTTGCAGATATAAACAACCGAGATTTGCAGGTGATTACGGTAGTGAAGCGCGT 9478
QY 1606 CGCGCAGAGTACGGGTGTCACATGGGAGAGCGGTAGCCAGAGATGTTCAACAATAAT 1665
Db 9479 CGCGCAGAGTAAAGGTTATTCACATGGGAAAGTGGTAAGCCGACAGCATTTTGAACAACAT 9538
QY 1666 CAATACGTTACAGCTACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTCGAACACCAA 1725
Db 9539 CAGTGGCGCTACAGCTACGATAATCTGCTTGGCTCCAGCAGCTTGAACCTCGATAGCGAA 9598
QY 1726 GGAACAATATTACGCGAGGAAGAGTATTATCCATTTGGCGGGAACAGCGCTGTGGGACGA 1785
Db 9599 GGGCAGATTCTCAGTCAGGAAGAGTATTATCCGTATGGCGGTACGGCGATATGGCGCGCG 9658
```

```
QY 1786 AACAGCCAAACAGAACCCAGCTATATAACGATTCGCTATTCGCGGCAAAAGAACGAGATGCC 1845
Db 9659 AGAATATCAGACAGAACCCAGCTACAAATTTATTCGTTACTCCGGTAAAGAGCGGATGCC 9718
QY 1846 ACCGGTTGTATATATACGGTTATCGTTATTAACCAACCGTGGCGGCGAGATGGTTAAGC 1905
Db 9719 ACTGGAATTGATTTATTAACGGCTACCGTTATTAATCAACCTTGGTGGGTGATGGTTGAGT 9778
QY 1906 GCGGACCCGCGAGGAACCAATTCATGGCTGGAATCTATACCGAATGTAAGAAATAATCTCT 1965
Db 9779 GCTGATCCCGCGGAACCGTGGATGGCTGAATTTGTACCGAATGGTGAGGAATACCCC 9838
QY 1966 GTGAGTTTACAAGATGAAAATGGAATAGCAGCC 1997
Db 9839 ATCAGATTGACTGACCATGACGATTAGCAC 9870

RESULT 15
AF346499
LOCUS
DEFINITION
  25655 bp DNA linear BCT 25-OCT-2001
  Photorhabdus luminescens strain W14 toxin complex tcc locus,
  partial sequence.
ACCESSION
  AF346499
VERSION
  AF346499.1 GI:16416908
KEYWORDS
SOURCE
  Photorhabdus luminescens
  Photorhabdus luminescens
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
ORGANISM
REFERENCE
  1 (bases 1 to 25655)
  Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and
  ffrench-Constant,R.H.
  The tc genes of Photorhabdus: a growing family
  Trends Microbiol. 9 (4), 185-191 (2001)
  11286884
  2 (bases 1 to 25655)
  ffrench-Constant,R.H., Bowen,D.J. and Waterfield,N.R.
  Direct Submission
  Submitted (19-JAN-2001) Biology and Biochemistry, University of
  Bath, Claverton Down, Bath BA2 7AY, UK
FEATURES
  Location/Qualifiers
    1..25655
      /organism="Photorhabdus luminescens"
      /mol_type="genomic DNA"
      /strain="W14"
      /db_xref="taxon:29488"
      <1..670
      /notes="orf1; similar to colicin E4 structural protein"
      /codon_start=2
      /evidence=not experimental
      /transl_table=11
      /product="unknown"
      /protein_id="AAL18467.1"
      /db_xref="GI:16416909"
      /translation="IRDEKSGRMTVQGVHVSPEGGLDKVPVRMMTLNRTTGNVEFWEP
      GETRPTILTPNEQFKVPAHTNEQFPISQITVLPIPKVGSIDIESLPMEEDKF
      RYVLVPEIPNMPVYVLSKPRNGLPQGDHYPAPKTEITGVSGLSRAKKTKPQ
      SGGKDRWDISKGRRIYEWDSQHGELVYVSDGHELCSDVYKTGKELKPAVKGRNI
      KQYL"
    1031..1489
      /notes="orf2; similar to colicin E4 immunity protein"
      /codon_start=1
      /evidence=not experimental
      /transl_table=11
      /product="unknown"
      /protein_id="AAL18468.1"
      /db_xref="GI:16416910"
      /translation="MTINVEALINSLKTYOEIFDEGLIPYRSKPNPGLVNLIGIDM
      VKSGILSPERSKILNEITLRLRDDKASFIPLNELPSPLTHSMRDKWIKENLGGPI
      KSLPPQILKRQGWKDLRPTDEISMQISYDMMERVKSVTFLPTSEVRW"
      1599..2066
      /notes="orf3; similar to pyocin S3 immunity protein"
      /codon_start=1
```

```

/evidence=not_experimental
/transl_table=11
/product="unknown"
/protein_id="AAL18469.1"
/db_xref="GI:16416911"
/translation="MTINIEALINSLGKTYQBIQFKGLIPYKTKSGPFGDSDISLDM
AKGAPLSPFLRNKLTETLLIHRRENFIPFNPPLPLPLMSRQWVHSHGEPE
KSLPRKRLTRIGWTELYLLDFRITPSMQVDYNLLEQVRMTFLPTSEVRW"
2300..2638
CDS
/notes="orf4; similar to pyocin S3 immunity protein"
/codon_start=1
/evidence=not_experimental
/transl_table=11
/product="unknown"
/protein_id="AAL18470.1"
/db_xref="GI:16416912"
/translation="MIKEGVHLAFKEDGRVLEAIGLILIDEKDSQVFNELPSPLIP
INSRQWHEQFGPEPNSPPRKRLTKIGWTELYLLDFRITPSMQVDYNLLEQVRV
LPTLPSAVRW"
3165..6062
CDS
/genes="tccA"
/notes="tccA"
/genes="tccA"
/codon_start=1
/evidence=experimental
/transl_table=11
/product="toxin complex protein"
/protein_id="AAL18471.1"
/db_xref="GI:16416913"
/translation="MNQASPLISRTTEEIHNLPGKLTDLGYTSFVDFVMPREPFIRE
HRADIGSAEKMYDLAAGVAHQVHLHFHFRNSLSEAVQFGLRFPFVSGPDYANQLFLDA
NKGWDKAPSGPEANDAPVAYLTHIYQLALQEKQKATPIIMNTLAERPVHGLALLIN
DKAINVETIQLQOLVNEILSKAIOKLSLTDLEAVNARLSTTRYPNNLPHYGHQIQT
AQSGLTTLQDITLPTQLDLPONFATAKGLSDTTASALTRLQIMASOFSPQOKII
TETVGQDFQLNAGUSSLVNFSFDMTMDRTSLTPVQVELMLSTVSGGSVTVKSDN
VSSGDTTPFAFYAGFIRHAGKEAITLSRGAERHFAFTVNNLTDDKLDNRINRVL
QKWLNPYEDILLVTSAMDGETNLSMNDNTLRMLGVFKHYQAKYGVSAKQFAGW
LRVAPFATPATPFDDQVFNSTFTDTPFVINDQDFVYTLTTGGDGRVKHISTALG
LNHRQPLLLANIRAOQNVSTOITLNCNLFVVSFAFRLANLARTILGINPEFSKLDVR
LDAGTIVNQLAGKPTITVPOKSLPADILSLLOALSIAIQMOQHDLPSALLL
LSDNPISTSGTDDQLNFIRQVWNLGSTFVGATILSRSGAFLVDNTHGAIDWPAALLS
AGNSPLIDKVDIAGIOSVIATVNVNTOSLDEKKAITLTITNLNQVKTQOGVA
VSLLAQTLNVSQLPALLRWSGQTYOWLSATWALKDAKVTAAIDIPADYLRQLREW
RSLLTQOFTLSPAMVQTLDDYPAYFGSAETVTDISLWMLYTLSCYSDLLQMGEG
GTEDDVLAVRTANATPLSQSDAACLATLLGWENELQAAWSVLGGIAKTTPLQDA
LRLQQAQNTGLGVTTQOQGYLLSRSDSYTLWQSGQALVAGVSHVSGSN"
6156..10853
CDS
/genes="tccB"
/notes="tccB"
/genes="tccB"
/codon_start=1
/evidence=experimental
/transl_table=11
/product="toxin complex protein"
/protein_id="AAL18472.1"
/db_xref="GI:16416914"
/translation="MLSTWEKOLNESQRDALVTGYMNFVAPTLKGVSGOPVTVEDIYE
YLLIDPEVADEVETSRVAQAIASIQYTRQEKSHYFSELETLNQNRDLDPDVODAVIAYLNEFA
IWAAGAEVRNAYENYISPIITROEKSHYFSELETLNQNRDLDPDVODAVIAYLNEFA
VSNLYVLSINQDFQDAIYFIRGTTTKPYVRWQMDLSKNRQDQPNAGNPTNCW
NDWQETITLPSGDTVLEHTVRPFVYNDRLYVAWVERDPAVKDADGKNTGKTHAYNIK
FGYKRYDDTWTPANTTTLTMOQAGESSETORSLLIDESTTLRQVNLATVDFSIDP
TREETDNPGRMLGVVFPFGEDGANRKNKVVGYLYCDSAFNRHLVRLPSKNPLF
STYRDETQNSLOFNAVYDKYVITKVVTGATEDPENTGWVSKVDDLKQGTGAYYI
DQQLTLHIQTTTGTFINRHTFGYNDLVDSKSGYGTWSGNEGYFLTDHGNYYTF
HNAINYPYSGGGVPGTGWALEQRIWEGWAIAPLLDTHVTYVKGYSIAWEGTP
TGNLYIPDGTWLDWFDTKINFALGNKLESFVTSPPWPTLTITKNFSIADNRKPYQ
EINAEYDGNLPRKYSTOTFGLTSGATSTVTTSEADFSDPDNDKNYLQVLPWVD
HYDRPSGKGYASWSKFWNVVYALQDSKAPDAIPRLVSRYDSKGLVQYLPWTSLL
PAKRLNTLPTVTRIEKANGLDLSLDYTLQADPSLEADLVDTGKSEPMDFNGSGLY
FWELFPHLPVTRATFANQFSPAQKSLHYIFDPAMKKNKPHNAPYMWVRPLVEGNS
DLSRHDDSIDPDQYAHPIYQKAVFIAYVSNLIAQDGMWYRQLTRDGLTQARYY
NLAAILGPRPDVSLSSIWTPQTLDTLAAGQKAVLRDFEHQLANSDTALPALPGRNV

```

```

YLKADNGYFNEPLNVLMLSHWDTLDARLYNLRHNLTVDGKPLSLPLYAAPVDFVALL
AQRASGTLTNGVSGAMLTTPPYRFSAMLPRAYSAVGTLTSGQNLLSLERSERACQ
BELAQQLLDMSSYAITLQOQALDGLAADRALLASAQATAQORHHDHYTYLYQNNISSA
EQLVMDTOTSAQSLSSSTGVCTASGALKVI PNIFGLADGSGRYEGVTEAIAIGLMAA
COATSVATERLATTENYRREEMQIOYQOQSEVDALQKOLDALAVRKAQOTSQOQ
AKAQOVQIRTMLTYLTTFQTATLQWLSQSALYIYQAYDAVVALCISAQACWQVEL
GDYATTFOTGTWMDHYGLQVGETLQNLHOMEAAYLVHRHRRLLNINVTAKSLG
DDGFKLTKTEKVDPLSEKFPDNDPGHYLRQIKTVSVTPTLTVGPYINVTAKSLG
SSSILAAIDINGVKELNDPTGEGDATHIVTNLRASQVQVLSGSDAGSFELRDE
RYSLEPGTGAWSKMTLNFPRSVDEHIDDKTKADEMQAALLANMDVLVQVHYTACDG
GASFANOVKKTLS"
10984..14115
CDS
/genes="tccc"
/notes="tccc"
/genes="tccc"
/codon_start=1
/evidence=experimental
/transl_table=11
/product="toxin complex protein"
/protein_id="AAL18473.1"
/db_xref="GI:16416915"
/translation="WSPSETTLYTOTPTVSVLDNRGLSTRDIGFHRIVIGGDTDRVT
RHOYDARGHLNYSIDPRLYDAQADNSVKPNFVMOHDLAGHALRTESVDAGRTVALND
TEGRSVMTNATGVQRTRYEGNTLPGRLLSVSEQVFNQESAKVTERFHWAGNTYSEK
EYNLSGLCIRHYDTAGVTSLQSAGLMSQHLLAEGQANSGDDTEVMQGMILA
SVYTTQSTTNAIGALLTQTDAGNIQRLAYDIAGQLKGSWLTVKQSQSVIVKLSW
SAAHGKLREHNGVVTYVSEYEPETQRLIGITTRAEQSGSARVLQDLRYKYPVGN
VTSIHNDAEATRFMRNOKVPEPNRYVYDLSYOLMSATGEMANIGQSNQLPSPVPIPV
PTDSTYNYLRTYTYDRGNLQVIRHSSPATONSYYTDTIVSSRNRNAVLSLTITDP
TRVDALFSGGHQMLIPQONLDWNIIRGELQVTPVSRNNSDSEWRYSSGDMRLLK
VSEQTNGSTQVRVYLPGLRITTVGADKTEDLVITVGEAGRAQVRVLHWESGK
PTDIDNNQVSYNDLGSQLELSEQILSQEYYPYGGTAIWAARQTESAKYFI
RYSGERATGLYGYRYQPWGRWLSADPAGTVGDLNLYRMVNNITLTDHGL
APSPNRNRTFWASFELPRKPDGMSAMRRGOKIGRALAGGIATGLAATTAATAGA
AIPVLVAVAGAGIGALMGVNVGSILLEKCALLARLVQKSTLVQSAGAAGASSA
AAYGAQGVASAGAVTAVGWSVINNADRGIGGAGVIGFGLDVASNPAGHLNLYAVG
HEVGAAGAGAGMITQGTGTHAGITGAGITGAGITGAGITGAGITGAGITGAGITGAG
YAAIGAEAVNRMINGGFLSRLLGRVSPYAAGLARQLVHFVSVARPEFIPSVLGG
LVGGITGLHRVMGRESWISALSAAAGSIDHVAGMIGNQIRGRVLTITTTGIANADYG
TSAVCAARRVFLS"
complement(14281..14682)
/genes="tccc2"
complement(14281..14682)
/genes="tccc2"
/codon_start=1
/evidence=not_experimental
/transl_table=11
/product="unknown"
/protein_id="AAL18474.1"
/db_xref="GI:16416916"
/translation="MKNLFVIMLLSVITGCSGKSTSNRQTOAEGLKFAFSGGNFI
LTHACTKIDYLGPDGNGDQIEIAIKNDKQCFAHFDALINKNGTQMAISFAGTHLA
TATQITPLNPSFRMGVKQKEQAISIMNALKN"
15131..16234
CDS
/notes="orf9; similar to Bacillus subtilis toxic cation
resistance protein"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAL18475.1"
/db_xref="GI:16416917"
/translation="MSTKVIPSPFRDMALNESTVLIDQEHINTLIEKIDISQPAAV
ISYGAQMGGIARFADTLLNVTKEADVGQKLSLVNMFIREHDALESPEKSRFLR
KLPLJGGIFPKAERTWIDQKTLTQOVDITATLHDSANMLLRDITVLQDLYDRNLGFY
KEISLYVANGKLAQIKTVELPSLQRAETSQDMDAQSKDLENINRFRRLHDL
ELSKATIQAPQIRIQVNNQALAEKQSSILSTLPIWKSQVNLNLSKASRAAKL
QKEVATDITELLRKNAILQSSSIATATEVERSIVDIETLRDVSQSLVNTIEDTMRIA
SBARKTIEKEKLSMEGNLRQLTAANAQY"
16292..17332
CDS
/notes="orf10"
/codon_start=1
/evidence=not_experimental
/transl_table=11

```

Query Match		35.0%;	Score 962;	DB 1;	Length 25655;				
Best Local Similarity		72.2%;	Pred. No. 3.3e-215;						
Matches 1323;		Conservative	0;	Mismatches	470;	Indels	39;	Gaps	4;
Qy	205	CCAAATTTCAATCGTGCTCTTTAACTCTTCCGGTCAAGTTTTCAGTGAAGAAAGTTTGAT	264						
Db	11203	CCTAAATTTGCTGGCAGCATGATCTGCCGGTCAATGCCCTGCGACAGAGAGTGTGAT	11262						
Qy	265	GCCGGTCGGACTATTACCTCAATGATATTGMAAGTCGCCGGTGTGATCATCAATGCA	324						
Db	11263	GCTGGTCGTACTGTGTAATGAAATGATATTGAAGGTCGTTCCGTAATGACAATGAATGG	11322						
Qy	325	ACCGGTGCGCAAAACCACTCGTTATGAAGATAACACCCCTTCCCGGTCTGCTCGCT	384						
Db	11323	ACCGGTGCTGTCAGACCCGCTGCTATGAAGGCAACACTTTCGCCGTGCGTTGTTATCT	11382						
Qy	385	ATCACCGAACAAGT- - - - -ACAGGCGAGGAGAGAAAACGACCGAAGCTCTTATCTGGGCC	438						
Db	11383	GTGAGCGAGCAAGTTTTCAACCAAGAGAGTGCTAAAGTGACAGAGCGCTTTATCTGGGCT	11442						
Qy	439	GGCAATACGGCGGCAAGAAAAGATTACAACTCTCGCTGGCGTGTGCTATCACAATCT	498						
Db	11443	GGGAATACAACTCTCGAGAAAGAGTATAACCTCTCCGGTCTGTGTATACGCCACTACGAC	11502						
Qy	499	ACCGCGGACTTACTCAACTCAATAGCTTTCTCTGCTGGCGTGTGCTATCACAATCT	558						
Db	11503	ACAGCGGAGTGACCCGGTTGATGAGTCAGTCACTGCGGGCGGCATGCTATCCCAATCT	11562						
Qy	559	CAACACTGCTTACCGATACACAGGATGCCGACTGGACAGGTGAAGACCAAGAGCTCTGG	618						
Db	11563	CACCAATTGCTGGGGAAGGCGAGGCTAACTGGAGCGGTGACGACGAACTGTCTGG	11622						
Qy	619	CAACAAAACCTGAGTAGTGATGCTCTATATCACCAAAAGTAACACTGATGCCACGGGGCT	678						
Db	11623	CAGGGAATGCTGGCAAGTGAGGTCTATACGACACAAAAGTACCACATAATGCCATCGGGCT	11682						
Qy	679	TTACTGACCCAGACCGATGCCAAGGCAACATTCCAGCGGCTGGCTATGATGTGGCCGGG	738						
Db	11683	TTACTGACCCAAACCGATGCGAAGGCAATATTGAGGCTGGCTTATGATGTGGCGGT	11742						
Qy	739	CAGCTAAAGGGAGTGTGGTTAACTCACTAAAGGTGAGCGGCAACAGGTGATTTACAAATCG	798						
Db	11743	CAGTTAAAGGGAGTGTGGTTGACGGTGAAGGCCAGAGTGAACAGGTGATTTGTAAGTCC	11802						
Qy	799	CTAACCTACTCCGCGCGGCAAAATTAAGTGAAGACGACGTAACGGATGTGTCACCT	858						
Db	11803	CTGAGCTGGTCAGCGCGAGGTCATAAATTGCGTGAAGAGCAACGGTAAACGGCGGTTCACG	11862						
Qy	859	GAATACAGCTACGAACCGGAAACCAACGGCTTATCGGCATTACCACTCGCC- - - - -	910						
Db	11863	GAGTACAGTTATGAGCGGAAACTCAAGCTCTGATAGGTATCACCAACCGCGGTGCCGAA	11922						
Qy	911	- - - - -GTCCATCAGACGCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCAGTAGGC	966						
Db	11923	GGGAGTCAATCAGGAGCCAGAGTATTGACGATCTACGCTATAAGTATGATCCGGTGGG	11982						
Qy	967	AATGTCATTAATTCGTAATGATGCGAAGCCACTCGCTTTTGGCGCAATCAGAAAAGTA	1026						
Db	11983	AATGTTATCAGTATCCATTAATGATGCGGAACTACCCGCTTTTGGCGGTAATCAGAAAAGTG	12042						
Qy	1027	GCCCCGGAGATAGCTATACCTACGATTCCTGCTGATCAGCTTATCAGCGCCACCGGGCGC	1086						
Db	12043	GAGCGGAGATCGCTATGTTTATGATCTCTGATCAGCTTATGATGCGACAGGGCGT	12102						
Qy	1087	GAATGGCCAATATCGGTGAGCAAAAACCAACTTCCCTCCCTG- - - - -CGCTACCT	1140						
Db	12103	GAATGGCTAATATCGGTGAGCAAAAAGCAACCACTTCCCTCAACCGTTATACCTGTTCT	12162						
Qy	1141	TCTGACAACAATACCTACACTAATATCTCGAGCTACAGCTATGATCAGTGGTAAT	1200						
Db	12163	ACTGACGACGACTTATACCAATTAACCTTCGTAACCTATCTATGACCGTGGCGGTAAT	12222						

Qy	1201	CTGACGCAAAATTCGGCACAGCTGCGCAGCTACCCAGAACAACTACACCGTGGCTATCACC	1260
Db	12223	TTGGTTCAATCCGACACAGTTTCACCCGGACTCAAAATAGTTATACACACAGATATCACC	12282
Qy	1261	CTCTAAAACGGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320
Db	12283	GTTCGAAGCGCAGTAACCGGGCGGTATTGAGTACATTAACGACAGATCCAAACCCGAGTG	12342
Qy	1321	GATACGTTGTTGATCCCGGTGCTACCAAAACCAAGTTTATACCCGGACAGACACTTATC	1380
Db	13243	GATGCCCTATTGTTATTCGCGCGGTATCAAGAGATGTTAATACCGGGGCAAAATCTGGAT	12402
Qy	1381	TGGACACCAACGAGGAGGTTAAAGCAGGT- - - - -TAATAATGCCCGCGGA	1425
Db	12403	TGGAATATTCCGGGTGAAATTGCAACAGAGTCACACCGGTGAGCGGTGAAAATAGCAGTGAC	12462
Qy	1426	AATGAGTGGTACCGCTACGACAGCAACGGCATGAGACAATGAAAGTGAAGTGAACAGCCA	1485
Db	12463	AGTGAATGGTATCGCTATAGCAGTGATGCGCTGCTAAAGTGAAGTGAACAGCAG	12522
Qy	1486	ACCCGAATACTACGACAGCAACAAACGGGTAATCTATTTCGCGGACTGGAGCTACGCACA	1545
Db	12523	ACGGGCAACAGTACTCAAGTACAACGGGTGACTTATCTGCGGGGATAGAGCTACGGACA	12582
Qy	1546	ACCAGAGCAACGCCACAACACGGAAGGTTACAGCTTATCACACTCGGTGAAGCGGT	1605
Db	12583	ACTGGGGTTGCAGATAAAACAACCGAAGATTTGCAGGTGATTACGGTAGGTGAAGCGGT	12642
Qy	1606	CGCGCACAGGTAGCGGTGTTGCACTGGGAGAGCGGTAAAGCCAGAAAGTGTCAACATAAT	1665
Db	12643	CGCGCACAGGTAAAGGTTATTGCACTGGGAAAGTGGTAAGCCGACAGATATTGCAACAAT	12702
Qy	1666	CAACTAGTTTACAGCTACGATATCTGCGGTCCAGCCAGCTTGAACTGGACAACCAA	1725
Db	12703	CAGTGGCTTACAGCTACGATATCTGTTGGCTCCAGCCAGCTTGAACTGGATAGCGAA	12762
Qy	1726	GGCAAAATATACAGCGAGGAAGTATTATCCAATTTGGCGGACAGCGCTGTGGCGACGA	1785
Db	12763	GGCGAGATTCTCAGTCAGGAAGAGTATTATCCGTATGGCGGTACGGCGATATGGCGGCG	12822
Qy	1786	AACAGCCAAACAGAACGCGACTATAAAACGATTTCGCTATTCGGGCAAAAGAACGATGCC	1845
Db	12823	AGAAATCAGACAGAAGCCAGCTACAAATTTATTTCGTTACTCCGGTAAAGAGCGGGATGCC	12882
Qy	1846	ACCGGGTTGTATTATTACGTTATCTGTTATTACCAACCGTGGCGGCGAGATGGTTAAGC	1905
Db	12883	ACTGGATTGTATTATTACGGCTACCGTTATTATCAACCTTGGGTGGTTCGATGGTTGAGT	12942
Qy	1906	GCGGACCCCGCAGGAACCAATTGATGGGCTGAAATCTATACCGAATGGTAAGAAATAATCCT	1965
Db	12943	GCTGATCCGGCGGGAACCGTGGATGGCTGAAATTTGTACCGAATGGTGAGGAATAACCCC	13002
Qy	1966	GTGAGTTTACAGATGAAAATGGAATTAGCGCC	1997
Db	13003	ATCACATTGACTGACCATGCGGATTAGCACC	13034

Search completed: December 13, 2005, 23:35:49
Job time : 13315 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 10:14:39 ; Search time 7364 Seconds
(without alignments)
5813.441 Million cell updates/sec

Title: US-10-647-956A-6

Perfect score: 4740

Sequence: 1 MSYNSAIDQKTPSIKVLND.....EAINRISAAIAENLGMRTS 915

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10647956/runat_12122005_091818_29607/app_query.fasta_1.1095
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1 8010 @runat_12122005_091818_29607 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	806	17.0	749	9 AQ991727	AQ991727 Rfc00357F
C 2	721.5	15.2	460	9 AQ991476	AQ991476 Rfc02418
C 3	716	15.1	605	9 AQ990411	AQ990411 Rfc01179
C 4	580	12.2	878	10 CZ547320	CZ547320 SRAA-aad7
C 5	559	11.8	733	11 AW901477	AW901477 RCO-NN101
C 6	529	11.2	494	9 AQ991400	AQ991400 Rfc02327
C 7	503	10.6	406	9 AQ990055	AQ990055 Rfc00763

C	8	487	10.3	594	9	AQ990688	AQ990688 Rfc01498
	9	409.5	8.6	547	9	AQ990013	AQ990013 Rfc00707
	10	371	7.8	312	9	AQ990147	AQ990147 Rfc00869
	11	309.5	6.5	644	1	AW901491	AW901491 RCO-NN101
C	12	180	3.8	795	10	CZ532972	CZ532972 SRAA-aac8
C	13	179	3.8	681	9	CC818388	CC818388 100004D09
	14	178.5	3.8	846	9	CC129231	CC129231 NDL.73B3.
C	15	172.5	3.6	850	9	CC110859	CC110859 NDL.20H16
	16	165.5	3.5	5087	10	AY405422	AY405422 Mus muscu
	17	155.5	3.3	3038	4	AK037897	AK037897 Mus muscu
	18	152.5	3.2	16425	11	DQ038516	DQ038516 Homo sapi
	19	152	3.2	5094	10	AY405420	AY405420 Homo sapi
	20	151	3.2	9714	11	DQ043368	DQ043368 Homo sapi
	21	147	3.1	3696	4	HSM804219	AL832908 Homo sapi
	22	146.5	3.1	848	10	CZ533828	CZ533828 SRAA-aac8
	23	145	3.1	689	3	BI385847	BI385847 BFL26_000
	24	144.5	3.0	6246	10	AY413475	AY413475 Homo sapi
	25	143.5	3.0	808	9	CC111285	CC111285 NDL.38D12
	26	143.5	3.0	6315	4	AY321333	AY321333 Rattus no
	27	142	3.0	19677	11	DQ051895	DQ051895 Homo sapi
	28	141	3.0	8025	10	CL961005	CL961005 ObiFCC005
	29	138	2.9	881	10	CZ545184	CZ545184 SRAA-aad6
	30	138	2.9	4741	4	AK029802	AK029802 Mus muscu
	31	137	2.9	7787	11	DQ048663	DQ048663 Homo sapi
	32	136.5	2.9	1383	9	BZ565560	BZ565560 p8c82-164
	33	135	2.8	3064	4	AK004607	AK004607 Mus muscu
	34	135	2.8	3836	4	AK088238	AK088238 Mus muscu
C	35	134.5	2.8	614	9	AQ991166	AQ991166 Rfc02049
C	36	134	2.8	1016	9	BZ571923	BZ571923 mah2_2138
	37	133.5	2.8	874	9	BZ567033	BZ567033 p8c82-164
C	38	133	2.8	340	2	BE092381	BE092381 IL2-BT073
	39	133	2.8	2173	10	AY409388	AY409388 Mus muscu
	40	133	2.8	2415	4	CR858297	CR858297 Pongo pyg
	41	133	2.8	3750	4	AK019545	AK019545 Mus muscu
	42	132.5	2.8	843	9	BZ570678	BZ570678 mah2_1482
	43	132.5	2.8	4609	11	DQ050672	DQ050672 Homo sapi
	44	132	2.8	2439	10	CL982610	CL982610 ObiFSC048
	45	131.5	2.8	814	9	CC851172	CC851172 NDL.121N1

ALIGNMENTS

RESULT 1

AQ991727/c

LOCUS

DEFINITION

Photorhabdus luminescens genomic clone PLG00357F, genomic survey

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

AQ991727 749 bp DNA linear GSS 14-AUG-2000

Rfc00357F Photorhabdus luminescens strain W14 M13 library

Photorhabdus luminescens genomic clone PLG00357F, genomic survey

sequence.

AQ991727

AQ991727.1 GI:9650223

GSS.

Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 749)

french-Constant,R.H., Waterfield,N., Buxland,V., Perna,N.T.,

Daborn,P.J., Bowen,D. and Blattner,F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

10919786

Contact: french-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bssr@bath.ac.uk

This is one of a selected subset of flipped clones from the M13

library. For annotation of identified clones (BLASTX, BLASTN and

mapping to E. coli K12 genome) please see french-Constant et al.

2000, Nucleic Acids Res.

QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
 DB 242 CAACGGGTAACTATTTCGGCGACTGGAGCTACGCACACACCCAGAGCAACGCCACAACA 301
 QY 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
 DB 302 ACCGAAGAGTTACACGTTATACACACTCGGTGAAGCGCGGTGCGCCACAGGT-CGGGTGTG 360
 QY 543 HisTTPGluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSer-TyrAs 562
 DB 361 CACTGGGAGCGGTAAAGCAGAGATGTCAACATAATCACTACGT---TCAGCTCGA 417
 QY 562 pAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGly 576
 DB 418 TAATCTGATCGGTTTCAACCGCTTTGACTGGACACCCCAAGGG 460

RESULT 3
 AQ990411 605 bp DNA linear GSS 14-AUG-2000
 LOCUS Rf001179 Photorhabdus luminescens strain W14 M13 library
 DEFINITION Photorhabdus luminescens genomic clone PLG01179, genomic survey sequence.
 ACCESSION AQ990411 GI:9649005
 VERSION AQ990411.1
 KEYWORDS GSS.
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 605)
 AUTHORS fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 JOURNAL 10919786
 PUBMED
 COMMENT Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.

FEATURES
 source Location/Qualifiers
 1..605
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01179"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
 Alignment Scores: 6.96e-67 Length: 605
 Pred. No.: 716.00 Matches: 140
 Score: 84.85% Conservative: 28
 Best Local Similarity: 70.71% Mismatches: 24
 Query Match: 15.11% Indels: 6
 DB: 9 Gaps: 1

US-10-647-956A-6 (1-915) x AQ990411 (1-605)

QY 140 ThrGluArgLeuIleTyrPalaGlyAenthProGlnGluLysAspTyrAsnLeuAlaGly 159
 DB 3 ACAGACGGCTTATCTGGCTGGGAATACAACCTCGGAGAAAGAGTATAACCTCTCGGT 62
 QY 160 GlnCyeValArgHisTyrPalaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
 DB 63 CTGTGTATACGGCCTACACACAGCGGAGGTACCCCGTTGATGAGTCAGTCAGCTGGCG 122
 QY 180 GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThr 199
 DB 123 GGGCCATCTATCCCAATCTCACCATTTGCTGGCGAAGGGCAGGAGCTAACTGGAGC 182
 QY 200 GlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSer 219
 DB 183 GGTGACGACGAAACTGCTCTGGCAGGGAATGCTGGCAAGTGAGGTCTTATACGACACAAGT 242
 QY 220 AsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyValAsnIleGlnArg 239
 DB 243 ACCACTTAATGTCATCGGGCTTTTACTGACCCCAACCGATGCGAAGGCAATATTACAGCT 302
 QY 240 LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTyrPLeuThrLeuLysGlyGlnAla 259
 DB 303 CTGGCTTATGACATGTCGGTCACTTAAAGGGAGTTGGTTGACGGTGAAGGCCAGAGT 362
 QY 260 GluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
 DB 363 GAACAGGTGATTGTTAAGTCCCTGAGTCGTCAGCCGAGGTCAATAATTCGCTGAAGAG 422
 QY 280 HisGlyAsnGlyIleValThrGluTyrSerTyrGlu-ProGluThrGlnArgIleGlu 299
 DB 423 CACGGTAACGGCGTGGTTACCGAGTACAGTTATGAGCCCGGAAACTCAACGCTCTGATAG 482
 QY 299 YIleThrThrArgArgPro-----SerAspAlaLysValLeuGlnAspLeuAr 315
 DB 483 TATACACCGCGCGTCCCAANGGAGTCAATCANGAGCCAGAGTATTCAGGATCTACG 542
 QY 315 gTyrGlnTyrAspProVal-GlyAsnValIleAsnIleArgAsnAspAla 331
 DB 543 CTATAAGTATGATCCCGTGGGGAATGTTATCAGTATTCATATGATGATGCC 592

RESULT 4
 CZ547320/c 878 bp DNA linear GSS 13-MAY-2005
 LOCUS SRAA-aad73b07.b1 Strongyloides ratti whole genome shotgun library
 DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
 ACCESSION CZ547320
 VERSION CZ547320.1 GI:64683141
 KEYWORDS GSS.
 SOURCE Strongyloides ratti
 ORGANISM Strongyloides ratti
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloidea; Strongyloides.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D., Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H., Clifton,S.W. and Wilson,R.
 TITLE Genome Survey sequences from the rat parasitic nematode Strongyloides ratti
 JOURNAL Unpublished (2005)
 COMMENT Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK.
 Class: shotgun.
 Location/Qualifiers

FEATURES


```
source
1. .878
/organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="isofemale line ED321 heterogenic"
/db_xref="taxon:34506"
/dev_stage="infective larval stage (iL3)"
/lab_host="GS10"
/clone_lib="Strongyloides ratti whole genome shotgun library (SRAGSS 004)"
/notes="vector: pOrw13; Site 1: BatX1; Site 2: BatX1; Strongyloides ratti genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 kb fragments. Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."

ORIGIN
Alignment Scores:
Pred. No.: 8.13e-52 Length: 878
Score: 580.00 Matches: 128
Percent Similarity: 63.41% Conservative: 28
Best Local Similarity: 52.03% Mismatches: 45
Query Match: 12.24% Indels: 45
DB: 10 Gaps: 8

US-10-647-956A-6 (1-915) x CZ547320 (1-878)

Qy 480 ArgTyrAspSerAsnGlyMetArgGlnLeuLysValSer-----GluGln 494
Db 867 GGTATGACGCGGG-----CAGCCAGCGTATCCTGAATCCCGTACAGAAAT 817
Qy 495 ProThrGlnAenThrThrGlnGlnArgValleTyLeuProGlyLeuGluLeuArg 514
Db 816 CCC---GCTAACAGTACACACAGCGGTGTTTATCTCGCGGTCTGGAACCTCGC 760
Qy 515 ThrThrGlnSerAenAlaThrThrGluGluLeuHisValleThrLeuGlyGluAla 534
Db 759 AGCGGAAGAAATA-----TATCAGGGGATCTCGCGGGTGTGCC 718
Qy 535 GlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 554
Db 717 GGGCGGCACAGTACGGCTGCTGCTGCGCGGACGGTAAA-----AAA 673
Qy 555 AsnGlnLeuArgTyrSerTyrAspAsnLeulleGlySerSerGlnLeuGluLeuAspAsn 574
Db 672 GATCACCAGCGGTTTCAGTTATGGAATCTGATCGCAGCAGCGGCTGGAAACGGATGC 613
Qy 575 GlnGlyGlnlleleSerGluGluGluTyTyTyProPheGlyGlyThrAlaLeuTrpAla 594
Db 612 GACCGTAACGCTGAGTACAGGAGGAATACTATCCGTTCCGCGGCACGGCGGTGCTGGT 553
Qy 595 AlaAsnSerGlnThrGluAlaSerTyTyLysThrIleArgTyTySerGlyLysGluArgAsp 614
Db 552 GCCATCGGCACAGCGGTATTGACTACAAACCCACCGTTATTCGGCAAGACGGGAT 493
Qy 615 AlaThrGlyLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 634
Db 492 CGCAGCCGACTGTATTACTACGGCTACCGCTACTATCAGCCGTCGGCGAGGCGCTGCTG 433
Qy 635 SerAlaAspProAlaGlyThrIleAspGlyLeuAenLeuTyTyTyTyTyTyTyTyTyTy 654
Db 432 AGTTACAGCCCGCGGGAACCGCTGATCTGTATTCATGTTGTTAAATAAATAAT 373
Qy 655 ProValSerLeuGlnAspGluAsnGlyLeu-----AlaProGluLysGlyLys-Ty 671
Db 372 CCGGTCTCATTCAGAGATATTAAATGGATTATGATGTCGGTAAAGAAAGAGATGAAC 313
Qy 671 rThrLysGluValAsnPhePheAspGluLeuLysPheLysLeuAlaLysSer----- 689
Db 312 TTCAGCAAG-----AAACTCAAAACAAAGACAGAGT 280

Qy 690 -----SerHisValValLysTrpAsnGluLysG1 699
Db 279 CACTTAACACACAGCTTCGGTAACTAAACAGACATCTGCTCCGTTTGTGGCGGA 220
Qy 699 uSerSerTyThrLys 704
Db 219 GCTGGAATATCAGAAG 204

RESULT 5
AW901477/c
LOCUS
DEFINITION
RCO-NN1012-270300-031-a08 NN1012 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW901477
VERSION
AW901477.1 GI:8065682
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 733)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=RCO-NN1012-270
300-031-a08&t3=2000-03-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 691.
FEATURES
source
1..733
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1012"
/notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 136,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1.18e-49 Length: 733
Score: 559.00 Matches: 115
Percent Similarity: 60.74% Conservative: 32
Best Local Similarity: 47.52% Mismatches: 73
Query Match: 11.79% Indels: 22
DB: 1 Gaps: 4

US-10-647-956A-6 (1-915) x AW901477 (1-733)

Qy 455 ProGlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsn----- 471
```

```

Db 678 CCGCGCGAAGTGGATGGATGACGAAACAACTGAGCCATGTCATATGGTGGAG 619
Qy 472 -----AsnGlyProGlyAsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGln 488
Db 618 CGCACGTGGCCCTCAATGACACCGAGCGGTAGCTTACGGTCCGACGCGCATGGCCAG 559
Qy 489 LeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgValIleTyrLeu 508
Db 558 CGCAAGGTGGCGACGACGCAACCAACCGCCGACCTTGGTCAGTGAGACCCGATATCTA 499
Qy 509 ProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisVal 528
Db 498 CCAGGGCTGGAACCGCGCATGGGATGGC-----GAGAAACTGCACGTC 454
Qy 529 IleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLys 548
Db 453 GTCAACCGTC---CAGGCGGCGCCGACCCAGCGTGCAGGTGTTCATTTGGGAAGCGCGCG 397
Qy 549 ProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSer 568
Db 396 CCGCAGCAACTGGCGAATGATCAATACCGTTACACCTTAGCCGATCATCTGGGCTCTTGT 337
Qy 569 GlnLeuGluLeuAspAsnGlnGlyGlnIleSerGluGluGluTyrTyrProPheGly 588
Db 336 TCCTGGAAGTGGACAGTGAAGCGAGGATCATCTCGCGAGACGATCATCTCGTTTGGT 277
Qy 589 GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyr 608
Db 276 ACAGCGCCCTTCAGCAGAGGGGTGATTCGAGCGAGAGAGTATTCGACGTTGGTTAT 217
Qy 609 SerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnPro 628
Db 216 TCGGCAAGGAGCGGATGCGACGGGGCTTTATTACTATGGTTTCAGGTACTACGTGCGC 157
Qy 629 TrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr 648
Db 156 TGGTTACAGGTGGATTAACCTGATCCGCGGAGCGGATCAGCGGTTTGAATCTGTAT 97
Qy 649 ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLys 668
Db 96 AGAATGTCAGAAATAATCCGTTTTCCTCAGAGATGATGAAGTCTGGTACTACGAAA 37
Qy 669 GlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeuAlaLys 688
Db 36 -----GAAGAGATCTACAGTCGGCTCGCCCTCTCT 7
Qy 689 SerSer 690
Db 6 ATGTCA 1

RESULT 6
LOCUS AQ991400/c
DEFINITION AQ991400 494 bp DNA linear GSS 14-AUG-2000
            Photobacterium luminescens strain W14 M13 library
            Photobacterium luminescens genomic clone PLG02327, genomic survey
            sequence.
ACCESSION AQ991400
VERSION AQ991400.1 GI:9649994
KEYWORDS GSS.
SOURCE Photobacterium luminescens
ORGANISM Photobacterium luminescens
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photobacterium.
            1 (bases 1 to 494)
AUTHORS Ifrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
            Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
            Photobacterium luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10519786
COMMENT Contact: french-Constant RH
            Department of Biology and Biochemistry

```

```

University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
    source
        1..494
        /organism="Photobacterium luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clone="PLG02327"
        /dev_stage="primary phase variant"
        /clone_lib="Photobacterium luminescens strain W14 M13
        library"
        /notes="Genomic DNA from strain W14 was size selected (1-2
        kb) and then cloned into M13 Janus."
ORIGIN
Alignment Scores:
Pred. No.: 1,15e-46 Length: 494
Score: 529.00 Matches: 107
Percent Similarity: 80.86% Conservative: 24
Best Local Similarity: 66.05% Mismatches: 28
Query Match: 11.16% Indels: 4
DB: 9 Gaps: 1
US-10-647-956A-6 (1-915) x AQ991400 (1-494)

```

```

Qy 90 GlyArgThr-IleThrLeuAsnAspIleGluSerArgProValLeuIleIleAlaLath 109
Db 485 GGTGCTGCTGTTGTCATTAATGATATTAAGAGTCTGTCGTAATGACAATGATGGCC 426
Qy 109 rGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAla 129
Db 425 CGGTGTTGCTGACAGCCCGTCGCTATGAGGCAACACCTTGCCCGT-CGCTTGTATCTGT 367
Qy 129 eThrGluGlnVal-----GlnAlaGlyGluLysThrThrGluArgLeuIleTrpAlaG 147
Db 366 GAGCGAGCAAGTTTCAACCCAGAGAGTGTAAAGTGACAGAGCGCTTTATCTGGGCTGG 307
Qy 147 YAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspTh 167
Db 306 GAATACAACTCGGAGAAAGAGTATAACCTCTCCGGTCTGTGTATAGCCACTACGACAC 247
Qy 167 rAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerG 187
Db 246 AGCGGAGTGACCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 187
Qy 187 nGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpG 207
Db 186 CCAATTGCTGGCGAAGGGCAGGAGCTAACTGAGCGGTGACGACGAAACTGTCTGGCA 127
Qy 207 nGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAla 227
Db 126 GGAATGCTGGCAAGTGAGGTCTTATACGACACAAAGTACCACCTAAATGCCATCGGGGCTTT 67
Qy 227 uLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyG 247
Db 66 ACTGACCCCAACCGATCGGAAAGGCAATATTTCAGCGTCTGGCTTATGACATTCGCGGTCA 7
Qy 247 nLeu 248
Db 6 GTTA 3
RESULT 7
AQ990055

```

```

LOCUS      AQ990055              406 bp    DNA          linear      GSS 14-AUG-2000
DEFINITION Rf00763 Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG00763, genomic survey
            sequence.
ACCESSION  AQ990055
VERSION    AQ990055.1 GI:9648649
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 406)
            ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
            A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
            Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL    10919786
PUBMED
COMMENT    Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bsr@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.
FEATURES   source
            Location/Qualifiers
            1..406
            /organism="Photorhabdus luminescens"
            /mol_type="genomic DNA"
            /strain="W14"
            /db_xref="taxon:29488"
            /clone="PLG00763"
            /dev_stage="primary phase variant"
            /clone_lib="Photorhabdus luminescens strain W14 M13
            library"
            /note="Genomic DNA from strain W14 was size selected (1-2
            kb) and then cloned into M13 Janus."
ORIGIN
Alignment Scores:
Pred. NO.: 5.67e-44 Length: 406
Score: 503.00 Matches: 100
Percent Similarity: 88.80% Conservative: 11
Best Local Similarity: 80.00% Mismatches: 12
Query Match: 10.61% Indels: 2
DB: 9 Gaps: 0

US-10-647-956A-6 (1-915) x AQ990055 (1-406)

Qy 483 SerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrGlnGln 502
Db 1 AGCAACGGCATACGCCACCTAAAGTGAATGAACAACAACTCAGATATCCCCGACAA 60
Qy GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
Db 61 CAAGGGTAACTTATCTACCGGGGTGAATACGTACACCCAGAACACGCCACCAACA 120
Qy ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
Db 121 ACAGAAGAGTTACACGTTATCACACTCGTGAAGCCGCCGCCGACGATTCGAGTATG 180
Qy HisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuAtgTyrSerTyrAsp 562
Db 181 CATTGGGAGACGGTAAACAGAGATATATATACATCATAGCTTCGTTACAGTACGAT 240
Qy AsnLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSerGlu-Gl 582

```

```

Db 241 AATCTTATTGGTCCACCAACTTCAATTAGATAGACGACGGCAAAATTATCAAGTGAAGA 300
Qy 582 uGluTyrTyrProPheGlyGlyThr-AlaLeuTyrAlaAlaAenSerGlnThrGluAlaAs 602
Db 301 AGAATATTATCCATTGGTGGTACAGCGCTGTGGCGGNAGGGATTAAACCGACCAAG 360
Qy 602 erTyrLysThr 605
Db 361 CTNTTAAACA 371

RESULT 8
LOCUS      AQ990688/c
DEFINITION Rf001498 Photorhabdus luminescens strain W14 M13 library
            Photorhabdus luminescens genomic clone PLG01498, genomic survey
            sequence.
ACCESSION  AQ990688
VERSION    AQ990688.1 GI:9649282
KEYWORDS   GSS.
SOURCE     Photorhabdus luminescens
            Photorhabdus luminescens
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
REFERENCE  1 (bases 1 to 594)
            ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
            A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
            Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL    10919786
PUBMED
COMMENT    Contact: ffrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bsr@bath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.
FEATURES   source
            Location/Qualifiers
            1..594
            /organism="Photorhabdus luminescens"
            /mol_type="genomic DNA"
            /strain="W14"
            /db_xref="taxon:29488"
            /clone="PLG01498"
            /dev_stage="primary phase variant"
            /clone_lib="Photorhabdus luminescens strain W14 M13
            library"
            /note="Genomic DNA from strain W14 was size selected (1-2
            kb) and then cloned into M13 Janus."
ORIGIN
Alignment Scores:
Pred. NO.: 5.78e-42 Length: 594
Score: 487.00 Matches: 111
Percent Similarity: 64.00% Conservative: 17
Best Local Similarity: 55.50% Mismatches: 68
Query Match: 10.27% Indels: 5
DB: 9 Gaps: 0

US-10-647-956A-6 (1-915) x AQ990688 (1-594)

Qy 428 GlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
Db 593 GGTGTGTCAGACCCCTAACAGGATCCCAATCTGTTGATTCATTCATTCATTCAGGT 534
Qy 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuLeuThrPro--ArgGlyGluL 467

```

```
Db 533 GGTCAATCAACCCAGTTTGTATCAGGCATTCTTTAAGCTGNNACCCCGGNAGAACTCCAC 474
Qy eulyserGlnValAsnAsnGlyProGlyAsnGluTyrArgTyrAspSerAsnGlyMetA 487
Db 473 CNANTGACCAAGTGGTAAACAGCGCGCGAATGGTC-CGCTATGACAGTGATGGAATGC 415
Qy 487 rg-GlnLeuYsValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgValle 506
Db 414 GGCTATTGTAATAAATGAACAGCAACCAACCCCTATGCCACTGCAACACACGCGAGTCNCT 355
Qy 507 TyrLeuProGlyLeuGluLeuArgTyrThrGlnSerAsnAlaThrThrThrGluGluLeu 526
Db 354 TACTTCGACGGTGGTAATACANACCACTCAAGCGCGCCCAATATACCGAAGACTTG 295
Qy 527 HisValle-ThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSe 546
Db 294 CAAGTTATTGCTGTCGACCAAGCAGNAGACCAAGTACGCGTTCTACANTGNAAAA 235
Qy 546 rGlyYsProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleG1 566
Db 234 AGGCCANCCNCTCGNATAGATNACNATCAGTACAGTACAGTACAGTATCTTNCACA 175
Qy 566 ySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTrp 586
Db 174 CAGCAGCGAATTAGAACTGNATATGACGGGTTAATTATCAGTTGGNAGAGATTATACC 115
Qy 586 oPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrIysThr11 606
Db 114 CTATGCCGCGACCCATATGNCNCAAGAAATCAGTTGTAAGCTGTWACAAAACCAT 55
Qy 606 eArgTyrSerGlyYsGluArgAspAlaThrGlyLeuTyrTyrTrpGlyTyr 623
Db 54 TCGTTATTACGNCAAGAGCGCTGATGCAACAGGACTGTACTATTACGGCTAC 3

RESULT 9
LOCUS AQ990013 547 bp DNA linear GSS 14-AUG-2000
DEFINITION Rfc00707 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00707, genomic survey
sequence.
ACCESSION AQ990013
VERSION AQ990013.1 GI:9648607
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 547)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1..547
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
```

```
ORIGIN
Alignment Scores:
Pred. No.: 1,39e-33 Length: 547
Score: 409.50 Matches: 73
Percent Similarity: 88.89% Conservative: 7
Best Local Similarity: 81.11% Mismatches: 7
Query Match: 8.64% Indels: 3
DB: 9 Gaps: 1
US-10-647-956A-6 (1-915) x AQ990013 (1-547)
Qy 585 TyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLys 604
Db 1 TATCCGTATGGCGGTACGGCGATATGGCGCGAGAAATCAGACAGAAAGCCAGCTACAAA 60
Qy 605 ThrIleArgTyrSerGlyYsGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArg 624
Db 61 TTTATTGCTTACTCCCGTAAAGAGCGGGATGCCACTGGATTGTATTATTACGGCTACCGT 120
Qy 625 TyrTyrGlnProTrpAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGly 644
Db 121 TATTATCAACCTTGGTGGTGCATGGTTGAGTGTGATCCGCGGGACCGTGGATGGG 180
Qy 645 LeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeu 664
Db 181 CTGAATTTGTACCGAATGGTGAGGAATAACCCCATCATTGACTGACCATGACGGATTA 240
Qy 665 AlaProGlu-----LysGlyLysTyr 671
Db 241 GCACCCGCTCTCCAATAGAAATCGAAATAC 270

RESULT 10
LOCUS AQ990147 312 bp DNA linear GSS 14-AUG-2000
DEFINITION Rfc00869 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00869, genomic survey
sequence.
ACCESSION AQ990147
VERSION AQ990147.1 GI:9648741
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 312)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
FEATURES
source
1..312
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
```


QY 557 LeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGly 576
 Db 492 TACGGTTACACCTTACGATCATCTGGGCTCTTGTTCGCTGAACCTGGACAGTGAAGCG 551
 QY 577 GlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTyrPalaAlaAsn 596
 Db 552 AGGATCATCATCGGAGACGTATCATCCGTTGGTACGAGCGCCCTTCAGCAGAGGGGT 611
 QY 597 SerGlnThrGluAlaSerTyrLysThrIleArg 607
 Db 612 GATTCGACGAAGAGAGCTTATCGCACGTTGCGT 644

RESULT 12
 CZ532972/c
 LOCUS
 DEFINITION
 (SRAA-aac82c03.g1 Strongyloides ratti whole genome shotgun library
 (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
 CZ532972
 CZ532972.1 GI:64646528
 GSS.
 STRONGYLOIDES RATTI
 ORGANISM
 Strongyloides ratti
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Panagrolaimoidea; Strongyloidea; Strongyloides.
 1 (bases 1 to 795)
 Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
 Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
 Clifton,S.W. and Wilson,R.
 Genome Survey sequences from the rat parasitic nematode
 Strongyloides ratti
 Unpublished (2005)
 Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 Genomic DNA was provided by Fiona Thompson
 (F.Thompson@bristol.ac.uk) and Mark Viney
 (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
 UK.
 Class: shotgun.
 Location/Qualifiers
 1. 795
 /organism="Strongyloides ratti"
 /mol_type="genomic DNA"
 /strain="isofemale line ED321 heterogonic"
 /db_xref="taxon:34506"
 /dev_stage="infective larval stage (L3)"
 /lab_host="G510"
 /clone_lib="Strongyloides ratti whole genome shotgun
 library (SRAAGSS 004)"
 /notes="vector: pOTW13; Site 1: BstXI; Site 2: BstXI;
 Strongyloides ratti genomic DNA was randomly sheared,
 end-repaired and size fractionated to enrich for 2-4 kb
 fragments. Genomic DNA was provided by Fiona Thompson
 (F.Thompson@bristol.ac.uk) and Mark Viney
 (Mark.Viney@bristol.ac.uk) at the University of Bristol,
 Bristol, UK. Sequencing by Washington University Genome
 Sequencing Center, St. Louis, MO."

ORIGIN
 Alignment Scores:
 Pred. No.: 2,45e-08 Length: 795
 Score: 180.00 Matches: 69
 Percent Similarity: 32.90% Conservative: 33
 Best Local Similarity: 22.26% Mismatches: 80
 Query Match: 3.80% Indels: 128
 DB: 10 Gaps: 12

US-10-647-956A-6 (1-915) x CZ532972 (1-795)

QY 368 GlyGlnAsnAsnGlnLeuProSerProAlaLeuProSerAspAsnAenThrTyr--- 386
 Db 668 GGAGCGCAACCTGAGAAAGAGCGCCCTTAACCTTCCAAAACAGGAGTGGTTCGGTTATACC 609
 QY 387 -----ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIle 404
 Db 608 TCAATTACGGATTATCTGGATGGTTCCCAATAC----- 576
 QY 405 ArgHisSerSerProAlaThrGlnAsnAenTyrThrValAlaIleThrLeuSerAsnArg 424
 Db 576 ----- 576
 QY 425 SerAsnArgGlyValLeuSerThrLeuThrAspProAsnGlnValAspThrLeuPhe 444
 Db 575 -----CTGAGTACGGTAGGAAGCAACCAATAGATGGATCCTATT--- 534
 QY 445 AspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTyrProArg 464
 Db 534 ----- 534
 QY 465 GlyGluLeuGlnValAsnAsnGlyProGlyAsnGluTyrTyrArgTyrAspSerAsn 484
 Db 533 -----GAGTATGCCTATGAACAGGAA 513
 QY 485 GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArg 504
 Db 512 GCCTTTCTAGAGCAACAGCATGCGGAGCAGCCG-----ANTCCAACGCTCCAC--- 465
 QY 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrGlu 524
 Db 464 -----TTTTTCCCA-----ACTGGCGAA 447
 QY 525 GluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrp 544
 Db 446 GGATTTTAT----- 438
 QY 545 GluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeu 564
 Db 437 -----GATTATGAAAATAATGAGTATATTTACCAGTACAAAGATCAT 396
 QY 565 IleGlySerSerGlnLeuGluLeu-----AspAsnGlnGlyGlnIleIleSer 580
 Db 395 TTGGGAATGTACGGTAAGCTATAAAGAGGCTCTGATGGTCTTCACAGATTACCGAC 336
 QY 581 GluGluGluTyrTyrProPheGly-----GlyThrAlaLeuTrpAla 594
 Db 335 CAGAAATGATTACTATCTTTCGGGATGAATATTTCCAAGGGAAGAGCGGCTTTGGG 276
 QY 595 AlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAsp 614
 Db 275 ACCAATAGTTTA-----TACAACATAAG-----TACAACGGTAAGGAACCTCAA 231
 QY 615 AlaThrGlyLeuTyrTyrTyrArgTyrTyrGlnProThrPalaGlyArgTrpLeu 634
 Db 230 GAGACAGGAATGATGATTATGAGCGAGATTTTATATCGCGGATATTGGGAGATGGGT 171
 QY 635 SerAlaAspPro---AlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
 Db 170 GTGGTGGATCCGTCGCGGAGAAATATACAGAAATGCTCTCCATATATCTATGTTGGAAT 111
 QY 654 AsnProValSerLeuGlnAspGluAsnGly 663
 Db 110 AACCTTCAATATTTGTTGATTATGATGGT 81

RESULT 13
 CC818388/c
 LOCUS
 DEFINITION
 100004D09R Oxytricha plasmid UUGC10 library Sterkiella
 histriomuscorum genomic clone UUGC100004D09 R, genomic survey
 sequence.
 CC818388
 CC818388.1 GI:32897684
 GSS.
 ACCESSION
 VERSION
 KEYWORDS

SOURCE
ORGANISM Sterkiella histriomyscorum (Oxytricha trifallax)
Sterkiella histriomyscorum
Eukaryota: Alveolata: Ciliophora: Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.

REFERENCE
AUTHORS Dunn,D., Doak,T., Herrick,G. and Weiss,R.
TITLE Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0004 row: D column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 681.

FEATURES
source
1. .681
Location/Qualifiers
/organism="Sterkiella histriomyscorum"
/mol_type="genomic DNA"
/db_xref="taxon:94289"
/clone="UUGC10004D09"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Oxytricha plasmid UUGC10 library"
/notes="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polynucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2.45e-08 Length: 681
Score: 179.00 Matches: 53
Percent Similarity: 47.12% Conservative: 37
Best Local Similarity: 27.75% Mismatches: 85
Query Match: 3.78% Indels: 16
DB: 9 Gaps: 6

US-10-647-956A-6 (1-915) x CC818388 (1-681)

Qy 137 GlulysThrThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsn 156
::: ||| ||| ::::: |||
Db 551 GATAATACGGTTGAGCTCTTGTATATCGCGAGGCCAATCGAATGCTACACTCGAGAAC 492
::: ||| ||| ::::: |||
Qy 157 LeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeu 176
::: ||| ::::: ||| ::::: |||
Db 491 CTGAGAGGAAACTTTTTCAGCATTTATGACTCAGGAGCGCTGGAAGAACACCGACTTAT 432
::: ||| ::::: ||| ::::: |||
Qy 177 SerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuThrAspAsnGln--Asp 195
::: ||| ||| ::::: |||
Db 431 AACCTCAAGGACAAATCCATAAATGATCGCGCTTGCCATTGATACACAGGTGCTC 372
::: ||| ||| ::::: |||
Qy 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
::: ||| ||| ::::: |||
Db 371 GCCGATTGG-----AGGCTCATCGCGGTAGCTGGAAGCAATAGCTAC 327
::: ||| ::::: |||
Qy 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
::: ||| ||| ::::: |||
Db 326 CAGATCAGGACAAGCATATGATGCCCTCGCGAGGATTAAACCGGCATCGGCTCCTGACCAT 267
::: ||| ||| ::::: |||

Qy 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
::: ||| ||| ::::: |||
Db 266 AGCATCATTAATCTCTTCTTATAGCAGCGCTGTGTACTGTAAGCGAAACGGTA----- 213
::: ||| ||| ::::: |||
Qy 256 LysGlyClnAlaGluGlnValIle-----IleLysSerLeuThrTyrSerAlaAla 272
::: ||| ||| ::::: |||
Db 212 -----GAACAAAGTTCTGTGTGTGACGACACATCTGCAAAACATTGAAATATGATGCGAAA 159
::: ||| ||| ::::: |||
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
::: ||| ||| ::::: |||
Db 158 GGGCAGCAATGAGCGTGACCTACGCGAATGGTGATTAACCACTATGAATACGATGAT 99
::: ||| ||| ::::: |||
Qy 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgPro---SerAspAlaLysValLeu 311
::: ||| ||| ::::: |||
Db 98 GAAACTTTTAGGATCAACACGCTGAAACCTTGAGCGCCATCAGTGTCTCT-----TTA 45
::: ||| ||| ::::: |||
Qy 312 GlnAspLeuArgTyrGlnTyrAspProValGly 322
::: ||| ||| ::::: |||
Db 44 CAGGATCTACATTTTCACGATATGACGCGCTCGGA 12
::: ||| ||| ::::: |||

RESULT 14
CC129231/c
LOCUS CC129231 846 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.73B3.T7 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.73B3, genomic survey sequence.
ACCESSION CC129231
VERSION CC129231.1 GI:29998286
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE 1 (bases 1 to 846)
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.73B3.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: entae@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .846
Location/Qualifiers
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.73B3"
/clone_lib="Notre Dame Liverpool"
/notes="Vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched 1d larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"

ORIGIN
Alignment Scores:
Pred. No.: 3.95e-08 Length: 846
Score: 178.50 Matches: 90
Percent Similarity: 37.64% Conservative: 41
Best Local Similarity: 25.86% Mismatches: 127
Query Match: 3.77% Indels: 91
DB: 9 Gaps: 13

US-10-647-956A-6 (1-915) x CC129231 (1-846)

Qy 473 GlyProGlyAsnGluTrp-----TyrArgTyrAspSerAsnGlyMetArgGlnLeu 489
::: ||| ||| ::::: |||

```
Db 832 GGGCCGAGGCGAGTTTCGAGGCGCATATCATTTACGATGCGTGGCCGCCGAGCCGC 773
Qy 490 LysVal-----SerGluGlnProThrGlnAenThrThrGlnGlnGln 503
Db 772 AAGCGCGTGCCTACAGGCGCAAAACGACAGACCGTTCCTGTGCGCGGCTAC 713
Qy 504 ArgValIleTyrLeuProGlyLeuGluLeuArgThrGln-SerAenAlaThrThr 523
Db 712 CGGTTGCTG-----CAGGAGCAGCGCAGCAGCGC 683
Qy 523 rGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHi 543
Db 682 AGCGCGCGAGCTGAGCTACGATCCGCGCAGCC-----CGTGAGGCCCA 638
Qy 543 sTyrGluSerGlyLysProGluAepValAenAenAenGlnLeuArgTyrSerTyrAepAs 563
Db 637 CTGGCGCGCTGGAGCAGCGCGGCGCAGCGCTCGGCAGATATT-TACTGGTATCACAC 579
Qy 563 nLeuIleGlySerSerGlnLeuGluLeu---AspAenGlnGlyGlnIleIleSerGluGl 582
Db 578 CGATCTCAACAGCGCGCGCTGGAAGTGACCGACGCGCGCGCAACCTGTGCTGCTCGG 519
Qy 582 uGluTyrTyrProPhe-----GlyGlyThrAlaLeuTrpAlaAenSerGl 598
Db 518 GCATACGACACCTTCGCGCAAGCTGCAGGCGCGCAGCGTGGCGCGCGCGAAGCGCA 459
Qy 598 nThrGluAlaSerTyrLysThrIleArgTyrSerGlyLys---GluArgAspAlaThrGl 617
Db 458 GGGTGCGCAATACAGCAGCGCTGCGCTAGCGCGGCAATATACAGCAGCAGCAAGCGG 399
Qy 617 YLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAs 637
Db 398 CTGCACTACAACTGTTCCGTACTACGAACCGAGGTGGGCGTTTCCACCGCAGGA 339
Qy 637 pProAlaGlyThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValse 657
Db 338 TCCGATAGGGCTGCGCGCGGTTGAACCTTTATCAGTATGCA---CCGAACCGCTGAT 282
Qy 657 rLeuGlnAspGluAenGluAlaProGluLysGlyLysTyrThrLysGluValAenPh 677
Db 281 GTGGTGATCCGCTGGGTTGAGTGTAAAGCTTTGTAAGCAACAGAAAGAG----- 230
Qy 677 ePheAspGluLeuLysPheLysLeuAlaAlaLysSerSerHisValVallysTrpAenGl 697
Db 229 -----CCGAAGATTCTTAT----- 215
Qy 697 uLysGluSerSerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAs 717
Db 214 -----GAACAAGCTAGGAATAAAGCACTCAA----- 188
Qy 717 pProSerGlyTyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIl 737
Db 188 ----- 188
Qy 737 eileTyrSerArgLeuGluAenSerSerLeuSerGluLysSerLysThrAenLeuSe 757
Db 187 -----TGGCTTAGGAACGTGGTTTCAAGCGGAAAGTCAATACAGG---AA 141
Qy 757 rLeuGlySerGluIleSerGlyTyrMetAlaAArgThrIleGlnAspThrIleSerGluTy 777
Db 140 ATTTGGCGCAACAGAGCAACCTGTGCGGAATGACCACCTTGATGGTAAACAGGGTT 81
Qy 777 rAlaGluGluHisLysTyrArgSerAenHisProAspPheTyr-SerGluThrAspPhePh 797
Db 80 TAGGATTGAATATGATGAGAGAAGTGGT-----GCTCATATAAATGTCCT 36
Qy 797 eAlaLeuMetAspLysSerGlu 804
Db 35 TAGTGGGAAGGATGAAGGAGAG 14
```

RESULT 15
CC110859

```
LOCUS CC110859 850 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.20H16.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.20H16, genomic survey sequence.
ACCESSION CC110859
VERSION CC110859.1 GI:29979914
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE 1 (bases 1 to 850)
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.20H16.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.
FEATURES             Location/Qualifiers
     source            1..850
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /strain="Liverpool"
                     /db_xref="taxon:7159"
                     /clone="NDL.20H16"
                     /note="Vector: pECBAC1, Site 1: Hind III; The library was
                     prepared from whole body tissue of newly hatched 1st larvae
                     by David Severson at the University of Notre Dame and
                     Hongbin Zhang"
ORIGIN
Alignment Scores:      1.79e-07      Length:      850
Pred. No.:            172.50        Matches:     79
Score:                35.67%        Conservative: 43
Percent Similarity:   23.10%        Mismatches:  118
Best Local Similarity: 3.64%        Indels:      102
Query Match:          9
DB:                    13
US-10-647-956A-6 (1-915) x CC110859 (1-850)
Qy 329 AsnAspAlaGluAlaThrArgPheTrpArgAenGlnLysValAlaProGluAenSerTyr 348
Db 24 AATATTGCGGAACACTGACTGGGCAACACAAAATGACGGAACACTAGACCGCTTAGCTAC 83
Qy 349 ThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrArgGluMetAlaAenIleGly 368
Db 84 CAATATGATGTTACTAATCGTTA-----AAAGAGGTAATATTGGGCAATGCCGA 137
Qy 369 GlnGlnAenAenGlnLeuProSerProAlaLeuProSerAspAenAenThrTyrThrAen 388
Db 138 GCT-----ACAGCTGGATCT 152
Qy 389 TyrThrArgSerTyrSerTyrAspHisSerGlyAenLeuThrGlnIleArgHisSerSer 408
Db 153 TATGCGGAGAAATGGAATTATGACTTAAACGGGAATATTACTGGTGTGCAAGAACAGGT 212
Qy 409 ProAlaThrGlnAenAenTyrThrValAlaIleThrLeuSerAenArgSerAenArgGly 428
Db 213 -----CAGGTGCCGA 224
Qy 429 ValLeuSerThrLeu-----ThrThrAspProAenGlnValAspThr 442
Db 225 GTAATGATCAGCTCAGTTATACCTACGATCAATCGGGAATAGTAATAAAGTATGAG 284
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: December 14, 2005, 12:23:18 ; Search time 387 Seconds
(without alignments)
4202.762 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKTPSIKVLN.....EAINRRAIAENLGMRTS 915

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10647956/runat_12122005_091818_29634/app_query.fasta_1.1095
-DB=Issued Patents NA -QFMT=faostat -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1 290 @runat_12122005_091818_29634 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4740	100.0	2745	3	US-09-817-514A-5
2	2501.5	52.8	37948	3	US-09-251-645-11
3	2467	52.0	3132	3	US-08-851-567B-60
4	336	7.1	4884	3	US-09-328-352-2478
5	322.5	6.8	2997	3	US-09-252-991A-11853
6	307	6.5	2925	3	US-09-252-991A-7069
7	286.5	6.0	4881	3	US-09-252-991A-7234
8	281	5.9	4320	3	US-09-543-681A-3388
9	273.5	5.8	4281	3	US-09-492-709A-180

10	262	5.5	31960	3	US-09-453-702B-11	Sequence 11, Appl
11	282	5.5	31960	3	US-10-114-170-11	Sequence 11, Appl
12	256	5.4	5519	3	US-09-453-702B-226	Sequence 226, App
13	256	5.4	5519	3	US-10-114-170-226	Sequence 226, App
14	254.5	5.4	4134	3	US-09-711-164-296	Sequence 296, App
15	253.5	5.3	11613	3	US-09-453-702B-42	Sequence 42, Appl
16	253.5	5.3	11613	3	US-10-114-170-42	Sequence 42, Appl
17	248.5	5.2	4791	3	US-09-328-352-1416	Sequence 1416, Ap
18	246	5.2	9717	3	US-09-251-645-1	Sequence 1, Appl1
19	242	5.1	4998	3	US-09-543-681A-304	Sequence 304, App
20	235	5.0	4761	3	US-09-543-681A-1157	Sequence 1157, A
21	227.5	4.8	1857	3	US-09-252-991A-11787	Sequence 11787, A
22	219.5	4.6	1857	3	US-09-252-991A-7125	Sequence 7125, Ap
23	216	4.6	7841	3	US-09-902-540-816	Sequence 816, App
24	213.5	4.5	3003	3	US-09-902-540-1863	Sequence 1863, Ap
25	201	4.2	3660	3	US-09-453-702B-12	Sequence 12, Appl
26	201	4.2	3660	3	US-10-114-170-12	Sequence 12, Appl
27	197	4.2	3387	3	US-09-252-991A-14461	Sequence 14461, A
28	184	3.9	1683	3	US-09-252-991A-6977	Sequence 6977, A
29	184	3.9	1683	3	US-09-252-991A-11588	Sequence 11588, A
30	183.5	3.9	1035	3	US-09-328-352-2531	Sequence 2531, Ap
31	179	3.8	26012	3	US-09-902-540-1212	Sequence 1212, Ap
32	172.5	3.6	11091	3	US-09-134-001C-2243	Sequence 2243, Ap
33	171.5	3.6	4770	3	US-09-543-681A-826	Sequence 826, App
34	171	3.6	30549	3	US-09-134-001C-322	Sequence 322, App
35	170.5	3.6	2495	3	US-09-668-113A-1	Sequence 1, Appl1
36	169	3.6	1764	3	US-09-252-991A-14908	Sequence 14908, A
37	169	3.6	3840	3	US-09-710-279-3187	Sequence 3187, Ap
38	168.5	3.6	9319	3	US-08-976-259-85	Sequence 85, Appl
39	168.5	3.6	9319	3	US-09-956-004-85	Sequence 85, Appl
40	168.5	3.6	22671	3	US-08-976-259-14	Sequence 14, Appl
41	168.5	3.6	22671	3	US-09-956-004-14	Sequence 14, Appl
42	167	3.5	4453	3	US-09-453-702B-90	Sequence 90, Appl
43	167	3.5	4453	3	US-10-114-170-90	Sequence 90, Appl
44	166.5	3.5	1515	3	US-09-902-540-2019	Sequence 2019, Ap
45	166.5	3.5	3543	3	US-09-710-279-4149	Sequence 4149, Ap

ALIGNMENTS

RESULT 1
US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: firench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-09-817-514A-5

Alignment Scores:
Pred. No.: 0
Score: 4740.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 2745
Matches: 915
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-647-956A-6 (1-915) x US-09-817-514A-5 (1-2745)			
Qy	1	MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Ds	1	ATGAGCAGTTCACAATCTGCAATTTGACAAAGACCCCTCGATTAAGGTATTAGATAAC	60
Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Ds	61	AGGAAATTAATGATGACGTCTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Ds	121	GAATTAATGATGTTATGAGTTCAATATTTCCGGGATTTTCAGGTAAAGACCCGATCT	180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Ds	181	CGTAAAAATAAAACCCAGCGGCCCAATTTCAATCGTGTCTTTAAATCTTGCCGGTCAA	240
Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Ds	241	GTTTTACGTGAAGAAAGTTGATGCCGTCGGACTATTAACCTCAATGATATTGAAAGT	300
Qy	101	ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHisArgTyrGluAspAsn	120
Ds	301	CGCCCGGTGTGATCATCAATGCAACCGTGTCCGCCAAACCATCGTTATGAAGATAAC	360
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
Ds	361	ACCTTCCCGTCTGCTCGCTATCACCCGAAAGGTACAGCGGAGGAGAGAAACGACC	420
Qy	141	GluArgLeuIleTrrAlaGlyAenThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Ds	421	GAACGTCTTATCTGGCGCGCAATACGCCGCAAGAAAGATTAACAACCTCGCCGGTCAG	480
Qy	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Ds	481	TGTGTCCGCATACGATACCGCGGACTTACTCACTCAATAGCCTTCTCTGGCTGC	540
Qy	181	ValValLeuSerGlnSerGlnLeuLeuThrAspAenGlnAspAlaAspTrrThrGly	200
Ds	541	GTCTGTCTATCACAACTCTCAACACTGTCTACCGATACAGGATGCCGATGACACAGT	600
Qy	201	GluAspGlnSerLeuTrrGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Ds	601	GAAGACCAAGCCCTCTGCAACAAACTGAGTAGTGATGTATATCACTCAAAAGTAAC	660
Qy	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240
Ds	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	720
Qy	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrrPheLeuThrLeuLysGlyGlnAlaGlu	260
Ds	721	GCCTATGATGTGGCGGCGAGCTAAAGGGAGTTGGTTAACTCAAAAGGTCAGCGCGAA	780
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis	280
Ds	781	CAGGTGATTTACAAATCGCTAACTCTCCGCGCGCGGCAAAATTAACGTGAAGAGCAC	840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Ds	841	GGTAACGGGATGTCTCACTGAATACAGCTACGAAACCGGAAACCCACCGCTTATCGGCATT	900
Qy	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Ds	901	ACCACTCGCGTCCATCATCAGCCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA	960
Qy	321	ValGlyAenValIleAsnIleArgAenAspAlaGluAlaThrArgPheTrrArgAsnGln	340
Ds	961	GTAGGCAATGCTATTAATTCGTAAATGATCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	341	LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Ds	2101	AGTTATACAAAAATAAATCATTTGAAAGTGGTTCTGTCGTGATTCGCGTCCGTCGCGGT	2160
Ds	1021	AAAGTAGCCCCGAGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCCACC	1080
Qy	361	GlyArgGluMetAlaAsnIleGlyGlnGlnAenAsnGlnLeuProSerProAlaLeuPro	380
Ds	1081	GGCGCGAAATGGCCAAATATCGGTACGCAAAACACCAACTTCCCTCCCTGGCTACCT	1140
Qy	381	SerAspAsnAsnThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAen	400
Ds	1141	TCTGACAAACAATACCTACACTAATCTCGCAGCTACAGCTATGATCACAGTGGTAAT	1200
Qy	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAsnTyrThrValAlaIleThr	420
Ds	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGAACACTACACCTGGCTATCACC	1260
Qy	421	LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Ds	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320
Qy	441	AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Ds	1321	GATACGTTGTTTGATCGCGTGTGTACCAAAACCACTTATATCCCGGACAGACACTATC	1380
Qy	461	TrrThrProArgGlyGluLeuLysGlnValAenAsnGlyProGlyAenGluTrrTyrArg	480
Ds	1381	TGGACACCCAGGAGAGTTAAAGCAGGTTAAATGATGCGCCGGAAATGAGTGGTACCGC	1440
Qy	481	TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Ds	1441	TACGACAGCAACCGCATGAGACAACTGAAAGTGAGTGAAACAGCAACCCAGAAATACTACG	1500
Qy	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Ds	1501	CAGCAACAACGGGTATCTATTTCGGGACTGAGACTACGCAACAACCCAGAGCAACGCC	1560
Qy	521	ThrThrThrGluGlnLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Ds	1561	ACAACAACGGAAGAGTTACACGTTATCACCTCGTGAAGCCGCTCGGCACAGGACGG	1620
Qy	541	ValLeuHisTrrProGluSerGlyLysProGluAspValAenAsnAenGlnLeuArgTyrSer	560
Ds	1621	GTGTTCACCTGGGAGAGCGGTAAAGCAGAAAGATGTCAACAAATTAATCACTACGTTACAGC	1680
Qy	561	TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyIleLeuSer	580
Ds	1681	TACGATATCTGATCGCTCCAGCCAGCTTGAATCTGACAAACCAAGGACAAATATCAGC	1740
Qy	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrrAlaAlaAenSerGlnThrGlu	600
Ds	1741	GAGAAAGATTTATTCATTTGCGGGACAGCGCTGTGGGACGAAACAGCCAAACAGAA	1800
Qy	601	AlaSerTrrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Ds	1801	GCAGCTTATAAACAGATTCGCTATTCGGCAAAAGACGAGATGCCACCGGGTTGTATTAT	1860
Qy	621	TyrGlyTyrArgTyrTyrGlnProTrrAlaGlyArgTrrPheLeuSerAlaAspProAlaGly	640
Ds	1861	TACGTTATCGTTATACCAACCGTGGCGGGCAGATGGTTAAGCGCGGACCCCGCAGGA	1920
Qy	641	ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp	660
Ds	1921	ACCATTCGCTGGAATCTATACCGAAATGCTAAGAAATAATCTCTGTGAGTTTACAAGAT	1980
Qy	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu	680
Ds	1981	GAAATGAGTATAGCGCCAGAAAAGGAAATATACCAAGAGGTAAATTTCTTTGATGAA	2040
Qy	681	LeuLysPheLysLeuAlaLysSerSerHisValValLysTrrPheAenGluLysGluSer	700
Ds	2041	TTAAATTCAAATGGCAGCCAAAGTTTCACATGTTGTCAATGGAACGAGAGAGAGAGC	2100
Qy	701	SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720
Ds	2101	AGTTATACAAAAATAAATCATTTGAAAGTGGTTCTGTCGTGATTCGCGTCCGTCGCGGT	2160

```

Qy 721 TyrLeuLeuSerHisGluGluLeuLeuLeuGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2161 TATTGTGTAAGCCACGAGAGTTACTAAAAAGGTATAGAAAAAGTCAAAATCATATATAGC 2220

Qy 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
Db 2221 CGACTTGAAGAAACACGCTCCCTTCAGAAAAATCAAAAAAGAACTCTTCTTTAGGATCT 2280

Qy 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAAGAG 2340

Qy 781 HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAAATATAGAAATATCATCCCTGATTTTATTTCAGAAACCGATTTCTTTGGCTTAATG 2400

Qy 801 AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 2401 GATAAAAGTGAATAAAATGATTTATTCGGTGAAGAAAAATTTATGCGCAATGGAGGTT 2460

Qy 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 2461 AAGGTTTATCATGATTTAAAAATAAACATCAGAAATTAATCATGTCAACTATGCTGGCC 2520

Qy 841 HisProTyrThrGlnLeuSerAenGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 2521 CATCCCTATACGCAATTGAGTAATGAAGAAAGCGCTGTTCAGAAAGAACAGAACCCGCT 2580

Qy 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTTCAGAAATTCCTGACAAATGAAGCA 2640

Qy 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAenIle 900
Db 2641 ATTAAAAAATCATTTGAAGACATATAATTAATAGGATATCAACAGAGGCTATTAATTT 2700

Qy 901 ArgSerAlaIleAlaGluAenLeuGlyMetArgThrSer 915
Db 2701 CGCTCTCGCGCTATCGTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 2
US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCES: CC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 37948
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15171)..(18035)
; OTHER INFORMATION: orf5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23768)..(31336)
; OTHER INFORMATION: hph2
; FEATURE:

```

```

; NAME/KEY: CDS
; LOCATION: (31393)..(35838)
; OTHER INFORMATION: orf2
US-09-251-645-11

Alignment Scores:
Pred. No.: 2,696-244 Length: 37948
Score: 2501.50 Matches: 505
Percent Similarity: 74.33% Conservative: 103
Best Local Similarity: 61.74% Mismatches: 159
Query Match: 52.77% Indels: 51
DB: 3 Gaps: 13

US-10-647-956A-6 (1-915) x US-09-251-645-11 (1-37948)
Qy 1 MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAen 20
Db 15171 ATGAAAAACATCGATCCTAAACTTTATCAAAAGACCCCTGTGTCACACATCTACGATAAC 15230

Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp 40
Db 15231 CGAGGTCTAACGATCGTAACATCGACTTTCACCGTACCACCGCAACCGCGATACCGAT 15290

Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db 15291 ATCCGTTATTACTCGCCATCAATATGACTCCCTTGGGCACCTAAGCCAAAGCACCGATCCG 15350

Qy 61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80
Db 15351 CGTCTATATGAAGCCAAACAAAATCTAACTTCTCTGCAGTATGATTGACCGGTAAT 15410

Qy 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer 100
Db 15411 ATTTTGTGTACAGAAAGCGTCGATGCTGTCGCACTGTCCCTTGATGATATTGAAGGC 15470

Qy 101 ArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAspAen 120
Db 15471 CGTCCGCTACTGACAGTAACTGCAACAGGTGTATACAAACCCGACCAATATGAACGTCT 15530

Qy 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 139
Db 15531 TCCCTACCCGGTGTGTGTCTGTACCGAAACAAATACCA-----GAAAAACATCC 15584

Qy 140 -----ThrGluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyrAenLeu 157
Db 15585 CGTATCACCGAACGCTGATTTGGGCTGGCATAGCGAGCAGAGAGAAACCATATATCTT 15644

Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSer 177
Db 15645 GCCAGCCAGTGGCTGCCCACTATGACCGCGGAGTCCCGATTAGAGAGTTTGTCA 15704

Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAspAlaAap 197
Db 15705 CTGACCGGCTACTGTTTTATCTCAATCCAGCAACATATTGAGCGACACTCAAGAAAGTAGC 15764

Qy 198 TrpThrGlyGluAspGlnSerLeuTrpGlnLysLeuSerSerAspValTyrIleThr 217
Db 15765 TGGACAGGTGATAATGAACCGCTCTGGCAAAACATGCTGGCTGATGACATCTACACAACC 15824

Qy 218 GlnSerAenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIle 237
Db 15825 CTGAGCGCCTTTGTGTCACCGCGCTTTACTCTACAGCCGATGCGAAAGGGAACATT 15884

Qy 238 GlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLysGly 257
Db 15885 CAGAGGCTAACCTATGATGTGGCCGGCAGCTAAACGGGAGCTGGTTAACTTTAAAGAC 15944

Qy 258 GlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArg 277
Db 15945 CAACCGGAACAAGTATATCATGATTCCTTGACCTTTCGCCCGCGGACAAATAATACGC 16004

Qy 278 GluGluHisGlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeu 297

```


16005	GAGGAACACGGCAATCGTGTATTACCGGAATACAGTTATGAACCGGAAACCCAAACAGCTT	16064
298	IleGlyIleThrThrArgProSerAspAlaIysValLeuGlnAspLeuArgTyrGln	317
16065	ATCGGTACCAAAACCCACCGTCCGTCAAGATGCCAAAGTTGCAAGATCTACGTTATGAG	16124
318	TyrAspProValGlyAsnValIleAsnIleAraGsnAspAlaGluAlaThrArgPheTrp	337
16125	TATGACCCGGTAGGCAATGTCTACAGTATCCGTAAATGACGCAAGACCAACCGCTTCTGG	16184
338	ArgAsnGlnIysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIle	357
16185	CACAAATCAGAAAGTGGCGCGGAAACACTATACCTACGACTCCTCTGTATCAGCTTATC	16244
358	SerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerPro	377
16245	AGCGCAACCGGCGCGAGATGGCAATATATAGTCAAGCAAGATPAACCAACTTCCCTCCCTC	16304
378	AlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHis	397
16305	ACCCTACCTTCTGATAACAACACCTACACCAACTATACCGTACTTATATTATGACCGT	16364
398	SerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrVal	417
16365	GGCGGCAATTTGATATAAAATCAGCAAGTTCACCGCGCAGCAAAACAACCTACACCA	16424
418	AlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspPro	437
16425	AACATACCGTGTCTAACCGAGCAATCCGGCAGTACTCAGCACCTCTGACCGAAGATCCG	16484
438	AsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGln	457
16485	CGCAAGTAGATGCTTTATTTGATGCGCGGACATCAACAACACGCTTGATATCAGGACAA	16544
458	ThrLeuIleTrpThrProArgGlyGluLeuLysGlnVal-----AsnAsn	472
16545	AACTCGAAGTGGAAATACACGCGTGAACTACACAACATGTGACATTCGTGAAACGGGCAAG	16604
473	GlyProGlyAsn-----GluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLys	490
16605	GGCGCCNATGATCGGGNATCGTATCGCTATAGTAGTGCAGGGAAGGATATTAAAA	16664
491	ValSerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGly	510
16665	ATCAATGAACACGACGACCGACCAACTCTCAAAACACAGAGAATAACTTATTTGCCGAGC	16724
511	LeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThr	530
16725	TTAGAATTCGTCTAAACAAAAACAGCAGCATCACAAACCGAAGATTTGCAAGTTATCACA	16784
531	LeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGlu	550
16785	GTAGGAGAACGGGTCCGGCACAGGTACAGATATTACATTTGGGATAGCGGTCAACCGGAA	16844
551	AspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeu	570
16845	GATATCGACAAATATCAGCTACGTTATAGCTACGATAATCTTATCGGTTCCAGTCACTT	16904
571	GluLeuAspAsnGlnGlyIleIleSerGluGluGluTyrTyrProPheGlyGlyThr	590
16905	GAATTTAGACAGCAAAAGGAGAAATTAATAGTGAGGAAGAGTACTATCCTCTATGCGCGCAGC	16964
591	AlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrIysThrIleArgTyrSerGly	610
16965	GCAATATGGGCAACAAGGAAGCGCGACAGAACCCAGTTATAAAACCACTCCGTTATTTCAGGT	17024
611	LysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAla	630
17025	AAAGAGCGGGATGGCACCGCACTATATTATACGGTTACCGATATTATCAGGCTTGGGTA	17084
631	GlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet	650
17085	GGACGATGGTTAAGTGCCTATCCGACGGAACAGTAGATGGGTTGAATTTATCCGATG	17144

Qy	651	ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaPro-----	666
Db	17145	GTAAGGAATAATCCGGTTACTCTGCTTGAATCTGTGAATTAATGCCAAATTCAGAA	17204
Qy	667	-----GluLysGlyLysTyr-----ThrLysGlu	674
Db	17205	CGCATAGCAGCACTGCANAAAAATAAAGTAGCAGAGATTGACGCCTTCGCCAACAAATGCC	17264
Qy	675	ValAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLys	694
Db	17265	ACAAAGTAGCGATAAACATCGCGCGCGTAGCACCACAAACCTTACC--TTATCCCAA	17321
Qy	695	TrpAsnGluLysGluSerSerTyrThr-----LysAsnLysSerLeuLysValVal	711
Db	17322	GCATCAACGAGTAGCCAAATCAACTACATACCCCATCAAAATCTGCAGCACTAAACCAACG	17381
Qy	712	ArgValGlyAspSer-----AspProSerGlyTyrLeuLeuSerHisGlu	726
Db	17382	ACGTCGGGATCATCCATTACTGCTCCACTGAGTCCAGTAGGAATAAATCTACTCCTGAA	17441
Qy	727	GluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLeuGluGluAsnSer	746
Db	17442	ATATCTCTTCCA-----GAAAGCACTCAA-----AGC	17468
Qy	747	SerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMet	766
Db	17469	AATCTTCAAGCGCTATTTCACAAATCTACAGAAAAGTCA-----TTTACTTTATATAGA	17525
Qy	767	Ala-----ArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHisLys	782
Db	17526	GCGGATAATAGATCCCTTTCAAGACATGCAGAGATAAATCCCTGGAAGGATTAA	17579

RESULT 3

US-08-851-567B-60
; Sequence 60, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhapinda, Kitisri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow AgroSciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```
/ APPLICATION NUMBER: US 08/063,615
/ FILING DATE: 18-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/395,497
/ FILING DATE: 28-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/007,255
/ FILING DATE: 06-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/608,423
/ FILING DATE: 28-FEB-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/705,484
/ FILING DATE: 28-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.93804
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 60:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3132 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-851-567B-60

Alignment Scores:
Pred. No.: 1,61e-242 Length: 3132
Score: 2467.00 Matches: 470
Percent Similarity: 81.25% Conservative: 89
Best Local Similarity: 68.31% Mismatches: 111
Query Match: 52.05% Indels: 18
DB: 3 Gaps: 5

US-10-647-956A-6 (1-915) x US-08-851-567B-60 (1-3132)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
DB 1 ATGAGTCCGTCGAGACTACTCTTTTACTCAAAACCCCAACAGTCAGCGGTGTAGATAAT 60
QY 21 ArgLysLeuAsnValArgThrLeuArgTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
DB 61 CCGCGTCTGTCATTCGTATGTTGTTTCCACCGTATTGTAATCCGGGGGATACGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB 121 ACCCGCGTCACCGTCACCATGATGATGCCGTGGACACCTGAACCTACAGTATTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
DB 181 CGCTTGATGATCAAGCAGCGCTGATAACTCAGTAAGCCCTAAATTTGTCTGGCAGCAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
DB 241 GATCTGGCGGTGATCCCTGCGGACAGAGAGTGTGATGCTGCTGCTACTGTGTGATG 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
DB 301 AATGATATTGAAGGTGTTCCGGTAAATGACAAATGAATCGCACCCTGTTTCTGACACCCGT 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
DB 361 CGCTATGAAGCAACACCTTGCCCGTCGCTTCTTATCTGTGAGCGAGCAAGTTTCAAC 420
QY 134 GlnAlaGlyGluLysThrThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLys 153
DB 421 CAAGAGGTGCTAAAGTGACAGAGCCGTTTATCTGGGCTGGGAAATACACCTCGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
```

```
DB 481 GAGTATAACCTCTCCGGTCTGTGTATACGCCACTACGACACAGCGGAGTGACCCGGTTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
DB 541 ATGAGTCACTGTCGGGGCGCCATGCTATCCCAATCTCACCNAATGCTGGCGGAAGGG 600
QY 194 GlnAspAlaAspTTPThrGlyGluAspGlnSerLeuTTPGlnGlnLysLeuSerSerAsp 213
DB 601 CAGGAGGCTAACTGGAGCGGTGACGACGAACTGTCTGGCAGGAAATGCTGCGCAAGTAG 660
QY 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
DB 661 GTCTATACACACAAAGTACCCTAATGCTCGGGGCTTTACTGCCCAACCCGATGCG 720
QY 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTTPLeu 253
DB 721 AAAGGCNAATTTCAGCGTCTGGCTTATGACATTCGCGGTGAGTTAAAGGAGTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGly 273
DB 781 ACGGTGAAAGGCCAGAGTGAACAGGTGATTGTTAAGTCCCTGAGCTGTCAGCGCAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
DB 841 CATAAATTCCGTGAAGAGACCGGTAAACGCGGTGTTACGGAGTACAGTTATGAGCCGAA 900
QY 294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAspAlaLys 309
DB 901 ACTCAACGTCGTATAGTATACACCCCGCGGTGCCGAAGGGAGTCAATCAGAGGCCAGA 960
QY 310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
DB 961 GTATTGAGGATCTACGCTATAAGTATGATCGGTGGGAAATGTTATCAGTATCCATAAT 1020
QY 330 AspAlaGluAlaThrArgPheThrArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
DB 1021 GATGCCAAGCTACCCGCTTTTGGCGTAATCAGAAAGTGGAGCGCGAGAAATCCGCTATGT 1080
QY 350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
DB 1081 TATGATTCCTGTATCAGCTTATGATGTCGACGAGCGCGTGAATGCTAATATCGGTGAG 1140
QY 370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAsnAsnThrTyrThr 387
DB 1141 CAAAGCAACCAACTTCCCTCACCGTTATACCTGTTCTCTACTGACGACGACCTTATACC 1200
QY 388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
DB 1201 AATTACCTTCGTACCTTATCTTATGACCGTGGCGTAATTTGGTTCAAAATCCGACACAGT 1260
QY 408 SerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
DB 1261 TCACCCGCGCATCAAAATAGTTACACACAGATATCCCGTTTCAAGCGCAGTAACCGG 1320
QY 428 GlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
DB 1321 GCGGTATTGAGTACATTAAACGACAGATCAACCCCGAGTGGATGCGCTATTGATTCGGC 1380
QY 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467
DB 1381 GGTCTATCAGAAGATGTTAATACCGGGGCAAAATCTGGATTGGAAATATTCGGGGTGAATTG 1440
QY 468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTyrTyrAsgTyrAsp 482
DB 1441 CAACGAGTCAACCCGCTGAGCCGCGTGAATAGCAGTACAGTGAATGTTATCCGCTATAGC 1500
QY 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
DB 1501 AGTGATGGCATCGCGTCTAAAGTGAGTGAACACGACGACGCGGCAACAGTACTCAAGTA 1560
QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
```


736 GAATACGACGTGCACCAAGGGCAATCGCACGCCCGCAGCGCATCAAGGACGCCAGCGGC 795
Qy
160 GlnCysValArgHis-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
Db
796 AGCCTGGTGGCGCCAGCAGCAATGGCGCTACGACGAGCTTGGC-----CGCTGCTCCGTGGC 852
Qy
176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
Db
853 GTCCGCCCGCGGCCAGACACGCGAGTTGGCTACGAC-----CTCAACGACAAATCCG--- 906
Qy
196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
Db
907 -----GTCCGCGAAACCAACCCG-----CGCCAGTTGGCCACAGCGAGCGCTTC 951
Qy
216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
Db
952 -----GAGCGCTCGACCGGTGGTGGCCAGAGCGATCCCTCGGC 993
Qy
236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu-----Lys 249
Db
994 GGCAGACCGGACTCGGCTAGCAGCCCGCAGACAACTCACCGAGGTCAAGGACCCCGCGC 1053
Qy
250 GlySerTrpLeuThrLeuLys-----GlyGlnAlaGluGlnValIle 263
Db
1054 GGC-----GTCACCAACCGCTACGAATACGACGGCCTCGGCAACCTGACCGACTGGTC 1107
Qy
264 -----IleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
Db
1108 AGCCCGGACAGCGCACCCACCTTCGAGCAGACGCGCGGCAACGTCATCCGCGCGC 1167
Qy
279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db
1168 ACCGACCTCGGTGGTCCGTCACCGATTCGTCACGAC-----GCCCTCAATCGGCTG--- 1221
Qy
299 GlyIleThrThrArgArgProSerAspAlaLysVal----- 310
Db
1222 --GTCGAGCGCCGCTCGCCGAGCGACCCGAGCCTCGACGTACAGTACCGCTACGACCTC 1278
Qy
311 -----LeuGlnAsp 313
Db
1279 ACGCCGACGCAACCAAGGCGATCGCGCGCTGGCGGCCCATCGAAGTGGCCGCGACAGC 1338
Qy
314 LeuArgTyrGlnTyrAspProValGlyAsnValIle-----AsnIleArgAsn 329
Db
1339 CTGGTGTACCGCTACGACGAGCGCGCAACCTGTGTGAGCAGGTACGCGAGCATCCGCTC 1398
Qy
330 AspAlaGlu----- 332
Db
1399 GACGAGCAGACCTGCTCGACCGGTGACCTACCGCTACGACGCGGCGCAACCACTGTGT 1458
Qy
333 -----AlaThrArgPheTrpArgAsn----- 339
Db
1459 GAGATCGGCTACCCCTCGGCGCTCGCCATCGGCTACCGCGCAACGCGCGCGCCAGGTC 1518
Qy
339 ----- 339
Db
1519 GCCAGCTGACCCCTGGGCGCAAGGCGCGGAGCACCCCTGGTTGGCGCATCGCC 1578
Qy
340 -----GlnLysValAlaProGluAsnSerTyrThr----- 349
Db
1579 TACCTGCCCTTCGGCCCGCTGACGCGCTGACCTGGGGCAACGCGCATCTCTCAGCGCGC 1638
Qy
350 ---TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGly 368
Db
1639 GAGTACGACCAAGGATACCAACTGCTGCG-GCAGAAGGTGCGGCCCTGGCA----- 1688
Qy
369 GlnGlnAsnGlnLeuProSer----- 376
Db
1689 -----GAGCGACTACGACGATGCGCAATGGCAATATCCAGCAGCACCCCGCAG 1739
Qy
377 -----ProAlaLeuProSerAspAsnAsnThrTyr 386
Db
1740 CCTCTGGGGCACCCCTGGACTACGACTACGACCCGCTGACCGCGCTGACCGAGGAACGCGG 1799

Qy
387 -ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHis 406
Db
1800 CGTCCAGGCGCGCGCAGCTACGCCCTACGACGGGTGCGCAACCGCACCCAA---CGCAG 1856
Qy
406 sSerSerPro-----AlaThrGlnAsnAsnTyrThrValAlaIleThrLe 421
Db
1857 CGACAACCCCGCTCAGGCGGCGCACCGCCAGCAGCAGGACTACCACTACGTCGCG----- 1908
Qy
421 uSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAs 441
Db
1909 -----CCGACAGCAACCGA-----TTACCGCCATCGGCGCGCAAGCGGT 1949
Qy
441 pThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTr 461
Db
1950 GACC---AGCGACCGCGCGCAACCTCACCCAGGACCGCGCGCGCAACTGGGCTA 2006
Qy
461 pThrProArgGlyGluLeuLysGlnValAsn---AsnGlyProGlyAsnGluTrpTyrAr 480
Db
2007 CGACGCCAGGCGCGCTGCAAAAGCTGACGCTCGACGGCGCAGCAGGTCCGCAATACCG 2056
Qy
480 gTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrTh 500
Db
2067 CTACAAGCGCTCGCGCAGCGCATCTCAAGCTCAC---CCCGAGAGCATCACAC 2120
Qy
500 rGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAl 520
Db
2121 C-----TACTCTACGCTCCGAGCGCCAGTTG----- 2148
Qy
520 aThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly----- 535
Db
2149 -----CTCGCGAAGCGCAACACGACGCGCAGCGG 2177
Qy
536 -----ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysPro----- 549
Db
2178 CCGGAAATCGGAGCCCGACTACCTG-----TGGCTGGACAGCTGCCGCTGGCCAC 2231
Qy
550 -----GluAspValAsnAsnGlnLeuArgTyrSerTy 561
Db
2232 CATCGACGCGCATACGACGCCCGAGGCAAGGTGGCAACCCGACCTGTCTACTCTCCA 2291
Qy
561 rAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleSerG1 581
Db
2292 TGGCGACCACTCGACACCCCGCGCTTGGCTACCGACGCGCGCGCAGATCGCTGGCA 2351
Qy
581 uGluGluTyrTyrProPheGly---GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrG1 600
Db
2352 GTGGCAGTCCGACGCTTCGGCGCGCGGCAAGCGCTGAGCCAGGCGCAGCCCAAGGTC-- 2409
Qy
600 uAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla---ThrGlyLeuTy 619
Db
2410 -----AACCTGGCTTCCCGGGCAGTACTAGATCGGAGAGCGGCTGCA 2456
Qy
619 rTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAl 639
Db
2457 CTACAACCTACTCCGCGACTATGATCCGAGACTGCGCGGTATGTGGAGAGTATCGCAT 2516
Qy
639 aGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuG1 659
Db
2517 TGGACTAAGTGGGGAGTGAACACATACGATATGTACAGGAGGCCCCCTCAACCGTAT 2576
Qy
659 nAspGluAsnGlyLeuAla 665
Db
2577 TGATCCTTTAGTCTAGCA 2595

RESULT 6

US-09-252-991A-7069
; Sequence 7069, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7069
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7069

Alignment Scores:
Pred. No.: 7,66e-21 Length: 2925
Score: 307.00 Matches: 212
Percent Similarity: 33.22% Conservative: 91
Best Local Similarity: 23.25% Mismatches: 280
Query Match: 6.48% Indels: 331
DB: 3 Gaps: 43

US-10-647-956A-6 (1-915) x US-09-252-991A-7069 (1-2925)
QY 46 TyrGluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsn 65
DB 349 TACAGCTACAACCGCCCTCGGCTGATCAAGCGCGCGACGGTCCGGCGCACCGATGTGCAG 408
QY 66 -----GlnSerGlyProAsnPheIleArgValPheAsnLeuAla 78
DB 409 GAGCTCACCCCTATGCTTACGACAGTCGCGGCAACCTGACCAGGTGACCAACGCCCTC 468
QY 79 GlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIle 98
DB 469 GGCAGGTACCCGC-----CTCGCGGACTAT 495
QY 99 GluSerArg-----ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArg 116
DB 496 GACGAGCGGGCAAGCCCGGCGAGCATCACCGATGCCAACCGCGTCAACGACGACCTCGCC 555
QY 117 TyrGlu-----GlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
DB 556 TACACCGCGGCTGACGGCTGGCTGCTCGTCAGCACCGCGCGACACACCTCGGCGAAGCCTC 615
QY 119 AspAsnThrLeuProGlyArgLeuLeuAlaIleThr----- 130
DB 616 GACTATGACCGGTGCGGCAGATACCCCGGTCAACCGCGCGGCGGCGGCGAGTGGCTGAGC 675
QY 131 -----GlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
DB 676 TACGAATACGACGACGACGCGGCTGGTAGCGATCGGCAACACCTCGGCGAAGCCTC 735
QY 144 IleTrp-----AlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
DB 736 GAATACGACGTCGACACCAAGGCAATCGCACCGCGCGCATCAAGCAGCGCGCGGCG 795
QY 160 GlnCysValArgHis-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
DB 796 AGCTGTGTGGCGGACGAGCAATGGGCTACGAGAGCTTGGC---CGGCTGCTCGGTGCG 852
QY 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
DB 853 GTCGGCGCGCGCGGCGGACGACGACGCTTCGCTACGAC---CTCAACGACATCCG--- 906
QY 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
DB 907 -----GTGCGCGAACAACCGC-----CGGCAGTTCGCCACACGCGGCGCTC 951
QY 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
DB 952 -----GATGCCCTCGACCGGCTGTGCGGCGAGACGCGATCCCTCGGC 993
QY 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu-----Lys 249

```

```

994 GGCAAGACCGGCTCGCTACGACGCGCCAGGACAACTCAACGAGGTCAAGGACCCCGCG 1053
250 GlySerTrpLeuThrLeuLys-----GlyGlnAlaGluGlnValIle 263
1054 GGT-----GTCAACACCGCTACGAATACGACGCGCTCGGCAACCTGACCCGACTGGTC 1107
264 -----IleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
1108 AGCCCGGACAGCGGACACCACTTCGAGACGACGCGCGCGCAACGTCAACCGCGCG 1167
279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeu 298
1168 ACCGACGCTCGCGGTGCGGTACCGAGTATCGCTACGAC---GCCCTCAATCGGCTG--- 1221
299 GlyIleThrThrArgArgProSerAspAlaLysVal----- 310
1222 ---GTCGAGCGCGCTCGCGGAGGACCGGAGCTCGACGTACAGTACCGCTACGACCTC 1278
311 -----LeuGlnAsp 313
1279 ACGCGGACGCAACAAAGGCGATCGGCGCGCATCGATGGCGCTCGCGACAGC 1338
314 LeuArgTyrGlnTyrAspProValGlyAsnValIle-----AsnIleArgAsn 329
1339 CTGGTGATACCGCTACGACGCGCGCAACCTGGTCGACAGGTGCGCAGCATCCGCTC 1398
330 AspAlaGlu----- 332
1399 GACCAGACACCTGCTCGACCGGTGACCTACCGGTACGACGCGGCGCAACCACTGCTG 1458
333 -----AlaThrArgPheTrpArgAsnGln----- 340
1459 GAGATCGGCTACCCCTCGCGCTCGGCATCGGCTACCGCGCAACCGCGCGCGCAGGTC 1518
341 -----LysValAlaProGluAsn----- 346
1519 GCCAGCGTGACCTGCGAGTGGGCGACAGGCGCGCAGCACCCCTGTCGCGGAGATCGCC 1578
347 -----SerTyr 348
1579 TACCTGCCCTTGGCCCGCTGCTGCGCCTGACCTGGGGCAACGGCATCACTCTCAGCGCG 1638
349 ThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGly 368
1639 GAGTACGACGAGGACTACCACTGCTGCG- GCAGAAGGTGCGGCCCTTGSCA----- 1688
369 GlnGlnAsnAsnGlnLeuProSer----- 376
1689 -----GAGCGACTACGACGACGATGCCAATGGCAATATCCAGCAGCAGCGCCACAG 1739
377 -----ProAlaLeuProSerAspAsnAsnThrTyr 386
1740 CTTCTGGGACACCTCGATACAGTACGACCGCTGGACCGCTGACCGAGGAGCGCG 1799
387 -ThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgH1 406
1800 CGTCCAGGCGGGCGGAGCTATGCTTACGACGCGGTGCGCAACCGCACCCAA---CGCAG 1856
406 sSerSerPro-----AlaThrGlnAsnAsnTyrThrValAlaIleThrLe 421
1857 CGACAACCCCGCTCAGGCGGACCGCCAGCAGCAGCAGGACTACAGTACGCG----- 1908
421 userAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAs 441
1909 -----CCGACAGCAACCGA-----TTGACCGCATCGGCGCGCAACGGGT 1949
441 pThrLeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTr 461
1950 GACC---AGGACCGCGCGGCAACCTCACCAGGACCGCGCGCGCAACTGGCCTA 2006
461 pThrProArgGlyGluLeuLysGlnValAsn---AsnGlyProGlyAsnGluTrpTyrAr 480

```



```
Db 2007 CGACGCCAGCGCGCTCGAAGCGTCAGCGCCAGCGAGTCCGCAATACCG 2066
Qy 480 gTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrTh 500
Db 2067 CTAAACGCCCTCGCGCAGCGCATCGCAAGCTCAC-----CCGAGAGCGTCCACC 2120
Qy 500 rGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAl 520
Db 2121 C-----TACTCTATGGTCCGCGCGCCAGTTG----- 2148
Qy 520 aThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly----- 535
Db 2149 -----CTCGCGAAGCCGCAACACGACGCGCAGCGG 2177
Qy 536 -----ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysPro----- 549
Db 2178 CCGGAAACTCGGAGCCAGTACTACTG-----TGGCTGGACAGCGCTCGCGTGGCCAC 2231
Qy 550 -----GluAspValAsnAsnAsnGlnLeuArgTyrSerTy 561
Db 2232 CATCGACGCCGACTACAGCGCCAGGCGCAGGTCCGCAACCGACCTGTCTACTCTCCA 2291
Qy 561 rAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGl 581
Db 2292 TGGCGACCACTCGACACCCCGCGCTGGCCAGCGCGCAGCGCCAGATCGCTGGCA 2351
Qy 581 uGluGluTyrTrpProPheGly---GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGl 600
Db 2352 GTGCGACTCGGACGCTTCGCGCGCGCGAAGCGCTGAGCCAGCGGCGACCCAGGTC-- 2409
Qy 600 uAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla---ThrGlyLeuTy 619
Db 2410 -----AACCTGGCGCTTCGCCGGCGACTACTACATCGGAGAGCGGGCTGCG 2456
Qy 619 rTyrTyrGlyTyrArgTyrTrpGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAl 639
Db 2457 CTAAACTCTAAGAAAGCTCAACACCCCTGAAATGACATTTTAAATTCTGCGCAGAGCAT 2516
Qy 639 aGlyThrIleAspGlyLeuAsn----- 646
Db 2517 AGAAACTCTAAGAAAGCTCAACACCCCTGAAATGACATTTTAAATTCTGCGCAGAGCAT 2576
Qy 647 -----LeuTyrArgMetVa 651
Db 2577 GCTCAAGCCACTCCGATTGGGAACATGGATTTCACGCCGATCAATCACTACATACTC 2636
Qy 651 lArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLys-- 670
Db 2637 CGATAACATCCAACTGCNAAAGCGACAGCATGGTCTTTCACCAACCCCTACGGACAA 2696
Qy 671 -----TyrThrLysGluValAsnPheAspGluLeuLysPheLys----- 684
Db 2697 CTTGATCTACACCTGACACCACTGCATGATGATACATTAGATGCAAGAAAAAATTATC 2756
Qy 685 -----LeuAlaLysSerSerHisValVally 694
Db 2757 TGGAAATGGAAAGTCTTTCCTTGGGAGCTCTATGTAGCAAAAGCCAC-CACCCCGTCT 2815
Qy 694 sTrpAsnGluLysGluSerSerTyrThrLysAsn 705
Db 2816 TTGGGGAGTAGTATGCATAGCACATAGTAAT 2849

RESULT 7
US-09-252-991A-7234
; Sequence 7234, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

```
; PRIOR APPLICATION NUMBER: US 60/074,789
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7234
; LENGTH: 4881
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7234

Alignment Scores:
Pred. No.: 2,24e-18 Length: 4881
Score: 286.50 Matches: 178
Percent Similarity: 35.63% Conservative: 91
Best Local Similarity: 23.58% Mismatches: 239
Query Match: 6.04% Indels: 250
DB: 3 Gaps: 34

US-10-647-956A-6 (1-915) x US-09-252-991A-7234 (1-4881)

Qy 8 lLeAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAsnValArgThr 27
Db 2581 ATAGAAGAAGAGCTTCGCGACGTCAGCTG-----CGCGCTATCGCTACGACACA 2631
Qy 28 LeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGlu 47
Db 2632 CTGGGTAGACAGATACCGCCAGGACGAAAGCGGC-----CCCATCACCCGGTTCAA 2685
Qy 48 PheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSer 67
Db 2686 TGGGATGACGACGCGCGCTGAGCCAGATCACCTGCCCC-----GGT 2727
Qy 68 GlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuArgGlu-----Glu 85
Db 2728 GCGCGCCAGCGCATGTACCGCTACAAACGCTTACGCAAGGTCAACGCGAGTGGCGAGAA 2787
Qy 86 SerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu-----SerArgProVal 103
Db 2788 CAGGCGCGATGATCCCGCTACGAAATATCTTGACGACTGACACCTGTCAGCCGCGCGG-- 2844
Qy 104 LeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuPro 123
Db 2845 -----ATCAACCCGCGCGCAGTCAGCTGCGCTACCGCTACGAAAC----- 2886
Qy 124 GlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
Db 2887 GCGCGGCTACTGCTCAGCGAGATCGAGAACGAAACGCGCGCAACGC-----TATCGCCTC 2940
Qy 144 lLeTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCysValArg 163
Db 2941 GATTACACCGCAACCGCGCTGATCAGCAGAAACCGGCTTCGACGCGCGCGCACCGCC 3000
Qy 164 His-----TyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 182
Db 3001 TATCGCTACGACCTCAAGGC----- 3021
Qy 183 LeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGluAsp 202
Db 3022 -----CAGCTTCTGGAGAAAAACGAGTACGCGCAGCAGCGCGCAACTG 3066
Qy 203 GlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAsp 222
Db 3067 CGACCACTTACCGCGC----- 3087
Qy 223 AlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyr 242
Db 3088 AGTACCGGGCGCTGTCTGGCGAAGACACTCTCCCGCAGCGCAATCGGTCGACTACCGGTAC 3147
Qy 243 AspValAlaGlyGlnLeu-----LysGlySerTrp-----LeuThrLeuLysGly 257
Db 3148 GATACGCTCGAGCGCTGGTGGCGTGCAGCAGCGCACCTGGCGCTGGCTACGAAATAC 3207
```


Qy 84 GluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProVal 103
Db 2053 CATACTGATGCTCAGGCAACAACATATTGGTGTATGATGACGAGCGCGTGTGTT 2112
Qy 104 LeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAsnThrLeuPro 123
Db 2113 TCTCAAAACCAACGCGCTTGCAGGAAGCCACCGAGTACCAGTACGATGAG-----GTG 2163
Qy 124 GlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArgLeu 143
Db 2164 GSAACACCTCGCTCGCATATA-----TTGCCCGCATTAATCTACCGTGCAACTG 2211
Qy 144 IleTyr-----AlaGly-----AsnThrProGlnGlu 152
Db 2212 GCATGGAAATCCCGAGAGATTACTTACTCATCATCAACGCAATGACATACCCCATGTCAA 2271
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArg----- 163
Db 2272 TGGCAATACAAACGCGCTTGGTGGTGTCCACACAGAAATTGATAAATCTCGCTCGGCATATC 2331
Qy 164 -----HisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
Db 2332 CACTACCATTTACAATGCACAAGGT-----GCATTAATTTTCAATT 2370
Qy 182 ValLeuSerGlnSerGlnGlnLeuLeuLeuThrAspAsnGlnAspAlaAspTyrThrGlyGlu 201
Db 2371 GAAATCCCAATGGCGGGGTATCTCTC---AACCGTATGTC-----GAA 2415
Qy 202 AspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr 221
Db 2416 GATCGGTAGTGC-----GAAGAAATACGTCCTGATGAGCGCTACTCCAATACACCTAT 2469
Qy 222 AspAlaThrGlyAlaLeuLeuThrGln----- 233
Db 2470 AACCTCGCTGGACACTGGTTGAAGAAAGCTCACTTAGCGGACCGAGTCTTCACATCTGCA 2529
Qy 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 2530 CCAGCGCAATA---TTACTCGACTATGATCGCGGGTAACTTGTCAAACGTGAGACC 2586
Qy 249 -----LysGlySerTyr----- 252
Db 2587 TTAACGTATCGCTATCAATATGATGATAGTATGAACCGCTATTGGTCGCGCAGCAA 2646
Qy 253 -----LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSer 266
Db 2647 CAACCTAATCAACGTGGTCTTTGAATGGGTTTGAAGCGAATCAAGTC-----CAC 2697
Qy 267 LeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlnHisGlyAsnGlyIleValThr 286
Db 2698 TTTACCTACGTACGTGGCGGATTTATTCGTGACAAACAGCGGAGGATATCGTC--- 2754
Qy 287 GluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSer 306
Db 2755 GAAATTAATATGAT---GAACTCAATAACCTAAGCGCTCTGACGTTACCTCAAGGT--- 2808
Qy 307 AspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsn 326
Db 2809 -----GACAGCGCTCAACTGGCTCTATTATGGCTCTGGGCATGCCACGGCT 2853
Qy 327 IleArgAsnAspAlaGluAlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsn 346
Db 2854 ATCAACCACTTGTGTATAGT-----CGTCTCATGTTAAAT--- 2892
Qy 347 SerTyrThrTyrAspSerLeuThrGlnLeuIleSerAlaThr----- 360
Db 2893 GAAATTTGAACGTGACGACCTACACCGTGAATCAGTCGAACCTCAAGGAGAGACTCACCCAA 2952
Qy 361 -----GlyArgGluMetAlaIleGlyGlnGlnAsnGln 373
Db 2953 TATCGGCAATACGATAAATCGGGCGAACCATTAGCACTTTTCAGCTCGCGTGAAGCAA 3012
Qy 374 LeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyr 393

Db 3013 CATCCATTAATGCTATT-----ACTTTATGCGCTAAGTGG 3048
Qy 394 SerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsn 413
Db 3049 TTTTATGATCCCCAAGGTAACTCTGCGCCATGGAAGAC-----ACCTATCGA 3096
Qy 414 AsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeu 433
Db 3097 GGTGGGTAGATACTGTATGACTCAGAGCAACGTTTAAAAAAGTCGCGACAGTGAA 3156
Qy 434 ThrThrAspPro-----AsnGlnValAspThrLeuPheAspAlaGlyGlyHis 449
Db 3157 AACCTCGATGCTATGCTGTTTTACGATCGCGGATAAATCTACTCGAAACCCCAATCC 3216
Qy 450 GlnThrSerLeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGlu---LeuLys 468
Db 3217 GAAATGGATGCTGAACACTCCCTACTTTAGAACTAAGTCCCAAGGGGATAAGTACGT 3276
Qy 469 GlnValAsnAsnGlyProGlyAsnGluTyr---TyrArgTyrAspSerAsnGly----- 485
Db 3277 CAATTTCAAGGC-----TGGCACTATCAGTATGATGCCTATGTTAATGTT 3321
Qy 486 ---MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArg 504
Db 3322 ATTGCTCGCGGTTACCCTAACCAATCATCAAAACCTATGCTTATGATGGTGAATACTGT 3381
Qy 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGlu 524
Db 3382 CTGGTTATCGCTCATTAATCAAGCATATAAAGCTCAATACACACTACGATGCCCTAGGCCGT 3441
Qy 525 GluLeuHis---ValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 3442 CGTATTCACAAACCGTTGAAACCCGAGAAAGTGGCAAGTTAAACGACAAAGACCAT 3501
Qy 544 -----TrpGluSerGlyLys-----ProGluAspValAsnAsnAsnGlnLeuArg 558
Db 3502 TTTATTTGGCAAGGGCTACGGTTACTGCAAGAGCAGCATATCAACACCGGTAAACACCAA 3561
Qy 559 ---TyrSerTyrAspAsnLeu----- 564
Db 3562 ACTTATTTGCTACGAAGAGACGCGCATATACCCCTCTTGCCCGTTATCGTGAACAAATCC 3621
Qy 565 -----IleGlySerSerGlnLeuGluLeuAsp 573
Db 3622 AGCGTTTTCATTATTACTGGCACCCTGTGATATTAAACAGCGCCCTTGAAGTACC 3681
Qy 574 Asn---GlnGlyGlnIleIleSerGluGluTyrTyrProPheGly----- 588
Db 3682 AATGCACAAGCAATACGATATGCTCAGGGAAATATGAACGCTTTGGCTTTGTTCCGAGT 3741
Qy 589 ---GlyThrAlaLeuTyrAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIle 606
Db 3742 AGCCCTCTGAGTTTATTCAGTCCCTGAACGCTGTGATGGCTCTTTGAGCAAAATCTA 3801
Qy 607 ArgTyrSerGlyLysGluArgAsp---AlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
Db 3802 CGCTATGCCGACAAATATTTTGCAATGAACCGGATACATTTTATACCTTTAGATTC 3861
Qy 626 TyrGlnProTyrAlaGlyArgTyrProLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 3862 TAGACCCACAGATAGCCCGTTTTATCATCGCTGACCAATTTGGATTATTTGGGTGGGATT 3921
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 3922 AATCTGTATCAATATGCG---CCGAATCCGTTGGGATGGATTGATCCGTGGGGTTGTCA 3978
Qy 666 ProGluLys 668
Db 3979 TCTCAGGAA 3987
RESULT 9
US-09-492-709A-180

```
; Sequence 180, Application US/09492709A
; Patent No. 6720139
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Twawick, John
; APPLICANT: Forevth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA.001A
; CURRENT APPLICATION NUMBER: US/09/492,709A
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 4281
; TYPE: DNA
; ORGANISM: E. Coli
US-09-492-709A-180

Alignment Scores:
Pred. No.: 3,91e-17 Length: 4281
Score: 273.50 Matches: 220
Percent Similarity: 30.66% Conservative: 136
Best Local Similarity: 18.95% Mismatches: 352
Query Match: 5.77% Indels: 453
DB: 3 Gaps: 52

US-10-647-956A-6 (1-915) x US-09-492-709A-180 (1-4281)
Qy 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 1141 AGTACCGCTATCTTTATGAGCAG-----GACCGATACCGTACCAGACG----- 1188
Qy 23 LeuAsnValArgThrLeuGluTyrLeuArgThrGlnAla----- 35
Db 1189 CTGAACCGCGGT-----GAGGTGCTGCATACAGAGGCGGGCGCGGCGGTAACACGGGTG 1242
Qy 36 -----AspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIleProGlyPhe 53
Db 1243 GTGAAAAAAGAACTGGCGGAGCGGCGGTACGCGCAGCGCGGTATGACGCGGCGAGGAAG 1302
Qy 54 GlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArg 73
Db 1303 CTCACGGCGCAGACGGCGCGCGGCGGAGGAGGACAGGTACCGTCTGAATGTGGTG--- 1359
Qy 74 ValPheAsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIle 93
Db 1360 -----TCCGGCGATATACCGGACATCACACACCGGACCGGCGGCGGAGACGAAA 1407
Qy 94 ThrLeuAsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGln 113
Db 1408 TTTTACTATAACGACGGAACCACTGACGCGGTGTGTCTCCCGGACGCGGTGAGAGC 1467
Qy 114 AsnHisArgTyrGluAspAsnThrLeuProGlyArgGluLeuAlaIleThrGluGlnVal 133
Db 1468 CGCGGGGAAATATGATGAA-----CCGGGCGAGGCTG-----GTATCGGAGACATCG 1512
Qy 134 GlnAlaGlyGluLys----- 138
Db 1513 CGCAGCGGGAGACAGTACCTACCGCTACGATGACGCGGACAGTACGATGATACCGGCGAGC 1572
Qy 139 -----ThrThrGluArgLeuIleTrpAla----- 146
Db 1573 ACAACGATGCGAGCGGACGACCGCGGACATACCTGGAGCGGCTACGCGGCGGTGCTG 1632
Qy 147 -----GlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
Db 1633 GCCTTACCAGCTGCTCGGGCTACGACCGGTTATGAATACGACCGCTTCGCGCCAGATG 1692
```

```
Qy 162 Val-----ArgHisTyrAspThrAlaGlyLeu 170
Db 1693 ACGCGGTCCACCGCGAGGAAGCATACGCTTTTACCGCGCTATGACAAACCGTGGC--- 1749
Qy 171 ThrGlnLeuAsnSerLeuSerLeuAla----- 179
Db 1750 ---CGGTTAACCTCGGTGAAGACGACAGGCGCGTGAACCGCGGTATGATACACACGCC 1806
Qy 179 ----- 179
Db 1807 GCAGGCGACTGACTCGCTATATCACCCCGGACGCAACCGGAGCGAGACACAGTACGAT 1866
Qy 180 -----GlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAspAlaAsp 197
Db 1867 GCGTGGGAAAGCGGTGACACACGACGAGGCGGCGCTGACGCGCATGTGGAGTACGAT 1926
Qy 198 TtpThrGlyGluAspGlnSerLeuTtpGlnGlnLysLeuSerAspValTyrIleThr 217
Db 1927 GCTGCCGAGCGTGTATCATCGCTGACCAACGAGACGCGGCGCTTTC----- 1980
Qy 218 GlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIle 237
Db 1981 -----AGTTACGATCGCTGACCGCTGTTACAGCAGCGGCGCTTTCGCGCGGACG 2034
Qy 238 GlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySer----- 251
Db 2035 CACCGTTATATTATGACCTGACCGGAAACTCACACAGATGAGGATGAGGACTTGTGTC 2094
Qy 251 ----- 251
Db 2095 ATCCTCTGTACTACGATGAATCGGACCGTATCATCTACCGCAGCGGTGAACGCGGAACCG 2154
Qy 252 -----TtpLeuThr----- 254
Db 2155 GCAGAGCAGTGGCAGTATGATGCCACCGCTGCTGACAGACATACGCCACCTGAGCGAA 2214
Qy 255 -----LeuLysGlyGlnAla 259
Db 2215 GGCCACCGTGTTCGCTCCACTATGCTATGACGATAAAGCGCGCTGACCGCGAATGC 2274
Qy 260 GluGlnVal----- 262
Db 2275 CACACGCTGGAGAACCCGAGAGCGGGGAACTCTCTGTGGCAGCATGAGACAAACACGCA 2334
Qy 262 ----- 262
Db 2335 TACAACGACGAGGGGTGGCAACCCGCTCACGCGGACAGCCTGCGCGGTGGAGTGG 2394
Qy 262 ----- 262
Db 2395 CTGACGTATGGCAGCGTTACCTGGCGGAATGAAGCTGGCGGAGCGCGCTGGTTCGAG 2454
Qy 263 -----IleLysSerLeu----- 267
Db 2455 TATACCGGAGACAGGTGACCGCTGAGACGCTGGCAGCTTCGCGCAGCATGGCAGGAGT 2514
Qy 268 -----ThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
Db 2515 AATGCCGCATACGAACTGACCGACACATACACCCCGGAGGCCAG---TTACAGAGCCAG 2571
Qy 280 HisGlyAsnGlyIleVal----- 285
Db 2572 CACCTGAACACCGCTGTATATGACTACCGGTGGAGTGAGTGAACACGCGACCTGGTG 2631
Qy 286 -----ThrGluTyrSerTyrGluProGluThrGlnArgLeu 297
Db 2632 CGCATCAGCGCGCGGACGACGCGGGAATACGGCTACAGC---GCCACGGCAGGCTG 2688
Qy 298 IleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGln 317
Db 2689 GAGAGTGTGGCACCCCTCGCACACGAC-----CTGGACATCCGCATCCCG 2733
```

```
Qy 318 Tyr-----AspProValGlyAsnValIle-----AsnIleArgAsnAspAlaGlu 332
Db 2734 TATGCCACGACCGCGGGGACACCGCTCCGGACCGGAGCTGCACCGCGACAGTACA 2793
Qy 333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
Db 2794 CTCACA---GTGTGGCGGATACCGCATCCGGAGGATCGCATATGTCTAC----- 2844
Qy 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
Db 2845 -----CGCCACGATGAATACCGCAGGCTGCAGGAGACGAGACGCGAC 2883
Qy 373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
Db 2884 CGATCCCGGGGGTGTATACCGACGAGCAGCAGCGG-----ACCCACCAC 2931
Qy 393 TyrSerTyrAspHisSerGlyAsnLeu-----ThrGlnIleArgHisSerPro 409
Db 2932 TACCACCTACGACGACCGACCGCTGTGTCTTCTACACGGGATACAGCATGGCGGACCA 2991
Qy 410 AlaThrGlnAsnAsnTyr-----ThrValAlaIleThrLeuSerAsnArgSer--- 415
Db 2992 CTGCTCAGAGCGGCTACTCTACACCCGCTGGACCGCGAATGGCAAAACGGGTCTGG 3051
Qy 416 -----ThrValAlaIleThrLeuSerAsnArgSer----- 425
Db 3052 CGCGCGGAGCGTGACCTGACGGGTGTATGCTGTGCGGTAAACCGGAGGTGACGTGG 3111
Qy 426 -----AsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThr 442
Db 3112 TATGGCTGGGACGAGCAGACGCTGACGACGGTGCAGACTGACACACACGATATCCAGACG 3171
Qy 443 LeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrpThr 462
Db 3172 GTATACGAGCGGGAAGCTTC---ACGCGCTCATCCGGGTGCGAGACA----- 3216
Qy 463 ProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyrAsp 482
Db 3216 ----- 3216
Qy 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db 3217 GAGAACCGCGAGCGGAA---AAGCGCAGCGCGGCGAGCTGGCAGAGACGCTCCAGACG 3273
Qy 503 Gln-----ArgValIleTyrLeuProGlyLeuGluLeuLeuArgThrThrGln 517
Db 3274 GAAGGAGTGAGAACCGCCACGCGCTGTGTTCCTCCGCTGAACCTGGTGGCGCTCTCGAC 3333
Qy 518 SerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAla 537
Db 3334 -----AGGCTGGAGGAAGAAATCCGGGCAGACCGCGTGACGAGTGAAGCCGGCG 3384
Qy 538 GlnValArgValLeuHisTrp-----GluSerGlyLysProGluAspValAsnAsn 555
Db 3385 -----TGCTTCGCGAGCGCGGCTGACGGTGAGCAACTGGCCAGA 3426
Qy 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
Db 3427 CAGGTGGAGCGGAATACACACCGCGCGAAGACTCATCTTTATCATCTGCGACCCCGG 3486
Qy 576 Gly-----GlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeu 592
Db 3487 GGACTCGCGTGGCGCTTATCAGCGAAGAC-----GGCAATACGGCG 3528
Qy 593 TrpAlaAla-----AsnSerGlnThrGluAlaSer----- 602
Db 3529 TGGACCGCGGAATATGATGAATGGGCAACACGCTTAATGAGGAGAACCCGCATCATGTG 3588
Qy 603 TyrLysThrIleArgTyrSerGlyLysGluArgAsp---AlaThrGlyLeuTyrTyr 621
Db 3589 TATCAGCGGTACCGTCTGCCAGGGCAGCATGATGAGGAATCAGGCGCTGCTACTAAC 3648
Qy 622 GlyTyrArgTyrTyrGlnProTrpAlaGlyTrpLeuSerAlaAspProAlaGlyThr 641
```

```
Db 3649 CGTCACCGGTACTACGATCCGTTGAGGGCGGTATATTACTCAGACCCGATGGGTTG 3708
Qy 642 IleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGlu 661
Db 3709 AAAGGGGATGGAATTTATATCAGTATCCTTTA---AATCCACTACAACAATTCACCT 3765
Qy 662 AsnGlyLeu----- 664
Db 3766 ATGGGATTTATGCGACACTTGGGATGATGCCAGATCTGGAGCATGTACGGGGGAGTTGT 3825
Qy 665 -----AlaProGluLysGlyLysTyrThrLysGluValAsnPhe 677
Db 3826 GGTGTTCTTTTACGTATAATAGGACCAAGTAAATTTGATAGTACTCGAGATGCT---GCG 3882
Qy 678 PheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAsnGlu 697
Db 3883 TTAGATGCTTTGAAA----- 3897
Qy 698 LysGluSerSerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAsp 717
Db 3898 -----GAAACGCGAGATAGATCTCTA-----TGTAAATGATATGGAA 3933
Qy 718 ProSerGlyTyrLeuSerHisGluGluLeuLysGlyLysGlyLysSerGlnIle 737
Db 3934 TACTCTGTTATTGCTCTGTAAGATACTAATGGAAAAATATTTTGCATCTTAAGCGAGAACT 3993
Qy 738 IleTyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSer 757
Db 3994 GATAATTTAAGA---AAGGAGTCATATCTCTGAAAAAGAAATGTCCACAGGTACAGAT 4050
Qy 758 LeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyr 777
Db 4051 AGAGTTGCTGCTTATCATCTACGCTGCAGATGATGATGCGCATTTGTTGATGATTT 4110
Qy 778 -----AlaGluGluHisLysTyrArgSer-----AsnHisProAspPheTyr 791
Db 4111 TTTTCAAGTAGCGATAAAATCTTGTAAAGAAATAAATAATCTTGAAGCATTTTAT 4170
Qy 792 SerGluThrAsp-----PhePheAlaLeuMetAspLysSerGlu----- 804
Db 4171 CTGCGAACACCTGATGCGACGATTTGAGCGCTTAATAATAAGGAGAAATATATTTTATC 4230
Qy 805 LysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHis 824
Db 4231 AGAAATAGTCTCCGGATGAGTTGATTCAGTATGATACCG-----TATCAT 4275
Qy 825 Asp 825
Db 4276 GAT 4278
```

RESULT 10

```
US-09-453-702B-11
; Sequence 11, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
```

	OPERATING SYSTEM:	PC-DOS/MS-DOS	
	SOFTWARE:	Word Perfect 8.0	
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER:	US/09/453,702B	
	FILING DATE:	03-Dec-1999	
	CLASSIFICATION:	<Unknown>	
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:	60/110,955	
	FILING DATE:	04-DEC-1998	
	ATTORNEY/AGENT INFORMATION:		
	NAME:	Seay, Nicholas J.	
	REGISTRATION NUMBER:	27386	
	REFERENCE/DOCKET NUMBER:	960296.95017	
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE:	(608) 251-5000	
	TELEFAX:	(608) 251-9166	
	INFORMATION FOR SEQ ID NO: 11:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	31960	
	TYPE:	nucleic acid	
	STRANDEDNESS:	double	
	TOPOLOGY:	linear	
	MOLECULE TYPE:	DNA (genomic)	
	SEQUENCE DESCRIPTION:	SEQ ID NO: 11:	
	US-09-453-702B-11		
	Alignment Scores:		
	Pred. No.: 1..57e-14 Length: 31960		
	Score: 262.00 Matches: 184		
	Percent Similarity: 29.83% Conservative: 97		
	Best Local Similarity: 19.53% Mismatches: 287		
	Query Match: 5.53% Indels: 374		
	DB: Gaps: 41		
	US-10-647-956A-6 (1-915) x US-09-453-702B-11 (1-31960)		
Qy	23	LeuAsnValArgThrLeuGluTyrLeu-----ArgThrGlnAla	35
Db	26734	CTGAACCGGGAGGTGCTGTACACGAGGCGGGTGCGCTGAACGCTGTGTGAAG	26793
Qy	36	AspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnVal	55
Db	26794	AAGAAATCATCGCAGCCGGAGCATCACCCGCAGGAGTAGATGATGAGCGGGAGGCGTTGAAG	26853
Qy	56	LysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	26854	GCACACGGATCGCGGGGACGGCGGACGGAGTCACG-----CTG	26895
Qy	76	AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu	95
Db	26896	CATATCGTCGGTTCGGTGACAGCGGTGACAGCGGCGCGGCGGAGCGGTGCCGTAT	26955
Qy	96	AsnAspIleGluSerArgProValLeuIleIleAsn---AlaThrGlyValArgGlnAsn	114
Db	26956	GGCTATAACAGCCAGCGCGAGGTGACTGAGTCAGTACCAGCGGGGCTGCGCAGCAGC	27015
Qy	115	HisArgTyrGluAspAsnThrLeuProGlyArgGluLeuAlaIleThrGluGln----	132
Db	27016	CGSGAGTATGATAGAAG-----GGNAGGCTGGCGCGGAGNACCTCGCGCAGCGGA	27066
Qy	133	-----ValGlnAla	135
Db	27067	GAGACGACGGGTACAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	27126
Qy	136	GlyGluLysThrThrGluArgLeuIleTrpAlaGly-----	147
Db	27127	GCGACGGCGAGTAACAACAGATGGCATGGAGCCGTTACGGTCAAGCTGCTGCTTTACG	27186
Qy	148	-----AsnThrProGlnGluLysAsp-	154
Db	27187	GACTGTCGGGTACACGACGGGTATGATGATGATGATGATGATGATGATGATGATGATGAT	27246
Qy	155	-----TyrAsnLeuAlaGlyGlnCysValArg	163

Db 28303 GAACTGCACCGGACAGCACCTCACGGCA---TGGCCGGATAACCCGATCGCGAAGAT 28359
Qy 346 AsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAla 365
Db 28360 GCGCACTATGTCTAC-----CGCTACGAT-----GAATACGGC 28392
Qy 366 AsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuProSerAspAsnAsnThr 385
Db 28393 AGCGTGGCGGAGAGACGGACCGGATCCCGAAGGGGTATC-----CGGATG 28440
Qy 386 TyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeu-----Thr 402
Db 28441 CACGACGAGCGCACCCACCACTACTACACAGCCAGCACCGCTGGTGTCCACACG 28500
Qy 403 GlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSer 422
Db 28501 CGGATACAGCAGCGCAACCAAGTGGAGAGCGGTAC----- 28539
Qy 423 AsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThr 442
Db 28539 ----- 28539
Qy 443 LeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTyrThr 462
Db 28540 CTCTATCACCGCTGGCGCGCGACGGGA-----AAACGGGTGTGGCG 28584
Qy 463 ProArgGlyGluLeu-----LysGlnValAsnAsnGlyProGlyAsnGluTyrTyr 479
Db 28585 CGGAGCGTCACTTCAGCGGGTGGATGCTGCTGCGGTAAACCGGAGGACCTGTATC 28644
Qy 480 ArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThr 499
Db 28645 GGGTGGACGGTGACAGCTG-----ACCACGTGTACG 28677
Qy 500 ThrGlnGlnGlnArgVal-----IleTyrLeuProGly----- 510
Db 28678 ACCCAACAGACAGAAATCCAGACGGTATACCGCCGGAGCTTCACGCCGCTCCTGAGA 28737
Qy 511 -----LeuGluLeuArg 514
Db 28738 ATCGAAACAGAGAAATGGTGAACAGCGGAAGCGCGCACCGTACCGTGGCGAGGTGTG 28797
Qy 515 ThrThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGly----- 532
Db 28798 CAGGAGACACGGGTGTGACCTACCGCGGAGCTGGCGGTGATG---CTGGGAGAGCTG 28854
Qy 533 -----GluAlaGlyArgAlaGlnValArgValLeuHisTyr-----GluSer 546
Db 28855 GAGCGGAGCTGCGCGAGGCGAGCTGAGTGAAGAAAGCCAGCAGCTGCTGCGCAGTGC 28914
Qy 547 GlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGly 566
Db 28915 GGGCTGACGGCGGAGCAGATGCCCGCAGCTGGAGCGGAATAC-----ATCCCG 28965
Qy 567 SerSerGlnLeuGluLeu-----AspAsnGlnGly-----GlnIleIleSer 580
Db 28966 GAGAGAAACTTCATCTTTACCATCGACACCGCGGAGCTGCCGCTGGCGCTCATCAGC 29025
Qy 581 GluGlu-----GluTyrTyrProPheGlyThrAlaLeuTyr 593
Db 29026 CCGGAAGGGGAAACCGCGTGGCAGGGGAGTATGACGAGTGGGGAACCTGCTG----- 29079
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyr-----LysThrIleArgTyrSerGlyLys 611
Db 29080 -----GGCGAAACCGCGCGCAGCACCTTCAACACAGTCACTCCGCTCCCGGGGCGAG 29130
Qy 612 GluArgAsp-----AlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTyrAla 630
Db 29131 CAGTATGATGAGGAGTCCGGGCTGTATCTACACCGCAACCGGTACTATGATCCGTTGCAG 29190
Qy 631 GlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet 650
Db 29191 GGGAGATATATACCCAGGACCCGATAGGGCTGGAGGGGGGATGGAACCTGTATCAGTAC 29250

Qy 651 ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGlyLysGlyLys 670
Db 29251 CCATCTC---AATCTATTGAACATATAGATCCGTTGGGGTTAGCACTTGATTGAATTAT 29307
Qy 671 TyrThr 672
Db 29308 TATTCT 29313

RESULT 11

US-10-114-170-11
; Sequence 11, Application US/10114170
; Patent No. 6855814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6855814e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31960
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-114-170-11

Alignment Scores:
Pred. No.: 1.57e-14 Length: 31960
Score: 262.00 Matches: 184
Percent Similarity: 29.83% Conservative: 97
Best Local Similarity: 19.53% Mismatches: 287
Query Match: 5.53% Indels: 374
DB: 3 Gaps: 41

US-10-647-956A-6 (1-915) x US-10-114-170-11 (1-31960)

Qy 23 LeuAsnValArgThrLeuGluTyrLeu-----ArgThrGlnAla 35
Db 26734 CTGAACCGCGGGAGGTGTGTACGCAAGAGCGGCGCTGGAACGCTGTGTGAAG 26793

Db 28738 ATCGAAACAGAGAATGCTGAACAGCGGAGCGCGCACCGTAGCTGCGGAGGTGTG 28797
Qy 515 ThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGly----- 532
Db 28798 CAGGAGCACCGGTGTGACGCTTACC GCGGAGCTGCGGTGATG---CTGGGAAGCGTG 28854
Qy 533 -----GluAlaGlyArgAlaGlnValArgValLeuHisTrp-----GluSer 546
Db 28855 GAGCGGAGCTGCGGAGCGGAGCGGTGAGTGAAGAAAGCAGCAGTGGCTGGCGCATGC 28914
Qy 547 GlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGly 566
Db 28915 GGGCTGACGGGAGCAGATGGCGCGCAGCTGGAGCGGAATAC-----ATCCCG 28965
Qy 567 SerSerGlnLeuGluLeu-----AspAsnGlnGly-----GlnIleIleSer 580
Db 28966 GAGAGGAACCTTCATCTTACCATTGCGACCCAGCGGAGCTGCGGCTGCATCAGC 29025
Qy 581 GluGlu-----GluTyrTyrProPheGlyGlyThrAlaLeuTrp 593
Db 29026 CCGGAAGGGGAAACCGGCTGGCAGGGGAGTATGACAGTGGGGAACCTGCTG----- 29079
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyr-----LysThrIleArgTyrSerGlyLys 611
Db 29080 -----GGCGAAACACGCGCGCAGCACCTTCAACAGTCACTCCGCTGCGCGGCGAG 29130
Qy 612 GluArgAsp---AlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAla 630
Db 29131 CAGTATGATGAGGAGTGGGGCTGTACTACAAACCGCAACCGGTACTATGATCCGTTGCAG 29190
Qy 631 GlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMet 650
Db 29191 GGGAGATATATCACCCAGGACCCGATAGGGCTGAGGGGGGATGGAACCTGTATCAGTAC 29250
Qy 651 ValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLys 670
Db 29251 CCACTC---AATCCTATTGAACATATAGATCCGTTGGGTTAGCACTTGATTTGAATTAT 29307
Qy 671 TyrThr 672
Db 29308 TATTCT 29313

RESULT 12

US-09-453-702B-226
; Sequence 226, Application US/09453702B
; Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 5519
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-702B-226

Alignment Scores:
Pred. No.: 3.7e-15 Length: 5519
Score: 256.00 Matches: 191
Percent Similarity: 33.98% Conservative: 126
Best Local Similarity: 20.47% Mismatches: 347
Query Match: 5.40% Indels: 270
DB: 3 Gaps: 45

US-10-647-956A-6 (1-915) x US-09-453-702B-226 (1-5519)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1809 CTGAGTCAGTACCGC---GCATACGACAGCGCGTGGACAGTAAATTCGCGTGAAGAC--- 1862
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 1863 -----ACGCGGGCCATGAA----- 1877
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 1878 -----ACGCGGTATGAATACAAACGCGCGGTGACCTGACACCGCTCATTTGCCCG 1928
Qy 61 ArgLysAsnLysAsn----- 66
Db 1929 GACGCGAGCAGAAACCGGACACAGTACGATCGGTGGGAAAAAGCCATCTGTACACGCGAG 1988
Qy 67 SerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuArgGluLys 86
Db 1989 GCGCGTCTGACGCGCAGTATGGAAATACGATGCTGCCGCGCGGTATCCGCTGACACAGT 2048
Qy 87 ValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProValLeuIle 106
Db 2049 GAAAACGCGCACACACCACTTCCTGTTACGATGTACTCGACCGG-----CTGATA 2099
Qy 107 AsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArgLeu 126
Db 2100 CAGGAAACCGGCTTTGACGCGCGCACACAGCGTTATCACACGACCTGACCGCGCAACTT 2159
Qy 127 LeuAlaIleThrGluGln-----ValGlnAlaGlyGluLysThr 139
Db 2160 ATCCGAGCGAGGATGAGGGGCTGGTCAACCACTGGCACTATGACGAAGCAGACCGGCTC 2219
Qy 140 ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
Db 2220 ACGACCGCACCGCTG---AAGGGTGAACCGCAGAGCGCTGGCAGTATGACGAACGCGGC 2276
Qy 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
Db 2277 -----TGGCTGCACACATCATGCCATATCATCGCAAGGG 2309
Qy 180 GlyValVal-----LeuSerGlnSerGlnGlnLeuLeuThrAspAsnGln 194
Db 2310 CACGGGTGACGCTGCATTTACGGGTATGATGAGAAAGGCGGCTGACCGGTGACGCTCAG 2369
Qy 195 AspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspVal 214
Db 195 AspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspVal 214

Db 2370 ACGGTGCATCACCGCAGACGGAGCAGCTCTCTGGCAGCATGAG----- 2414
Qy 215 TyrIleThrGlnSerAsnThrAspAlaThrGly---AlaLeuLeuThrGlnThrAspAla 233
Db 2415 -----ACCAGACAGCTTACAAACGGCAGCGAGGGCTGGCGAACCGCTGTATACCGGACAGC 2468
Qy 234 LysGlyAsnIleGlnArgLeuAlaTyrAsp-----ValAlaGlyGlnLeuLysGly 250
Db 2469 CTCCCGCGCGTGAATGGCTGACCTATGGCAGCGGCTGGCTGGCAGCGCATGAAGCTCGGC 2528
Qy 251 SerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeu----- 267
Db 2529 GACACACCGCTGTGGATTTCACCGCGGACCGGCTGCACCGGAAACGCTGCCAGATTC 2588
Qy 268 -----ThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Db 2589 GCGCGTTATGAATCTACACCGCTTATACCCCTGCGGGCAG--TTACAGAGCCAGCAC 2645
Qy 281 GlyAsnGlyIle----- 284
Db 2646 CTGAACAGCCTGCAGTATGACCGGATTCACCTGGAAACGACACCGCGAACTCATCCGC 2705
Qy 285 -----ValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db 2706 ATCAGACGCCCGCCAGACCCCGAGTTACAGCTACAGC---GACTCCGGCAGCGTAC 2762
Qy 299 GlyIle---ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGln 317
Db 2763 GCGGTTACACACCCAGCGCATCTGGATATCCGATC-----CCGTATGCC 2810
Qy 318 TyrAspProValGlyAsnValIle-----AsnIleArgAsnAspAlaGluAlaThr 334
Db 2811 ACGGACCCCGCAGTAACCCCTGCGCGACCGGAGCTGCACCGGACAGCACCCCTCAGC 2870
Qy 335 ArgPheTrpArgGlnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyr 354
Db 2871 ---ATGTGGCGGATACCGCTATCGCCGTCGCGGACCGCAGCTATCTTTAC----- 2915
Qy 355 GlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeu 374
Db 2916 ---CGGTATGACCGTCACGGCAGG-----CTGACAGAGAAACCGACTCATC 2960
Qy 375 ProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSer 394
Db 2961 CCGGAAGGGGTTATCCGACCGATGATGAGCGG-----ACTCACCGGTACCAT 3008
Qy 395 TyrAspHisSerGlyAsnLeu-----ThrGlnIleArgHisSerSerProAlaThr 411
Db 3009 TAGCAGCTCAGCAGCGCGCTGGTGCACTACACCGGACACAATATGAAGAGCCGCTGGTC 3068
Qy 412 GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSer 431
Db 3069 GAAAGCGCTAT----- 3080
Qy 432 ThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyHisGlnThr 451
Db 3081 -----CTTTACGACCGCTGGCGCCGAGGGTG 3107
Qy 452 SerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeu-----Lys 468
Db 3108 GCA-----AAACGGGTGGCGAGCGTGAACCGGACCTGACGGGCTGGATG 3152
Qy 469 GlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGln 488
Db 3153 TCCTGTACGGAACCGCAAGTGACCTGTAGCGGTGGGACCGCGGACCGGCTGACCACA 3212
Qy 489 LeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeu 508
Db 3213 ATA-----CAGAAGCAGAGAACCCGCATCCAGACGATTTATCAG 3251
Qy 509 ProGly-----LeuGluLeuArgThrThrGlnSerAsnAlaThrThrThr 523
Db 3252 CCGGGGAGCTTCACGCGCACTCATCAGGGTTGAACCGGCCACCGCTGAGCTGGCGAAACG 3311

RESULT 13

US-10-114-170-226

; Sequence 226, Application US/10114170

; Patent No. 6855814

Qy 524 GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 3312 CAGCGCCGC-----AGCCTGGCGGATCGCT-TCAGCAGCTCGGCGCGAAGACGG 3361
Qy 544 TrpGluSerGlyLysProGluAspValAsnAsnGlnLeu-ArgTyr-SerTyrAspAs 563
Db 3362 TGCAGATGGTGGTTCCCGCGGTGTGTGTGCAGATGCTCGACCGGCTGGAAAGTGAAT 3421
Qy 563 nLeuIleGly----- 566
Db 3422 CTGGCTGACCGGTGAGTGAGGAAAGCCCGCTGGTGGCATCTGGCGGCTGACTGT 3481
Qy 567 -----SerSerGlnLeuGlu----- 571
Db 3482 GCGCAGATGCAAGAGCAGATGAGACCGCGGTATACACCGCGCGGCGGAAAAATCCACCTGTA 3541
Qy 572 ----LeuAspAsnGlnGly-----GlnIleIleSerGluGluGluTyrTyrProPh 587
Db 3542 CCACCTCGGACCATCGGCGGCTCGCGCTGGCCCTTATCAGTAAGGAA----- 3587
Qy 587 eGlyGlyThrAlaLeuTrpAlaAla-----AsnSerGlnThrGluAl 601
Db 3588 ----GGGGCAACAGATGTCGCGCAGATACGATGAGTGGGCAACCTGCTGAATGAAGA 3643
Qy 601 aSer-----TyrLysThrIleArgTyrSerGlyLysGluArgAsp---AlaTh 616
Db 3644 GAACCGCATCAGCTGACGAGCTTATCGCCCTGCGCGGCGCAGCATGATGAGGATC 3703
Qy 616 rGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAl 636
Db 3704 CGCCCTGTATTACAACCGCCAGCGCTATTATGACCGCTGCAGGGGAGGTATATCATCTCA 3763
Qy 636 aAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProVa 656
Db 3764 GATCCGATGGCTGAGGGGGGAGGCTGTATATACATATATATATATATATATATATAT 3820
Qy 656 lSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAs 676
Db 3821 GAATGCGATGGATCCATTAGGATTATATGAATTTAAATCAAAAAATATAGATGATATGG 3880
Qy 676 nPhePhe-----AspGluLeuLysPh 683
Db 3881 AATATTTCATGGCGCAATGTAAATGGAGAAATCAATTAACGAGAAATAAAGAATATGGTGG 3940
Qy 683 eLysLeuAlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrTh 703
Db 3941 ACTAATATGAAGACCAAGGTGAATATTTCCTCCATGAATCCGATTAAGTTCAATGATAA 4000
Qy 703 rLysAsnLysSerLeuLysValVal-----ArgValGlyAspSe 716
Db 4001 TGATAGTGTAGACTTCGGAATATATAAATGCTCGTGAAGGTTTCAGAGAGAGTAGCGGATTA 4060
Qy 716 rAspProSerGlyTyrLeuLeuSerHisGluGluLeuLeuLysGly-----IleGluL 734
Db 4061 TCACACTACCGGTTTTTACTCTCAGCAT-----AAAGAAATAAAGTAACAAA 4108
Qy 734 sSerGlnIleIleTyrSerArgLeuGluGlnAsnSerSerLeuSerGluLysSerLysTh 754
Db 4109 AGAAATGATGTTTATGATAGTCTA-----AATTTTCAAGCAAGATTAAAC 4156
Qy 754 rAsnLeuSerLeuGly-----SerGluIleSerGlyTyrMetAlaArgThrI 770
Db 4157 GAATCTTATATGAATGGAATGGAAAAAAGAAATGCAAGTAGTACTTGGGA---ACACC 4213
Qy 770 eGlnAspThrIleSerGluTyrAlaGluGluHisLys 782
Db 4214 AAATAACACCTATCTAAAAATATAATATCCCAAGCTAAA 4250


```
Db 2961 CCGAAGGGGTTATCCGCCAGGATGATGACGG-----ACTCACCGGTACCAT 3008
Qy 395 TyAspHisSerGlyAsnLeu-----ThrGlnLeuArgHisSerProAlaThr 411
Db 3009 TACGACAGTCAGCAGCGGTGGTGCATACACCGGACACATATGAAGCGCGTGGTC 3068
Qy 412 GlnAsnAsnTyrThrValAlaLeuThrLeuSerAsnArgSerAsnArgGlyValLeuSer 431
Db 3069 GAAAGCGGCTAT----- 3080
Qy 432 ThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThr 451
Db 3081 -----CTTTACAGCCGCTGGCGCCGACGGTG 3107
Qy 452 SerLeuLeuProGlyGlnThrLeuLeuLeuThrProArgGlyGluLeu-----Lys 468
Db 3108 GCA-----AAACCGGTGGCGAGTGAACCGGACCTGACGGCTGGATG 3152
Qy 469 GlnValAsnAsnGlyProGlyAsnGluTyrArgTyrAspSerAsnGlyMetArgGln 488
Db 3153 TCGCTGTACGGAACCGCAAGTGACCTGTACGGCTGGGACGCGACCGCTGACCACA 3212
Qy 489 LeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgValLeuLeu 508
Db 3213 ATA-----CAGAACGACAGAACCGGCTCCAGACGATTTATCAG 3251
Qy 509 ProGly-----LeuGluLeuArgThrThrGlnSerAsnAlaThrThrThr 523
Db 3252 CCGGGAGCTTACGCCACCTCATCAGGTTGAAACCGCCACCGGTGAGTGGCGAAACG 3311
Qy 524 GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis 543
Db 3312 CAGCGCGC-----AGCTGGCGGATGGCT-TCACGACGTCCGGCGCGAAGACGG 3361
Qy 544 TrpGluSerGlyLysProGluAspValAsnAsnGlnLeu-ArgTyrSerTyrAspAs 563
Db 3362 TGGCAGTGTGTGTTCGCCCGGTGCTGTGTGTCAGATCTCGACCGGCTGGAAGTGAAT 3421
Qy 563 nLeuIleGly----- 566
Db 3422 CTTGGCTGACCGGTGATGAGGAACCGCGCTGCTGGCATCTGTGGCGCTGACTGT 3481
Qy 567 -----SerSerGlnLeuGlu----- 571
Db 3482 GCGCAGATCAAAAGCCAGATGACCCGGTATACACCGCGCGGAAATCCACCTGTA 3541
Qy 572 -----LeuAspAsnGlnGly-----GlnIleLeuSerGluGluGluTyrTyrProPh 587
Db 3542 CCACTGCGACCATCGCGGCTTATCCGCTGGCCCTTATCAGTAAGGAA----- 3587
Qy 587 eGlyGlyThrAlaLeuTrpAlaLeu-----AsnSerGlnThrGluAl 601
Db 3588 -----GGGGCAACAGATGGTGGCGAGAAATACGATGAGTGGGCAACCTGCTGAATGAAGA 3643
Qy 601 aSer-----TyrLysThrIleArgTyrSerGlyLysGluArgAsp---AlaThr 616
Db 3644 GAACCCGCATCAGTCGACGAGCTTATCCGCTCGCGGCGGACGAGTATGATGAGGATC 3703
Qy 616 rGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyrAlaGlyArgTrpLeuSerAl 636
Db 3704 CGGCGCTGATTACAAACCGCACCGCTATTATGACCCGCTGCGAGGGAGGTATATCACTCA 3763
Qy 636 aAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProVa 656
Db 3764 GSATCCGATTGGGCTGAAGGGGGATGGAACCTGTATACATATCCGCTG---AGCCCGGT 3820
Qy 656 lSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAs 676
Db 3821 GAATGGCATGATCCATTAGGATTATATGAATTTAAATCAAAAATATAGATGATATGG 3880
Qy 676 nPhePhe-----AspGluLeuLysPh 683
Db 3881 AATATTTGCATTGGCAATGTGTAATGGAGAATCAATTAACGAGAATAAAGAATATGTTGG 3940
```

```
Qy 683 eLysLeuAlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrTh 703
Db 3941 ACTAATATGTAGAAGCAAGGTGAATATTTCCCATGAATCCGATTAAGTTCAATGATAA 4000
Qy 703 rLysAsnLysSerLeuLysValVal-----ArgValGlyAspSe 716
Db 4001 TGATAGTGTAGACTTTCGGAATATATAAATGCCCTGAAGGTTACAGAGAGATGCGCGATTA 4060
Qy 716 rAspProSerGlyTyrLeuLeuSerHisGluGluLeuLeuLysGly-----lIeGluLys 734
Db 4061 TCACACTCAGGTTTTTACTCTGACGAT-----AAAGGAATAAAGTAACAAA 4108
Qy 734 sSerGlnIleIleTyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysTh 754
Db 4109 AGAAATGATGTTTATGATAGTCTA-----AATTTTCAAGCAAGATTAAAC 4156
Qy 754 rAsnLeuSerLeuGly-----SerGluIleSerGlyTyrMetAlaArgThrIl 770
Db 4157 GAATTCCTTATGTAATGGAATGGAAAAAAGAAATGCAGTAGTACTTGGGA---ACACC 4213
Qy 770 eGlnAspThrIleSerGluTyrAlaGluGluHisLys 782
Db 4214 AATAACACTATCTATAATATATATCCCAAGCTAAA 4250
RESULT 14
US-09-711-164-296
; Sequence 296, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERUTY
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4134)
US-09-711-164-296
Alignment Scores:
Pred. No.: 3 3e-15 Length: 4134
Score: 254.50 Matches: 167
Percent Similarity: 34.68% Conservative: 107
Best Local Similarity: 21.14% Mismatches: 279
Query Match: 5.37% Indels: 237
DB: 3 Gaps: 41
US-10-647-956A-6 (1-915) x US-09-711-164-296 (1-4134)
Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1705 CTGAGTCAGTACCGC---GCATACGACAGCGCGTGGACAGTTAATTCGCGTGAAGAC--- 1758
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 1759 -----ACGCAGGGCCCATGAA----- 1773
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 1774 -----ACGCGGTATGAATACATACATCGCCGCTGACCTGACCGCCGCTCATTCGCCCG 1824
Qy 61 ArgLysAsnLysAsn-----Gln 66
```


		: : : : :	
Db	1825	GACGGCAGCAGAAACGGGCACACACTACGATGCTGTGGGAAAGGCCGTCCTCCGTACCACCGCAG	1884
Qy	67	SerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeuValLeuArgGluGlusSer	86
Db	1885	GCGCGGCTAACCGCACGATATGAATAATCATGCTCCGGACGGGTCACTCCGCTGACCCAGT	1944
Qy	87	ValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProValLeuIleIle	106
Db	1945	GAATAACGGCAGCCACACACCTTCCTCGTTACGATGCTTGACCG-----CTGATA	1995
Qy	107	AsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArgLeu	126
Db	1996	CAGGAACCGCGCTTTGACGGCGGCACACAGCGTTATCACCAACGCTGACCGGCAAACTT	2055
Qy	127	LeuAlaIleThrGluGln-----ValGlnAlaGlyGluLysThr	139
Db	2056	ATCCGACGAGGATGAGGGTCTCGTCACCCACTGGCACTATGACGAAGCAGACCGGCTC	2115
Qy	140	ThrGluArgLeuIleTTPAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly	159
Db	2116	ACGCACGCGACCGTG---AAGGTTGAAAACCGCAGCGGTGGCAGTATGACCAACGTTGC	2172
Qy	160	GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuAla	179
Db	2173	-----TGCGTCAGACATCATGCCATATCATCGCAAAGG	2205
Qy	180	GlyValVal-----LeuSerGlnSerGlnLeuLeuThrAspAsnGln	194
Db	2206	CACCGGTGGCGTGTCATTACAGGTATGATGAGAAGCCGCGCTGACCGGTGACGTCAG	2265
Qy	195	AspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspVal	214
Db	2266	ACGTTGCATCACCCGCGCAGCAGGAGCACTGCTCTGGCAGCATGAG-----	2310
Qy	215	TyrIleThrGlnSerAsnThrAspAlaThrGly---AlaLeuLeuThrGlnThrAspAla	233
Db	2311	-----ACCAGACATGCGTACAACGCGCAGCGGGCTGGCGAAACCGCTGTATACCGACAGC	2364
Qy	234	LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeu	253
Db	2365	CTGCCCCCGTGGAA TGCTACCTACCTACCGC---AGCGGTTACCTGGCAGCGCATGAAACT	2421
Qy	254	-----ThrLeuLys---	256
Db	2422	GGCGACACACCGCTGGAGTACACCCGCGACCGCTGACCCGGGAAACGCTGCGCAGC	2481
Qy	257	---GlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys	275
Db	2482	TTCCGCGCTTATGAA-----CTCACCAACCGCTTATACCTCCCTGCGCGGCGAG---	2526
Qy	276	LeuArgGluGluHisGlyAsnGlyIleValThrGlu-----	287
Db	2527	TTACAGAGCCAGCACCTGAACAGCCTGCTGCTACCCGCGATTACACTGGGAACGACAAC	2586
Qy	288	-----TyrSerTyrGluProGlu	293
Db	2587	GGCGAACTCATCCGATCAGCAGCCCGCGCCAGACCCGGAGTTACAGCTACAGC---ACC	2643
Qy	294	ThrGlnArgLeuIleGlyIle---ThrThrArgArgProSerAspAlaValLeuGln	312
Db	2644	ACCGCAGGCTGACCGCGGTTACACCAACCGCAGCGAATCTGGATATCCGCACTC-----	2697
Qy	313	AspLeuArgTyrGlnTyrAspProValGlyAsnValIle-----AsnIleArgAsn	329
Db	2698	-----CGGTATGCCACAGACCCCGCAGGTAAACCGCTGCCCAGCCCGAGCTGCACCCG	2751
Qy	330	AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThr	349
Db	2752	GACAGCACCTTCAGC---ATGTGCCGATTAACGTATGCGCCCGTAGCCGCACTATCTT	2808
Qy	350	TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln	369
		: : : : :	

RESULT 15

US-09-453-702B-42/c
; Sequence 42, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Perna, Valerie
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11613
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Alignment Scores:

Pred. No.:	2,25e-14	Length:	11613
Score:	253.50	Matches:	156
Percent Similarity:	35.73%	Conservative:	102
Best Local Similarity:	21.61%	Mismatches:	261
Query Match:	5.35%	Indels:	203
DB:	3	Gaps:	36

US-10-647-956A-6 (1-915) x US-09-453-702B-42 (1-11613)

QY	102	ProValLeuIleleAenAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr	121
DB	5843	CCGGTGGCGGAAACGGACGGTGAAGCCACCGCTGGCAGTACCGCTACGATAAGACACG	5784
QY	122	LeuProGlyArgLeuLeuAlaIleThrGluGlnValGln---AlaGlyGluLysThrThr	140
DB	5783	-----CTGCNACTGACAGAGTCAITTAACCCGAGCGCGAGTCTTATCTT	5739
QY	141	GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln	160
DB	5738	TATATTGACAACTGTGGCCGGGTGACGGAAGACGTGACTGGGGC---GGCGTGGTC	5682
QY	161	CysValArgHisTyrAspThrAlaGlyLeu-----ThrGlnLeuAsnSerLeuSer---	177

DB	5681	TGTCGTTACCGTTATGACGCTGATGCCCTGTGTATCCGCCAGGGTCAACGGCCTGGAGAA	5622
QY	178	-----LeuAlaGlyValValLeuSerGlnSer	186
DB	5621	ACCATCTCTACAGCGCGGATCCGCGAGCCGCTGGCAGAAGTCACTACCGGAAGGC	5562
QY	187	GlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrp	206
DB	5561	AAA-----	5559
QY	207	GlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAla	226
DB	5558	-----AGCAGTATCGGTATGACAAATCCGGCAGG	5529
QY	227	LeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGly	246
DB	5528	CTGACGGGTATCTTCAGCCCGCAGCATACAGCGCACCGGCTATGATGAACGCGG	5469
QY	247	GlnLeuLys-----	249
DB	5468	CGGTGAATGTCAACACTCAGGCGCGACGGGCCATTGAATACACTACCCCGACGAACAC	5409
QY	250	-----GlySer	251
DB	5408	ACGTCATCCGCTGTATCTCTGCCACCGGAAGATGAACGCGACAGACACCCCGAGATCC	5349
QY	252	TrpLeu-----ThrLeuLysGlyGlnAlaGlnValIleIle---	264
DB	5348	CTGCTGAAACACACATACCGCTACACGCGCGGAGAACTGACGGAGGTATCTCTCGCG	5289
QY	265	-----LysSerLeuThrTyrSer-----AlaAlaGlyGlnLysLeuArgGluGluHis	280
DB	5288	GGGGATGACACGCTGACGCTTACGCGGTGATAGCGCGGACGTAAGTCTCCGCGCAGT	5229
QY	281	GlyAsnGlyIleValThrGluTyrSerTyr-----GluProGluThrGlnArg	296
DB	5228	AACCGGGTTTTCCTGTGTAACAGGCTGGATGACCGCGGTGAGCTGTACAGCCAGCGC	5169
QY	297	LeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeu-----	314
DB	5168	---GCCGACTTTTCCCGCGGAAGCACATGGGGGAGACTGCTCCTTCCTGCTACGG	5112
QY	315	ArgTyrGlnTyrAspProValGlyAsnValIleAenIleArgAsnAspAlaGluAlaThr	334
DB	5111	GAATACCGTTACGACAGCGCGGTAACTGATCAGCGGTCCAGCCCGCGGAAGATTACGGA	5052
QY	335	ArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyr	354
DB	5051	CGGGAACACACCGGGAG-----TAC	5031
QY	355	GlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeu	374
DB	5030	CGGCTT-----GACCGGAACGCCAGGTC	5007
QY	375	ProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSer	394
DB	5006	ACGGCGTGCACAGCCTCAGCCACCGGCTGGGTATGGGGAAGCGCACGACTTATGGC	4947
QY	395	TyrAspHisSerGlyAsnLeu-----ThrGlnIleArgHisSerProAlaThr	411
DB	4946	TATGACAGTGGCGCTACCTGAAGCGCAGTCTGCGGGCAGACACCGGATAACCGGAGAG	4887
QY	412	GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSer	431
DB	4886	ACTGACCATGATGCCGCGACGCCACCGGCTGAAACAGCGCCGGAAC-----	4842
QY	432	ThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGly-----	448
DB	4841	-----ACACAGTATGAC-----TATGACCGCCGACGCGCGGATGGTC	4806
QY	449	-----HisGlnThrSerLeuLeuPro---GlyGlnThrLeuIleTrpThrPro	463
DB	4805	AGCCGCACAAAACACCGCTACCGCTACCGCCCAAAACAGAGCGGTTCGCGTGGGACAGC	4746

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: December 14, 2005, 20:15:22 ; Search time 1433 Seconds
(without alignments)
5280.168 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKTPSIKVLON.....EAINRSAAIAENLGMRTS 915

Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlp
-Q=/cgn2_1/USPTO.spool.p/US10647956/runat_12122005_091821_29767/app_query.fasta_1.1095
-DB=Published Applications_NA_Main -QEXT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=biosum62 -TRANS=human4.0.cdi -LIST=45 -DOCALIGN=200 -THR SCORES=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1 1549 @runat_12122005_091821_29767 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4740	100.0	2745	US-09-817-514A-5	Sequence 5, Appl
2	4686	98.9	2748	US-10-609-113-45	Sequence 45, Appl
3	2960	62.4	2817	US-10-609-113-48	Sequence 48, Appl
4	2956	62.4	2817	US-10-706-424-15	Sequence 15, Appl
5	2956	62.4	2817	US-10-754-115-57	Sequence 57, Appl
6	2537.5	53.5	2883	US-10-706-424-11	Sequence 11, Appl
7	2537.5	53.5	2883	US-10-609-113-46	Sequence 46, Appl

8	2537.5	53.5	2883	8	US-10-754-115-46	Sequence 46, Appl
9	2512	53.0	2850	7	US-10-706-424-13	Sequence 13, Appl
10	2512	53.0	2850	7	US-10-609-113-47	Sequence 47, Appl
11	2467	52.0	3132	7	US-10-262-794A-60	Sequence 60, Appl
12	2467	52.0	3132	7	US-10-609-113-44	Sequence 44, Appl
13	2467	52.0	3132	8	US-10-754-115-25	Sequence 25, Appl
14	2187.5	46.1	2889	8	US-10-754-115-50	Sequence 50, Appl
15	2187.5	46.1	2889	10	US-11-020-848-9	Sequence 3, Appl
16	2187.5	46.1	2947	8	US-10-754-115-53	Sequence 53, Appl
17	2187.5	46.1	2947	10	US-11-020-848-8	Sequence 8, Appl
18	2187.5	46.1	7508	10	US-10-754-115-54	Sequence 54, Appl
19	2187.5	46.1	7508	10	US-11-020-848-9	Sequence 9, Appl
20	2168	45.7	3048	8	US-10-753-901-15	Sequence 15, Appl
21	2168	45.7	3048	7	US-10-754-115-21	Sequence 21, Appl
22	2168	45.7	3051	7	US-10-609-113-21	Sequence 15, Appl
C 23	2168	45.7	39005	8	US-10-753-901-6	Sequence 6, Appl
C 24	2168	45.7	39005	8	US-10-754-115-6	Sequence 6, Appl
25	2025.5	42.7	38258	6	US-10-365-319-1	Sequence 1, Appl
26	1558.5	32.9	2793	7	US-10-609-113-12	Sequence 12, Appl
27	1558.5	32.9	2793	8	US-10-754-115-41	Sequence 41, Appl
28	1558.5	32.9	2862	8	US-10-754-115-55	Sequence 55, Appl
29	1558.5	32.9	33521	7	US-10-609-113-1	Sequence 1, Appl
30	1219	25.7	2823	6	US-10-365-742-63	Sequence 63, Appl
31	643.5	13.6	858	7	US-10-609-113-40	Sequence 40, Appl
32	366.5	7.7	7092	6	US-10-156-761-284	Sequence 284, App
C 33	366.5	7.7	9025608	6	US-10-156-761-1	Sequence 1, Appl
34	339	7.2	2802	7	US-10-282-122A-8433	Sequence 8433, Ap
35	309	6.5	3957	6	US-10-369-493-34930	Sequence 34930, A
36	296.5	6.3	3750	6	US-10-156-761-22	Sequence 22, Appl
37	285	6.2	4539	7	US-10-282-122A-42202	Sequence 42202, A
38	291	6.1	2832	7	US-10-282-122A-11622	Sequence 11622, A
39	290	6.1	7158	6	US-10-156-761-201	Sequence 201, App
40	286	6.0	4716	7	US-10-282-122A-33231	Sequence 33231, A
41	281	5.9	4695	7	US-10-282-122A-8374	Sequence 8374, Ap
42	274	5.8	4095	7	US-10-282-122A-39125	Sequence 39125, A
43	273.5	5.8	4281	3	US-09-912-020-180	Sequence 180, App
44	273.5	5.8	4281	7	US-10-282-122A-6433	Sequence 6433, Ap
45	273.5	5.8	4281	8	US-10-771-241-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-09-817-514A-5
; Sequence 5, Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: ffrrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
; US-09-817-514A-5
Alignment Scores:
Pred. No.: 0
Score: 4740.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 2745
Matches: 915
Conservatives: 0
Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
US-10-647-956A-6 (1-915) x US-09-817-514A-5 (1-2745)			
Qy	1	MetSerSerTyrAenSerAlaileAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGAGCAGTTACAAATCTCGCAATTTGACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60
Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Db	61	AGGAAATTTAAATGATACGTACTTTAGAAATATCTAGCGCACTCAAGCTGACGAAAAACAGTCAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	GAATTAATATTCGTTCTATGAGTTCATATTTCCGGGATTTCAAGTAAAGACCCGATCCT	180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Db	181	CGTAAATAAACCAGAGCGGCCCAATTTCAATTCGTGCTTTAATCTTGCCGGTCAA	240
Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Db	241	GTTTTAGCTGAAGAAAGTGTGATCGCGGTCCGACTATTACCCCTCAATGATATTGAAAGT	300
Qy	101	ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHisArgTyrGluAspAsn	120
Db	301	CGCCCGGTGTGATCATCAATGCAACCCGGTGTCCGCCAAAACCATCGTTTGAAGAATAAC	360
Qy	121	ThrLeuProGlyArgLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr	140
Db	361	ACCCCTCCCGGTCTGCTCGCTATCACCGAAACAAGTACAGCGCAGGAGAAACCGACC	420
Qy	141	GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Db	421	GAACGCTTATCTGGCGCGCAATACGCCGCAAGAAAAAGATTACAACCTCGCCGGTCAG	480
Qy	161	CyeValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Db	481	TGTTGCCGCCAATACGATACCCGCGGACTTACTCAACTCAATAGCCITTTCTCGGTGGC	540
Qy	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAspAlaAspTrpThrGly	200
Db	541	GTCTGTCTATCACAACTCTCAACACTGCTTACCGATAACAGGATGCCGACTGGACAGGT	600
Qy	201	GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Db	601	GAAGACCAAGACCTCTGGCAACAAAACTGAGTAGTGATGTCTATATCACCCAAAGTAAAC	660
Qy	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGluArgLeu	240
Db	661	ACTGATGCCACGGGGCTTTACTGACCCAGACCGGATGCCAAAGGCCAACATTCAGCGGCTG	720
Qy	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db	721	GCCTATGATGTGGCGGGCAGCTAAAGGGAGTTGTTAAACACTCAAGGTCAGCGCGAA	780
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis	280
Db	781	CAGGTGATATCAAAATCGTAACCTACTCTCCGCGCGGCCAAAAATTAACGTGAAGAGCAC	840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	841	GGTAACGGGATGTCTCACTGAATACAGCTACGAACCGGAAACCCACGCGCTTATCGGCATT	900
Qy	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Db	901	ACCACTGCCCTCCATCAGACGCCAAGGTGTGCAAGACCTACGCTATCAATATGACCCA	960
Qy	321	ValGlyAenValIleAsnIleArgAenAspAlaGluAlaThrArgPheTrpArgAenGln	340
Db	961	GTAGGCAATGTCAATTAATATCCGTAAATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
Qy	341	LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Db	1021	AAAGTAGCCCCGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCCACC	1080
Qy	361	GlyArgGluMetAlaAenIleGlyGlnAenAenGlnLeuProSerProAlaLeuPro	380
Db	1081	GGCGCGAAATGGCCAAATATCGGTGACGAAAAACAACCACTTCCCTCCCTCGGCTACCT	1140
Qy	381	SerAspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAen	400
Db	1141	TCGACAAACAATACCTACACTACTATCTCGCAGCTACAGCTATGATACAGTGGTAAAT	1200
Qy	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAsnTyrThrValAlaIleThr	420
Db	1201	CTGACGCAAAATTCGGCACAGCTCGCCAGCTACCCAGACAACTACACCGTGGCTATCACC	1260
Qy	421	LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Db	1261	CTCTCAAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCCAGATCCAAATCAAGTG	1320
Qy	441	AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db	1321	GATACGTTGTTGATCCGGTGTCCACAAACCACTTATTACCCGACAGACACTTATC	1380
Qy	461	TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTrpArg	480
Db	1381	TGACACACACAGAGAGGTTAAAGCAGGTTAATAATGGCCCGGGAAATGATGGTACCGC	1440
Qy	481	TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Db	1441	TACGACAGCAACCGCATGAGCAACTGAAAGTGAAGTGAACAGCAACCCAGAAATCTACG	1500
Qy	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Db	1501	CAGCAACACCGGTAAATCTATTTGCCGGGACTGGAGCTACGCAACCCAGAGCAACGCC	1560
Qy	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db	1561	ACAAACACGGAAGTTTACACGTTATCACACTCGGTGAACCGGTCGCGCACAGGTACGG	1620
Qy	541	ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer	560
Db	1621	GTGTTGCACTGGGAGAGCGGTAAGCCAGAAAGATGTCAACAATAATCAACTACGTTACAGC	1680
Qy	561	TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer	580
Db	1681	TACGATTAATCTGATTCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATATCAGC	1740
Qy	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Db	1741	GAGGAAGATTTATTCATTTTGGCGGACAGCGCTGTGGGACCAACACAGCAACAGAA	1800
Qy	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Db	1801	GCCAGCTATAAAACGATTCGCTATTCGCGCAAGAACAGAGATGCCACCGGTTGTATTAT	1860
Qy	621	TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAenProAlaGly	640
Db	1861	TACGGTTATCGTTATTAACCAACCGTGGCGGGGAGATGGTTAAGCGCGGACCCCGCAGGA	1920
Qy	641	ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp	660
Db	1921	ACCAATTGATGGGTGAATCTATACCGAATGGTAAGAAATAATCTCTGTGAGTTTACAGAT	1980
Qy	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu	680
Db	1981	GMAAATGGAATAGCGCCAGAAAAAGGGAATATACCAAGAGAGGTAAATTTCTTTGATGAA	2040
Qy	681	LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Db	2041	TTAAATTTCAAAATTTGGCAGCCAAAAGTTTCACATGTTCTCAATGGAAACGAGAAAGAGC	2100
Qy	701	SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720

Db	2101	AGTTATACAAAAAATAAATCAITGAAGTGGTTTCGGTCCGGATTCCTCATTCGGGT	2160
Qy	721	TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer	740
Db	2161	TATTTGCTAAGCCACGAGGTTACTAAGAGGTATAGAAAAAGTCAATCATATATACG	2220
Qy	741	ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer	760
Db	2221	CGACTTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTAGGATCT	2280
Qy	761	GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu	780
Db	2281	GAAATATCCGGTTATATGGCAAGAACCATACAGATACCATATCAGAAATATGCCGAAGAG	2340
Qy	781	HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPheAlaLeuMet	800
Db	2341	CATAATATAGAAAGTAATCACCTGATTTTATTTCAGAAACCGATTTCTTCGGTTAATG	2400
Qy	801	AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal	820
Db	2401	GATAAAGTCAAAAAATGATTTATTCGGGTGAAGAAAAAATTTATCGCGCAATGCGAGTT	2460
Qy	821	LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAsnTyrAlaLeuAla	840
Db	2461	AAGGTTTATCATGATTTAAAAATAAACCAATCAGAAATTACATGTCAACTATGCATTGGCC	2520
Qy	841	HisProTyrThrGlnLeuSerAenGluGluArgAlaLeuLeuGlnGluThrGluProAla	860
Db	2521	CATCCCTATACCAATTTAGTAATGAAAGAGCGCTGTTGCAGAACACAGACCCGCT	2580
Qy	861	IleAlaIleAspArgGluTyrAenPheLysGlyValGlyPheLeuThrMetLysAla	880
Db	2581	ATTGCAATAGATAGACAATAAATTTCAAGGTGTTGGCAAAATTCCTGACAAATGAAAGCA	2640
Qy	881	IleLysLysSerLeuLysGlyHisLysIleAenArgIleSerThrGluAlaIleAenIle	900
Db	2641	ATTAAAAAATCATTTGAAGGACATAAAATTAATAGGATATCAACAGAGCTTAAATATT	2700
Qy	901	ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer	915
Db	2701	CGCTCTGGCGCTATCGCTGAGAAATTTAGGATGCGGAGAACTTCA	2745
RESULT 2			
US-10-609-113-45			
; Sequence 45, Application US/10609113			
; Publication No. US20040110184A1			
; GENERAL INFORMATION:			
; APPLICANT: Bintrim, Scott			
; APPLICANT: Bevan, Scott			
; APPLICANT: Zhu, Baolong			
; APPLICANT: Merlo, Donald J.			
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from			
; FILE OF INVENTION: Paenibacillus Species			
; FILE REFERENCE: DAS-101XC2			
; CURRENT APPLICATION NUMBER: US/10/609,113			
; CURRENT FILING DATE: 2003-06-27			
; PRIOR APPLICATION NUMBER: US 60/392,633			
; PRIOR FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: US 60/441,647			
; PRIOR FILING DATE: 2003-01-21			
; NUMBER OF SEQ ID NOS: 49			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 45			
; LENGTH: 2748			
; TYPE: DNA			
; ORGANISM: Photorhabdus strain W14			
US-10-609-113-45			

Alignment Scores: Pred. No.: 0 Length: 2748 Score: 4686.00 Matches: 902 Percent Similarity: 99.23% Conservative: 6

Best Local Similarity: 98.58%		Mismatches: 7
Query Match: 98.86%		Indels: 0
DB:		Gaps: 0
US-10-647-956A-6 (1-915) x US-10-609-113-45 (1-2748)		
Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAapAen 20
Db	1	ATGAGCAGTTCACAATTCGCAATTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC 60
Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp 40
Db	61	AGGAATTAATTAATGTAGTACTTTAGANATATCTACGCACCTCAAGCTGACGNAACAGTGAT 120
Qy	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db	121	GAATTAATTAATGTTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAAGCACCGATCCT 180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80
Db	181	CGTAAAAATAAAACCAGAGCGGCCCAAAATTCATTCGTGCTCTTTAATCTTCGCGGTCAA 240
Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer 100
Db	241	GTITTTACGTGAAGAAGTGTTCGCGGTGCGACTATTACCCCTCAATGATTTGAAAGT 300
Qy	101	ArgProValLeuIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAapAen 120
Db	301	CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCAAAAACCATCGTTATGAAGATAAC 360
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr 140
Db	361	ACCCTTCCCGTCTGCTCGCTATCACCGAACAAAGTACAGGCAGGAGAGAAAAACGACC 420
Qy	141	GluArgLeuIleTyrAlaGlyAenThrProGlnGluLysAspTyrAenLeuAlaGlyGln 160
Db	421	GAACTGCTTATCTGGCGCGCAATACCGCGCAAGAAAAAGATTACAACTCTCGCGGTGAG 480
Qy	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly 180
Db	481	TGTGTCCGCATTCAGATACCGCGGACTTACTCAACTCAATAGCTTTCTCTGGCTGGC 540
Qy	181	ValValLeuSerGlnSerGlnLeuLeuThrAspAenGlnAspAlaAspThrThrGly 200
Db	541	GTCTGCTATCACAATCTCAGCAACTACTCTGTCGATGATAAAAAATGCTGACTGGACAGT 600
Qy	201	GluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAen 220
Db	601	GAAGACCAAAAGCCTCTGGCAGCAAAACCTGACGAGTGATGCTATACCAACCCAAAAATAA 660
Qy	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeu 240
Db	661	GCCGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCAACATCCAGCGTCTG 720
Qy	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTyrPLeuThrLeuLysGlyGlnAlaGlu 260
Db	721	GCCTACGACGTAGCCGGCGAGCTTAAAGGCTGTTGGTTCACACTCAAAAGTCTCAGGCCGAG 780
Qy	261	GlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Db	781	CAAAGTGAATTCATAATCGCTGACCTACTCCGCGCGGACAAAAATTCACGGAAGACAC 840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
Db	841	GGTAACGGGGTTATCACTGAATACAGCTATGAACCGAAACCCACCGGCTTATCGGTATT 900
Qy	301	ThrThrArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro 320
Db	901	GCCACCGCGCTCCGTGACGCGCAAAAGTGTGCAAGACTTACGCTATCAATATGACCCG 960
Qy	321	ValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArgPheTyrPArgAenGln 340
Db	961	GTAGGCAATGTGATCAATATCCGTAATGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG 1020


```
QY 341 LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Db 1021 AAAGTGTCCGGGAGAAATAGCTATACACTCCCTGTATCAGCTTATCAGTGCACCC 1080
QY 361 GlyArgGluMetAlaAenIleGlyGlnAenGlnLeuProSerProAlaLeuPro 380
Db 1081 GGGGGGAATGGCTAATATAGGTACAGAAATAACCAACTGCCCTCCCTGGCTACCT 1140
QY 381 SerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAen 400
Db 1141 TCTGACAACAATACTACCTAACTAATCTCGAGCTACAGCTATGATCAAGTGGTAAT 1200
QY 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr 420
Db 1201 CTGACGCAAAATTCGCCACAGCTCCGCCAGCTACCCAGAACCACTACACCGTGGCTATCACC 1260
QY 421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal 440
Db 1261 CTCTCAAAACCGCAGCAATCGGGTGTCTCAGTACGCTAACCCACCGATCCAAATCAAGTG 1320
QY 441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 1321 GATACGTTGTTGATCGCGTGGTGCACCAACCAAGTTTATTCACCGGACAGACACTTATC 1380
QY 461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTrpTyrArg 480
Db 1381 TGGACACACAGAGAGAGTTAAAGCAGGTTAAATATGCGCGGAAATGAGTGATCCGC 1440
QY 481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr 500
Db 1441 TACGACACCAACGCGATGACACACTGNAAGTGAAGTGAACAGCCACCCAGATACATACG 1500
QY 501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrGlnSerAenAla 520
Db 1501 CAGCAACAACGGGTAAATCTATTTCCCGGACTGGAGCTACGCAACAACCCAGAGCAACGCC 1560
QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 1561 ACAACAACGGAAGAGTTACAGTTTATCACACTCCGTTGAAGCGGTCGCGCACAGGTACGG 1620
QY 541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer 560
Db 1621 GTGTTGACTGGAGAGCGGTAAACCCAGAGATGTCACCAATATCAACTACGTTACAGC 1680
QY 561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer 580
Db 1681 TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAAACCAAGGACAAATTTATCAGC 1740
QY 581 GluGluGluTyrTyrProPheGlyGlyThrAlaIleuTrpAlaAlaAenSerGlnThrGlu 600
Db 1741 GAGGAAGAGTATTTATCAATTTGGCGGGACACGCGCTGTGGCGAGCAAAACAGCCAAACAGAA 1800
QY 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 1801 GCCAGCTATAAAGCATTCGCTATTCCGGCAAAAGACAGAGTGCACCGGTTGTATAT 1860
QY 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 1861 TACGGTTATCGTTATTTACCAACCGTGGCGCGGAGATGGTTAAGCGCGACCCCGCAGGA 1920
QY 641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp 660
Db 1921 ACCATTGATGGCTGAAATCTATACCGAATGTAAGAAATAATCTCTGTGAGTTTACAAGAT 1980
QY 661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu 680
Db 1981 GAAATATGATTTAGCGCCAGGAAAGGGAATATATACCAAGAGGTAAATTTCTTTGATGAA 2040
QY 681 LeuLysPheLysLeuAlaAlaLysSerSerHisValVallyTyrAenGluLysGluSer 700
Db 2041 TTAAAAATTCAAATTTGGCAGCCCAAAAGTTTCACATGTTGTGTCAAATGCAACGAGAAAGAGAGC 2100
```

```
QY 701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2101 AGTTATACAAAATAAATCAATCAATGAAAGTGGTTCGTGTCGGTGATCCGATCCGTCGGGT 2160
QY 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2161 TATTTCTGAAGCCACAGAGTTACTTAAAGGTATAGAAAAAGTCAAAATCATATATAGC 2220
QY 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
Db 2221 CGACTTTGAAGAAACACAGCTCCCTTTTCAGAAAAATCAAAAAACGAATCTTTCTTAGGATCT 2280
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAAATATCCGTTATATGCGACAGAACCATACAGATACGATATCAGATATGCGAAGAG 2340
QY 781 HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAAATATAGAAGTAAATCACCCCTGATTTTATTTCAGAAAAACCGATTTCTTTGGCTTAATG 2400
QY 801 AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 2401 GATATAAGTCAAAAAATGATTTATCCGGTGAAGAAAAATTTATGCGCAATGGAGGT 2460
QY 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 2461 AAGTTTATCATGATTTTAAAAATAAACAATCAAGATTAATGATCACTGATGATGGCC 2520
QY 841 HisProTyrThrGlnLeuSerAenGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 2521 CATCCCTATACGCAATTGAGTAATGAAGAAAGAGCGCTGTTGCAAGAAAAACGACCCGCT 2580
QY 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAGATAGCAATATAATTTCAAAGGTGTTGGCAAAATTCCTGACAAATGAAAGCA 2640
QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 2641 ATTAAAAATCATTTGAAGACATATAAATTAATAGATATCAACAGAGGCTATTATATT 2700
QY 901 ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTCGCGCTATCGCTGAGATTTAGGAATCGGAGAACTTCA 2745

RESULT 3
US-10-609-113-48
; Sequence 48, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE OF INVENTION: Paenibacillus Species
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-48

Alignment Scores: 7.37e-243 Length: 2817
Pred. No.: 2960.00 Matches: 607
Score:
```


Db 901 CGGCTTATCGCATTTACCACTCCGCGTCCATCAGACGCCAAGGTGTGCAAGACCTTACGC 960
Qy 316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
Db 961 TATCAATATACCCAGTAGCAATGATAGTATCGTATAGTATCGGAGGACCATCGC 1020
Qy 336 PheTrpArgAsnGlnIysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGTATACCTACGATTCCTGTATCAG 1080
Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnAsnAsnGlnLeuPro 375
Db 1081 CTTATCAGCGCCACCGCGCGAGATGCGCAATATCGGTACGAAAGCAACCAACTTCCC 1140
Qy 376 SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
Db 1141 TCTCCGGCGTACTCTTGATACATATACCTACACCACTATATCTCGCACTTATCTAT 1200
Qy 396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
Db 1201 GACCGTGGCGCAATTTGACGAAATTCAGCATAGTTCACGACCGCGCAAAATACTAC 1260
Qy 416 ThrValAlaIleThrLeuSerAsnAsnArgSerAsnArgGlyValLeuSerThrLeuThr 435
Db 1261 ACACCGGATATACGGTTTCANATCGCAGAACCGCGCGGTACTCAGCACATTTGACCGCA 1320
Qy 436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
Db 1321 GATCCCACTCAAGTCGATGCTTATTTGATCGGGAGCCCATCAACACGCTTGTATCC 1380
Qy 456 GlyGlnThrLeuIleThrProArgGlyGluLeuIysGlnValAsnAsnGlyProGly 475
Db 1381 GGCCAAAGTCTAACTTGGACACCGCGAGCGGAATTTGAACAAGCCACCAATAGCGCAGGA 1440
Qy 476 AsnGluTrpTyrArgTyrAspSerAsnGlySerArgGlnLeuIysValSerGluGlnPro 495
Db 1441 AATGAGTGGTATCGCTACGATACGACGCGCATACCGCGATACCGCAATGATGAACACAA 1500
Qy 496 ThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
Db 1501 ACTCAGATATCCCGCNAACAAGGGTAACCTTACTACCGGGCTGGAAATACGTACA 1560
Qy 516 ThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 1561 ACCCAGAACCAACGCAACACAGAGAGTTACACGTTATCACACTCGGTAAAGCGCGC 1620
Qy 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyIysProGluAspValAsnAsn 555
Db 1621 CGCGCGCAAGTCCGAGTATTCGATTTGGGAGAGCGGTAAACAGAGATATTAATAACAA 1680
Qy 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
Db 1681 CAGCTTGTACAGTACGATATCTTATTTGGTCTCCAGCCAACTTCATATTAGATAGCGAC 1740
Qy 576 GlyGlnIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595
Db 1741 GGACAAATATCAGTGAAGAAGATATATCCATTTGGTGTACAGCGCTGTGGCGGCA 1800
Qy 596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyIysGluArgAspAla 615
Db 1801 AGGAATCAACCGAAGCAGCATATAAACCACTTCGTTATTCGTAAAGACGCGGATGTT 1860
Qy 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
Db 1861 ACCGGCTGTATTATATGCTACCGTTATACCAACCGGGCGGCGAGATGGTAGGT 1920
Qy 636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
Db 1921 GCAGACCCGCGAGAACCATTTGAGTGAATTTATATCGCATGTTGAGAAATAACCCG 1980
Qy 656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
|||||
|||||

Db 1981 GTACCGCAATTTGATGTTTCAGGGAATTATCACCGGCCAACAGAAAGCGGATATA 2040
Qy 667 GluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeuAla 686
Db 2041 AAACAGGGTTCCTTTACGGGA-----ATGGAAGAGCTGTTTATAAAAAATG 2088
Qy 687 AlaLys-----SerSerHisValValLysTrpAsnGluLysGluSer 700
Db 2089 GCTAAACCTCAAACTTTCAACGCCCAAGAGCTATCGTCCCAACACAGAGCAAGAGCC 2148
Qy 701 -----SerTyrThrLysAsnLysSerLeuValValArgValGlyAspAspPro 718
Db 2149 CATGAATCATTTGACCAACACCTAGTGTAGATATT-----AGCCCAATT 2193
Qy 719 SerGlyTyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIle 738
Db 2194 AAAAAGTACACACAGATAGTCCACAAATTAATGCGCGATAGGGAATAATCGTATTACG 2253
Qy 739 TyrSerArgLeuGluGluAsnSerLeuSerGlyLysSerLysThrAsnLeuSerLeu 758
Db 2254 CCAGCAGTGGAAAGTTTAGACGCCACATTTCTTCCCTACAGATAGACAAATGAGGTA 2313
Qy 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTTATCGGTGATGACCTATGTAGATAATTCACGCCATCGCTGGCACTGCCACAG 2373
Qy 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAATAGTATTAAATGTGTGTGATATCGTTTCGGATAACGCTTATTTATCAACATCG 2433
Qy 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe--- 796
Db 2434 GCCATCGTGGTTTCTCGAATTTTGTTCACAAAAAGAACCACTGAAACTCGATACGTC 2493
Qy 797 ---PheAlaLeuMetAspLysSerGluLysAsn-----AspTyr 808
Db 2494 AAGATCGCATTTTAAAGATCGGGTGTCAATGCCAGCAGCATCTATGTATAATAAT 2553
Qy 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
Db 2554 GCTGGCGGAGGACCAAGTATTAAATG-----GATTTAAACGAT 2592
Qy 829 LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAAGAAAGAGCCTCTGCTGAAAAATTAAGAGTCAAGTGCAGCCACCAATCGGACAA 2652
Qy 849 GluGluArgAlaLeuLeuGlnThrGluProAlaIleAlaIleAspArgGluTyrAsn 868
Db 2653 CGGGAATATTACTACTAGGGAACACAGTTCCGAAGTTGTT-----TCAATGAAA 2703
Qy 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAGGCGAGATACCTATGTATTATTCAGAGATATTAAACCAATCCGAGCCACTCAT 2763
Qy 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTCAGTAACACTTACCGCGTAATTTCAATCATCCACT 2808
|||||
|||||

RESULT 5

US-10-754-115-57
; Sequence 57, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schlexer, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia

```
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XCI
; CURRENT APPLICATION NUMBER: US/10/754,115
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens strain M14
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2817)
US-10-754-115-57

Alignment Scores:
Pred. No.: 1,62e-242 Length: 2817
Score: 2956.00 Matches: 608
Percent Similarity: 73.01% Conservative: 90
Best Local Similarity: 63.60% Mismatches: 186
Query Match: 62.36% Indels: 72
DB: 8 Gaps: 14

US-10-647-956A-6 (1-915) x US-10-754-115-57 (1-2817)
Qy 1 MetSerTyrAsnSerAlaileAaspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGGAACATTCAGCCCAAACTTTATCACCATACGCTACCGTCAGGTTCACGATAAC 60
Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAsp 40
Db 61 CGTGGACTAGTATCCGTAATATTAGTTTTCACCGCACCTACCGCAGAGCAAAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGTATTACCGGCATCAATATAATGCCGGCGGATTTTGAACCAAGCATTTGATCCT 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTGTATGACGCCAACACAGACTAACACGCTGTACACCGAATTTTATCTGGCGACAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTTCACCGCAATATCTCCGAACAGAGCGCTCGATGCCGTCGCGACGATTTACCCCTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAenAlaThrGlyValArgGlnAsnHis 115
Db 301 AACGATATTGAAGCCCGCCGGTGTGACCATCAATGACGCGGTGTCCGCCAAACCAT 360
Qy 116 ArgTyrGluAspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTACGAAGATAACACCTCGCCGTCGCTGCTCGCTATCAGCGAACAAGGACAGGCA 420
Qy 136 GlyGluLysThrThrGluArgLeuIleThrAlaGlyAenThrProGlnGluLysAspTyr 155
Db 421 GAAGAGAAACGACGAGCGCTTATCTGCGCGCGCAATACGCGCGCAAGAAAAAGACCAC 480
Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSer 175
Db 481 AACCTTCGCGTCAGTGGCTCGGCATTTACGATACCGCAGGACTCCTCAACTCAACAGC 540
Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
Db 541 CTGCGCTCGACCGCGCGCTTCTATCAACTCTCAACAACTGCTTACCGATAACCCAGAT 600
Qy 196 AlaAspThrThrGlyGluAspGlnSerLeuThrGlnGlnLysLeuSerSerAspValTyr 215
Db 601 GCCGACTGGACAGGTGAACAGCAGGCTCTGGCAACAAACAACTGAGTAGTGTCTAT 660
Qy 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
```

```
Db 661 ATCACCAAGTAACACTGATGCCCGGGCTTTACTGACCACGACCGATGCAAAAGC 720
Qy 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTyrLeuThrLeu 255
Db 721 AACATTCAGCGCTGCGCTATGATGTGGCGGCGAGCTAAAGAGGAGTTGGTTAACTC 780
Qy 256 LysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
Db 781 AAAGGTGAGCGGGAACAGGTGATATCAAACTCGTAACCTACTCCGCGCGCGGCAAAA 840
Qy 276 LeuArgGluGluHisGlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
Db 841 TTACGTGAGAGAGACACGTAACGGGATTGTCACTGAATACAGCTACGAACCGGAACCAA 900
Qy 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAaspLeuArg 315
Db 901 CGGCTTATCGGCATTTACCACTCGCGCTCATAGACGCCAAGGTGTTCGAAGACCTACGC 960
Qy 316 TyrGlnTyrAspProValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArg 335
Db 961 TATCAATATGACCAGTAGGCAATGTCATTAGTATCGTAAATGATGCGGAAGCCACTCGC 1020
Qy 336 PheTyrArgAenGlnLysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGln 355
Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAG 1080
Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuPro 375
Db 1081 CTTATCAGCGCCACCGCGCGAGATGGCCAATATCGGTGAGCAAAACCAACTTTCCC 1140
Qy 376 SerProAlaLeuProSerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
Db 1141 TCCTCGCGCTACTCTTGATATAATACCTACACCACTATATCTCGCACTTATCTACTAT 1200
Qy 396 AspHisSerGlyAenLeuThrGlnIleArgHisSerSerProAlaThrGlnAenAsnTyr 415
Db 1201 GACCGTGGCGCAATTTGACGAAATTCAGCATAGTTCCACGCGCGCAAAATAACTAC 1260
Qy 416 ThrValAlaIleThrLeuSerAenAenArgSerAenArgGlyValLeuSerThrLeuThr 435
Db 1261 ACGACGATATAACGGTTTCAAATCGCAGCAACCGCGGTACTCAGCACATTTGACCGCA 1320
Qy 436 AspProAenGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
Db 1321 GATCAAACTCAAGTCGATGCTTTATTTGATCGGGAGGCCATCAACACGACTTGTATTC 1380
Qy 456 GlyGlnThrLeuIleThrThrProArgGlyGluLeuLysGlnValAenAenGlyProGly 475
Db 1381 GGCCAACTTCTAATTGGACACCGCGAGCGGAATTGAAACAAGCAACAATAGCGCAGGA 1440
Qy 476 AsnGluTyrTyrArgTyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnPro 495
Db 1441 AATGAGTGGTATCGCTACGATAGCACGCGATACCGCAGCTAAAGTGAATGAACAACAA 1500
Qy 496 ThrGlnAenThrThrGlnGlnAlaGlyValIleTyrLeuProGlyLeuGluLeuArgThr 515
Db 1501 ACTCAGAAATATCCCGCAACCAACAAGGGAACCTTATCTACCGGGCTTGGAAATACGTACA 1560
Qy 516 ThrGlnSerAenAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 1561 ACCCAGAACCAACGCCCAACAAGAGATTACACGTATTACACTCGGTAAAGCGCGC 1620
Qy 536 ArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGluAaspValAenAsnAsn 555
Db 1621 CGCGCGAAGTCCGAGTATTGCAATTTGGGAGCGGTAAACCAAGAGATATTAAATAACAAT 1680
Qy 556 GlnLeuArgTyrSerTyrAspAenLeuIleGlySerSerGlnLeuGluLeuAaspAsnGln 575
Db 1681 CAGCTTGTACAGCTACGATAATCTTATTGGCTCCAGCCCACTTCAATTAGATAGCGAC 1740
Qy 576 GlyGlnIleLeuSerGluGluTyrTyrProPheGlyGlyThrAlaLeuThrAlaAla 595
```

```
Db 1741 GGACAAATTATCATGTAGAGAAAGAAATATTATCCATTTGGTGGTATCAGCGCTGTGGCGGCA 1800
Qy 596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla 615
Db 1801 AGGATCAACCGAGCCAGCTATAAACCATTCGTTATCTGGTAAAGAGCGGGATGTT 1860
Qy 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
Db 1861 ACCGGGTGTATTATTATGCTACCGTTATTACCAACCGTGGCGGCAGATGTTAGGT 1920
Qy 636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
Db 1921 GCAGACCCGCAGAACCATTTGAGCTGAATTTATATCGCATGGTGAGAAATAACCCG 1980
Qy 656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
Db 1981 GTGACGCAATTGATGTTCAGGGATTATCACCGGCCCAACAGACAGAGCAAGCATATA 2040
Qy 667 GluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeuAla 686
Db 2041 AAACAGGGTTCCTTTACGGGA-----ATGGAGAAAGCTGTTTATAAAAAAATG 2088
Qy 687 AlaLys-----SerSerHisValValLysTrpAsnGluLysGluSer 700
Db 2089 GCTAAACCTCAAACTTTCAAACGCCAAAGAGCTATCGCTGCCAAACAGAGCAAGAGCC 2148
Qy 701 -----SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspPro 718
Db 2149 CATGATCATGTGACCAACACCTGATGTAGATATT-----ACCCCAATT 2193
Qy 719 SerGlyTyrLeuLeuSerHisGluLeuLeuLysGlyIleGluLysSerGlnIle 738
Db 2194 AAAAACTACACACAGATAGCTCACAAATTAATGCCGCGATAGGGAATAATCGATTACG 2253
Qy 739 TyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeu 758
Db 2254 CCAGCATGGAAAGTTAGACGCGCACATTATCTCCCTCAAGATAGACAAATGAGGGTA 2313
Qy 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTATCGGTGATGACCTATGTAGATAATTCCACGCCATCGCTTGGCACTCGCCACAG 2373
Qy 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAAATAGTATTAAATGTTGGTGATATCGTTTCGGATAACGCTATTATCAACATCG 2433
Qy 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe--- 796
Db 2434 GCCCATCGTGGTTTCTGAAATTTTGTTCACAAAAAAGAAACCAACAGTGAAACTCGATCGTC 2493
Qy 797 ---PheAlaLeuMetAspLysSerGluLysAsn-----AspTyr 808
Db 2494 AAGATGCGCATTTTAAAGCATGGGTGTCAATGTCCACGACGATCTATGTATATAAT 2553
Qy 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
Db 2554 GCTGGCGAGCAGCAAGTATTTAAATG-----GATTTAAACGAT 2592
Qy 829 LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAAGAAAAACGCTTGTGAAAAATTTAAACATTAAGAGTCAGTGGACCAACATCGGGACAA 2652
Qy 849 GluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArgGluTyrAsn 868
Db 2653 GCGGAATATTACTACTAGGGAACACAGTTTCGAGTTGTT-----TCAATGAAA 2703
Qy 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAAGGCAGAGATACCTATGTATTATTGCAAGATATTAAACCAATCCGCGCACCTCAT 2763
Qy 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTACGTAAACACTTACACCGGTAAATTTCAAATCATCCAGT 2808
```

RESULT 6

```
US-10-706-424-11
: Sequence 11, Application US/10706424
: Publication No. US20040103455A1
: GENERAL INFORMATION:
: APPLICANT: ifrench-Constant, Richard
: APPLICANT: Waterfield, Nicholas
: TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
: FILE REFERENCE: 62878
: CURRENT APPLICATION NUMBER: US/10/706,424
: CURRENT FILING DATE: 2003-11-12
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 11
: LENGTH: 2883
: TYPE: DNA
: ORGANISM: Photorhabdus luminescens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(2880)
US-10-706-424-11
```

```
Alignment Scores:
Pred. No.: 1,12e-206 Length: 2883
Score: 2537.50 Matches: 518
Percent Similarity: 74.12% Conservative: 92
Best Local Similarity: 62.94% Mismatches: 159
Query Match: 53.53% Indels: 55
DB: Gaps: 12
```

US-10-647-956A-6 (1-915) x US-10-706-424-11 (1-2883)

```
Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAAACACATGTATCCCAAACTTTATCAAAACCCCTACTGTACGGTTTACGATAAC 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGTGGTCTGATAATCGTAACATCGATTTTCATCGTACTACCGCAAAATGGTGATCCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGTATTACCGCCCATCAATACGATATTACGGACACCTTAATCAAAAGCATCGATCCG 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTATATGAAAGCCAAAGCAACCAATACGATCAAAACCCCAATTTCTTTGGCAGTAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 GATTTGACCGGTAATCCCTATGTACAGAGAGCATTTGATCGAGTCCGACTGTCCACTTG 300
Qy 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AATGATATTGAAGCGCGCTCGCTACTTAACGGTCACTGCAACAGGGGTTATACAACTCGA 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CAATATGAACATCTTCTTCCTGCGCGTGTCTGTATCTGTTCCCGCAACCAACACCCGAG 420
Qy 136 GlyGluLysThr-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 421 ---GAAAAACATCCCGTATCATCCGAAACGCTGATTTGGCTGCGCAATACCGAAGCAG 477
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 478 AAAGACCAATAACCTTCCCGCCAGTCGTCGCTCACTATGACACACGGCGGAGTTACCCGG 537
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAsp 192
Db 538 TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCCACTATTGATCGAC 597
```



```
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-46

Alignment Scores:
Pred. No.:      1.12e-206      Length:      2883
Score:          2537.50      Matches:      518
Percent Similarity: 74.12%      Conservative: 92
Best Local Similarity: 62.94%      Mismatches: 159
Query Match:      53.53%      Indels:      55
DB:               7          Gaps:       12

US-10-647-956A-6 (1-915) x US-10-609-113-46 (1-2883)

QY      1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db      1 ATGAAACAAATTGATCCCAACTTTATCAAAAACCCCTACTGTACGCGTTTACGATAAC 60

QY      21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db      61 CGTGGTCTGATATCCGTAACATCGATTTTCATCGTACTACCCGCAATATGGTGATCCGAT 120

QY      41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db      121 ACCCGTATTACCCGCCATCAATACGATATTCACGGACACCTAATCAAGCATCGATCCG 180

QY      61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelleArgValphe 75
Db      181 CGCCTATATGAAGCCCAAGCAACCAACAAATACGATCAAAACCCCAATTTCTTGGCAGTAT 240

QY      76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db      241 GATTTGACCGGTAAATCCCTTATGTACAGAGAGCATTTGATCGAGTGCACGTGCACCTTG 300

QY      96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
Db      301 AATGATATTGAAGCCGTCGCTACTAAACGGTGACTGCAACAGGGGTATACAAACTCGA 360

QY      116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db      361 CAATATGAACATTCTTCCCTGCGCGTCTGTATCTGTTGCCGAACAAACACCCGAG 420

QY      136 GlyGluIysThr-----ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGlu 152
Db      421 ---GAAAAAACATCCCGGTATCACCGAACCGCTGATTTGGGCTGGCAATACCGAAGCAGAG 477

QY      153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db      478 AAAGACCATAACTTGGCGGCGAGTGGTGGTCTACTATGACACGCGGGGAGTTACCCGG 537

QY      173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
Db      538 TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCCACTATTGATCGAC 597

QY      193 AsnGlnAspAlaAspThrPheGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
Db      598 ACTCAAGAGCAAACTGGACAGGTGATAACGAAACCGCTCTGGCAAAACATATGCTGGCTGAT 657

QY      213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyValAlaLeuLeuThrGlnThrAsp 232
Db      658 GACATCTACAAACCTTGACACCTTCGATGCCACCGGTGCTTTACTGACTCAGACCGAT 717

QY      233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db      718 GCCAAAGGGAACATTACAGACTGGCTTATGATGTGGCCGGGCGAGCTNAACGGGAGCTGG 777

QY      253 LeuThrIleLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
Db      778 CTAAACACTCAAGGCCAGACGGAACAAGTGATTTATCAAAATCCCTGACCTACTCCCGCGCC 837
```

```
QY      273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db      838 GGACAAAAAATTACGTGAGGAACACGCGCAATATGTTATCACCGAATACAGTTATGAACCG 897

QY      293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
Db      898 GAAACCCAAACGGCTGATCGGTATCAAAACCCCGCGTCGTCAGACACTAAAGTGCTACAA 957

QY      313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
Db      958 GACCTGGCTATGAATATACCCCGGTAGGCAATGTCTATCAGCATCTCGTAATGACGCGAA 1017

QY      333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
Db      1018 GCCACCCGCTTTTGGCACAATCAGAAAGTGATGCGCGGAAACACTTATACCTACGATTC 1077

QY      353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
Db      1078 CTGTATCAGCTTATCAGCCGCCACCGGCGGAAATGCGGAATATAGGTCAACAAAGTCAC 1137

QY      373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
Db      1138 CAATTTCCCTCACCCTCTACTCTCTGATTAACAACACCTATACCACTATATACCCGTACT 1197

QY      393 TyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGln 412
Db      1198 TATACTTATGACCGTGGCGCAATCTGACCAAAATCCAGCACACAGTTTCACCGGCGACCA 1257

QY      413 AsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThr 432
Db      1258 AACAACTACACCAACCAATATCAGGTTTCAAAATCGCAGAACCGCGCAGTACTCAGCACA 1317

QY      433 LeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSer 452
Db      1318 TTGACGAGAGATCCGGCGCAGTAGATGCTTTGTTGTATGACGCGCGGACATACGAAACCC 1377

QY      453 LeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGlyLeuLysGlnVal----- 470
Db      1378 TTGATATCAGGACAAACCTGAACTACTCGTGGTGAACCTGCAACAAAGTAACACTG 1437

QY      471 -----AsnAsnGlyProGlyAsn-----GluTyrTyrArgTyrAspSerAsnGly 485
Db      1438 GTTAAACGGGCAACGCGGCCCAATGATGATCGGGAATGTTATCGTTATAGCGGTACGGA 1497

QY      486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
Db      1498 AGAAGATGTTTAAATAATCAATGAACAGCAGGCGCAGCAACAGCTCAACACAAACGTGTG 1557

QY      506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
Db      1558 ACTTATTTCCGAACTTAGAACTTCGTCTAACACAAAACAGCAGCAGCCCAACCGAAGAT 1617

QY      526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
Db      1618 TTGCAAGTTTATCACCGTAGCGAAGCGGCGCGGACAGGTACGAGTATTACATTGGGAG 1677

QY      546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
Db      1678 AGCGGTAAACCCGGAAGATATCGCAATAATAGTTGCGTTATAGTTACGATATCTTATC 1737

QY      566 GlySerSerGlnLeuLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
Db      1738 GGTTCAGTCACTTGAATTAGTAGCGGAAGGACAAATTTATCAGTGAAGAAGATATTAT 1797

QY      586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db      1798 CCTATGTTGGAACAGCATTTATGGGCGCGCGGACAGGAATCAGACAGACCCAGTTATAAA 1857

QY      606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
Db      1858 ATCCGTTATTGCGCAAGAGCGGATGCCCGGCTATATTTACTACGGCTATTCGGTAT 1917
```

```
Qy 626 TyrGlnProTpaAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TACCAACCGTGGATAGACGGTGTAAAGCTCCGATCCGACGAGAAACAAATCGATGGCTG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATTATATCGGATGGTGGAGGAATAATCCAGTACCCTCCTTGATCCTGATGATTAATG 2037
Qy 666 Pro-----GluLysGlyLysTyrThr----- 672
Db 2038 CCAACAATTGCGAAGCGCATAGCAGCACTAAATAAATAAAGTAACAGACTCAGCGCCT 2097
Qy 673 -----LysGluValAsnPheAspGluLeuLysPheLysLeuAlaAlaLysSer 689
Db 2098 TCGGCACAAATGCCAACAAGCTAGCGATAAACATCCGCCGCTGTAGCACCAAAACCT 2157
Qy 690 SerHisValVallystTpaAsnGluLysGluSerTyrThrTysAsnLysSerLeuLys 709
Db 2158 AGCTT-ACCGAAAGCATCAACAGAGTAGCAACCAACACACACACCTATCCGAGCTGCAAA 2216
Qy 710 -----ValValArg-ValGlyAspSerAspProSerGlyTyrLe 722
Db 2217 CATAAAAACCAACGAGCTGGGTCTATCTATTGTTGCTCCATTGAGTCCAGTAGGAATAA 2276
Qy 722 uLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
Db 2277 ATCTACTTCTGAATCTCTCTGCCA-----GAAAGCGCTCA----- 2313
Qy 742 uGluGluAsnSerSerLeuSerGluLysSerLysTyrAsnLeuSerLeuGlySerGluI 762
Db 2314 -----AGCAGTTCTTCAACGACACTACCTCCAGCAAAATCTACAGAAAAATCA---TT 2360
Qy 762 eSerGlyTyrMetAla-----ArgThrIleGluAspThrIleSerGluTyrAlaGlu 780
Db 2361 TACTTTATAGACGATACAGATCCTTTTGAAGAAATGCAAAAGTAAATTCCTCGAAGG 2420
Qy 780 uHisLys 782
Db 2421 ATTTAAA 2427

RESULT 8
US-10-754-115-46
; Sequence 46, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 46
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2880)
US-10-754-115-46
```

```
Alignment Scores:
Pred. No.: 1-12e-206 Length: 2883
Score: 2337.50 Matches: 518
Percent Similarity: 74.12% Conservative: 92
Best Local Similarity: 62.94% Mismatches: 159
Query Match: 53.53% Indels: 55
DB: 8 Gaps: 12

US-10-647-956A-6 (1-915) x US-10-754-115-46 (1-2883)
Qy 1 MetSerSerTyrAsnSerLalIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAAAAACATTGATCCCAACCTTTATCAAAAAACCCCTACTCTAGCGCTTACGATAAC 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGTGGTCTGATAATCCGTAACATCGATTTTCATCGTACTACCCCAATAGTGATCCCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGTATTACCGCCCATCAATACGATATTACGGACACCTAAATCAAAGCATCGATCG 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCCTATATGAGCCCAAGCAACCAACAATACGATCAAAACCCCAATTTCTTGGCAGTAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 GATTTCACCGGTAAATCCCTTATGTACAGAGAGCATTTGATGCGAGTGCACCTGTCACCTG 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AATGATATTGAGGCCGCTCGCTACTTAAACGGTACTGCAACAGGGGTATACAACTCGA 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CAATATGAAACTTCTTCCTGCGCGTCTGTATCTGTCTGCCGAAACAACACCCGAG 420
Qy 136 GlyGluLysThr-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 421 ---GAAAAAACATCCCGTATCACCAGACGCTGATTTGGGCTGGCAATACCGAAGCAGAG 477
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 478 AAGACCATTAACCTTGGCCGCCAGTGGTGGTCTACTATGCACAGCGGGAGTTACCCGG 537
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
Db 538 TTAGAGAGTTTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACCTATTGATCGAC 597
Qy 193 AsnGlnAspAlaAspThrThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
Db 598 ACTCAAGAGGCAAACTGGACAGGTGATAACGAAACCGCTCTGGCAAAACATGCTGGCTG 657
Qy 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
Db 658 GACATCTACCAACCCCTGAGCAGCTTCGATGCCACCGTCTTTACTGACTCAGACCGAT 717
Qy 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db 718 GCGAAAGGGAACATTCAGAGACTGGCTTATGATGTGGCCGGGAGCTAAACGGGAGCTGG 777
Qy 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrThrSerAlaAla 272
Db 778 CTAACACTCAAAGCCAGACGGAACAAGTATTATCAAAATCCCTGACTACTCTCGCCGCC 837
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db 838 GGACAAAAAATTCGTGGAGAACACGGCAATGATGTTATACCGGAATACATTGTAACCG 897
Qy 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
Db 898 GAAACCCCAACGGCTGATCGGTATCAAAACCCGCGTCCGTCCGACACACTAAAGTCTACAA 957
```

```
QY 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
Db 958 GACCTGGCTATGAATATGACCGGTAGGCAATGTCATCAGCATCGTATGACGGGAA 1017
QY 333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
Db 1018 GCCACCGGCTTTGGCCAACTAGAAGTATGATCGCGGAACAACACTTATACCTACGATTCC 1077
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
Db 1078 CTGTATCAGCTTATCAGCGCCACCGCGCGGAAATGCGGAATATAGTCAACAAGTCAC 1137
QY 373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
Db 1138 CAATTTCCCTCAGCGCTCTACCTTCTGTATAACAACACCTTATACCACTATACCGGTACT 1197
QY 393 TyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGln 412
Db 1198 TATACTTATGACCGTGGCGCAATCTGACCAAAATCGACACAGTTCACCGCGCAGCGAA 1257
QY 413 AsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThr 432
Db 1258 AACAACTACACCAATATCAGGTTTCAATCGCAGCAACCGCGCAGTACTCAGACA 1317
QY 433 LeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSer 452
Db 1318 TTGACCAAGATCGCGCGCAAGTAGATGCTTGTGTTGATCGCGCGACATCAGAACACC 1377
QY 453 LeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnVal----- 470
Db 1378 TTGATATCAGGACAAAACCTGGAATCTCGTGGTGAATCGCAACAACTGAACACTG 1437
QY 471 -----AsnAsnGlyProGlyAsn-----GluTrpTyrArgTyrAspSerAsnGly 485
Db 1438 GTTAAACGGACAAAGGCGCAATGATCGGGAATGGTATCGTTATACGGGTGACGGA 1497
QY 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
Db 1498 AGAAGGATGTTAAATAATCAATGAACAGCAGCGCCAGCAACACGCTCAACACACACGCTG 1557
QY 506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
Db 1558 ACTTATTTCGCGAACTTAGAACTTCGCTTAACACAAACACGACGCGCCACACCGAAGAT 1617
QY 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
Db 1618 TTGCAAGTTATACCGTAGCGGAAGCGCGCGGCGCACAGGTACAGTATTACATTGGGAG 1677
QY 546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
Db 1678 AGCGGTAACCGGAAGATATCGCAATAATCAGTTGCGTTATAGTTACGATAATCTTATC 1737
QY 566 GlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
Db 1738 GGTTCAGTCAACTGAATTAGATAGCGAAGGCAAAATTTATCAGTGAAGAAGAAATATTAT 1797
QY 586 ProPheGlyGlyThrAlaLeuTrpAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db 1798 CCCTATGGTGAACAGCAATTTATGGCGCGCCAGGAATCAGACGAAGCCAGTTATAAACT 1857
QY 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
Db 1858 ATCGGTTATTCAGCAAAAGCGGATGCCACCGGGCTATATTACTACGGCTATCGGTAT 1917
QY 626 TyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TACCAACCGTGGATAGACGGTGGTTAAGCTCCGATCCGATCCGCGACGGAACAATCGATGGCGTG 1977
QY 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATTTATATCCGATGGTGAAGGAATAATCCAGTTTACCCTCTCTGATGATTAATG 2037
```

```
QY 666 Pro-----GluLysGlyLysTyrThr----- 672
Db 2038 CCACAACATTGCAGAACGCATAGCAGCACTAAATAAAATAAGTAACAGACTCAGCGCCT 2097
QY 673 -----LysGluValAsnPheAspGluLeuLysPheLysLeuAlaLysSer 689
Db 2098 TCGCCAGCAAAATGCCAACAACGTAGCGATAAACATCTCGCGCGCTGTAGCACCAAAACCT 2157
QY 690 SerHisValValLysTrpAsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLys 709
Db 2158 AGCTT-ACCGAAGCATCAACGAGTAGCCACCAACCAACACACACCTTATCGGAGCTGCAA 2216
QY 710 -----ValValArg-ValGlyAspSerAspProSerGlyTyrLe 722
Db 2217 CATAAACCAACGACGCTCTGGGTCTATTTGCTTCATTGAGTCCAGTAGGAATAA 2276
QY 722 uLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
Db 2277 ATCTACTTCTGAAATCTCTCTGCCA-----GAAAGCGCTCAA----- 2313
QY 742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluI 762
Db 2314 -----AGCAGTTCTTCAAGCACTACCTCGACAAATCTACAGAAAAAATCA---TT 2360
QY 762 eSerGlyTyrMetAla-----ArgThrIleGlnAspThrIleSerGluTyrAlaGlu 780
Db 2361 TACTTTATATAGCAGCATACAGATCTTTTGAAGAAATGCAAAAGTAATTTCCCTGAAGG 2420
QY 780 uHisLys 782
Db 2421 ATTATAA 2427

RESULT 9
US-10-706-424-13
; Sequence 13, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: firench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2847)
US-10-706-424-13

Alignment Scores:
Pred. No.: 1.68e-204 Length: 2850
Score: 2512.00 Matches: 497
Percent Similarity: 76.17% Conservative: 88
Best Local Similarity: 64.71% Mismatches: 143
Query Match: 53.00% Indels: 40
DB: 7 Gaps: 10

US-10-647-956A-6 (1-915) x US-10-706-424-13 (1-2850)

QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAAARACATTGACCCAAACCTTTATCAACATACGCCCCACCGTTAACGTTACGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGTGGCTTACCAATTCGTAAACATCGACTTCCACGTCGCGGGAGCGCATACAGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
```

Db 121 ACTCGTATTACCGCCACCAATATGATACCGGAGCACCTTGAGCCAAAGCAITGATCCA 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGGCTGTATGACGCCAACCAACCAATACGACAAACCCCAACTTCCTCTGGCAATAC 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATCTCACCGCGACACTTTGGGACACAGAAAGTGTGATGCCGCGCTACGATAGCCCTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AATGATATTGAAGCGCGTCAAGTGTGATTGTAAACCGCAACCGCGCCCATTCAGACCCGA 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CAATATGAAGCCATATACCTGCCCGGTCTGCTATTATTCGTAAGTGAACAAGCC- --CCC 417
Qy 136 GlyGluLysThr-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 418 GGAGACAGACTCCCGCGTTACTAGACATTTTATTGGGCTGTGTAATACACAGCGCGAG 477
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 478 AAGATCATATCTTCGCGCCAGTATGTGCGCCACTACGACACAGCAGGAGTGAACGCA 537
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
Db 538 CTGAAAGCCCTGTCATTTGACAGAAACATCTTATCTCAATCCCGCTCATTTATTAGCCGAC 597
Qy 193 AsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
Db 598 GGTGAGGAAGCAGACTGACAGAGTAAAGATGAACCTCTGCGACACCAACTCAATAGC 657
Qy 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
Db 658 GAACACTTACACGACACAAAGCACCTTTGATGCTACCGCGCTTGCTGACCCAAACCGAT 717
Qy 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db 718 GCAAAGGCGACATCGCAACGTCTGGCTTACACGTGCGCAGGACAAATTACAAGGTAGCTGG 777
Qy 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
Db 778 CTGACATTGAAAAACCAAGTGGAGCAAGTCAATGTCANAATCCCTGACCTATTCCCGCGCA 837
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db 838 GGCCAGAAATTGCGTGAAGACACGCTAATGCGCTTATCACTGAATACAGCTATGAACCG 897
Qy 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
Db 898 GAAACTCTACGATTGATCGGTACCACTACTCGCGCTCAATCAGATAGCAAGGTGTACAA 957
Qy 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
Db 958 GATCTACGCTATGAACATGATCCTGTAGGGAATATTATTAGTCCGTAATGATGCAGAA 1017
Qy 333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
Db 1018 GCCACCCGCTCTCGCGCAATCAGANAATAGTCCCTGAAANATACCTACACCTACGATCC 1077
Qy 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
Db 1078 CTGTATCAGCTTATCAGTGCAACAGGAGCTGAGATGGCTAAACATCGGCGCACCAAGCAAC 1137
Qy 373 GlnLeuProSerPro-----AlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThr 390
Db 1138 CAACTTCCTCGCAATCATCCTCTTCTACTGATGAAAACCTCATATPACCACTATACT 1197
Qy 391 ArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAla 410
Db 1197

Db 1198 CGCAGCTATAATTACGATCGCGCGCAAAATTTGGTTCAAATCGGCACAGTTCCTCCCGCC 1257
Qy 411 ThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeu 430
Db 1258 GCCCAAAATAACTACACACAGATATCACCGTTTCGATTCGAGTAAACCGGCGAGTGTG 1317
Qy 431 SerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGln 450
Db 1318 AGTTTCGCTAACTCAGACCCCAACACAGGTGGAGGCACCTGTTTGTATCCGCGGACATCAA 1377
Qy 451 ThrSerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnVal 470
Db 1378 ACAAAATTTGTACCGGCGCAAGAGCTGAGTTGGAATACACGAGGTGAACCTTAAACACGGA 1437
Qy 471 -----AsnAsnGlyProGlyAsnGluTyrArgTyrArgTyrAspSerAsnGly 485
Db 1438 ACGCCAGTACGTCGCGAGAGCGCCAGCATCGGGAATGTTATCGTTACGGCAACGACGCG 1497
Qy 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgVal 505
Db 1498 ATCGACGCGTTAAAGTCAGTGAGCAACAGACTGGCAACAGCAGCAGCAGCAACAGTA 1557
Qy 506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
Db 1558 ACTTATCTTCCCGATCTGGAGCTACGTACAACAACAAAATGGGACTACTATACAGAAAG 1617
Qy 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
Db 1618 CTGCATGCTATTACCGTGGGAGCAGCGCCACGCAAGCTGCGAGTTCTACACTGGGAA 1677
Qy 546 SerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
Db 1678 ACTACGCCACCGCGGTATCAATAACATCAGCTTCGCTATAGCTATGATAATTTGATT 1737
Qy 566 GlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
Db 1738 GGTTCAGTCAACTGAACTGGATAACCGCAGGACAAATTTATCAGTCAGGAAGTATTAT 1797
Qy 586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db 1798 CCATTGGCGGCGACAGCAITATGGCAGCAAGAACCAATAGACCCAGCTACAAATC 1857
Qy 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
Db 1858 CTCGGTTACTCAGTAAAGAACCGATGCTACCGGCTCTATTATTACGCTACCGCTAT 1917
Qy 626 TyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TATCAGCCGTGGTGGTAGGTGGTTAAGCGCGCATCCGCTGGAAACAATCGATGGACTG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATCTATACCGGATGGTGAATAATAATCCGTCACACACTGGTTGATATTCTGGGCTTGCA 2037
Qy 666 ProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeu 685
Db 2038 CCTACG-----AAATACATATATCCCGGATTTTGCATTTGCAT----- 2073
Qy 686 AlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrThrLysAsn 705
Db 2074 -----GTAGAAATAGATGAGCAAAAAAGATCTAAATTTAAAAACCA 2112
Qy 706 LysSerLeuLysValValArgValGlyAspSer-----AspProSerGlyTyr 721
Db 2113 -----ACGTTGATAAGAAATCAAGATGAATTTTACATATTGCTCTGTAGATAAG 2163
Qy 722 LeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
Db 2164 CTGTTA-----GAAGAAAAAACCAGCGGCTCAATGTCACGAGGAGCTATTGTGATAGA 2217
Qy 742 LeuGluGluAsnSerSerLeuSer 749
Db 2218 GGTCCATCCGAGAATGAGTGTCA 2241

RESULT 10

US-10-609-113-47
; Sequence 47, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 47
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Photorhabdus strain W14
US-10-609-113-47

Alignment Scores:

Pred. No.: 1,686-204 Length: 2850
Score: 2512.00 Matches: 497
Percent Similarity: 76.17% Conservatives: 88
Best Local Similarity: 64.71% Mismatches: 143
Query Match: 53.00% Indels: 40
DB: 7 Gaps: 10

US-10-647-956A-6 (1-915) x US-10-609-113-47 (1-2850)

QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
||| : : : : :
DB 1 ATGAAACCATTCAGCCCAAACTTTATCAACATACGCCACCCTTAACGCTACGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
||| : : : : :
DB 61 CGTGGCCCTGACCAATCGTAACATCGACTTTCCAGCCGACGTCGCGGAGCGATACAGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
||| : : : : :
DB 121 ACTCGTATTACCGCCCAACCAATATGATACCCGAGGACACTTGAGCCCAAGCATTGATCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
||| : : : : :
DB 181 CGGCTGTATCAGCCCAACCAACCAATACCTCGACAAACCCCAACTTCCTCTGGCAATAC 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
||| : : : : :
DB 241 AATCTCACCGCGCACACTTTTCGGGACAGAAAGTGTGATGCGCGCGGTACCGTAGCCCTC 300
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
||| : : : : :
DB 301 AATGATATTAGGCCGTCAAGTGTGATTTGATTAACCCCAACCGCGCCGCTTACAGCCGA 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
||| : : : : :
DB 361 CAATATGAGCCCAATACCTGCGCGTCTGCTATTATTCGTAAGTGAACAAGCC---CCC 417
QY 136 GlyGluLysThr-----ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGlu 152
||| : : : : :
DB 418 GGAGAACAGACTCCCGCGTTACTAGACATTTTATTGGCTGGTAATACACAGCGCGAG 477
QY 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
||| : : : : :
DB 478 AAAGATCATTAATCTTTCGCGCCAGTATGTGCGGCACTTACGACACAGCAGGAGTGCACGA 537

QY 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
||| : : : : :
DB 538 CTGAAAGAGCTGTCAATTGACAGAAAACTCTTATCTCAATCCCGTCACTTATTATGCGCAG 597
QY 193 AsnGlnAspAlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSer 212
||| : : : : :
DB 598 GGTGAGGAGCAGACTGGACAGGTACGATGAACCCCTCTGGGACGACCAAACTCAATAGC 657
QY 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
||| : : : : :
DB 658 GAAACTTACAGCACACAAAGCAGCTTTGATGCTACCGCGCTTGTGACCCAAACCGAT 717
QY 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTyr 252
||| : : : : :
DB 718 GCAAAAGGCAACATGCAACGCTCTGGCTTACAACTGGCGGACGACAAATTACAAAGTAGCTGG 777
QY 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAla 272
||| : : : : :
DB 778 CTGACATTGAAAAACCAAGTGGCAGTCATTTGTCAATCCCTGACCTATTTCGCGCGCA 837
QY 273 GlyGlnLysLeuArgGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
||| : : : : :
DB 838 GGCAGAAATTGCGTGAAGAACACGCTAATGGCGTTATCACTGAATACAGCTATGAACCG 897
QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
||| : : : : :
DB 898 GAAACTCTACGATTGATCGGTACCTACTCGCGCTCAATCAGATCAGAAAGTGTATACAA 957
QY 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
||| : : : : :
DB 958 GATCTACGCTATGACATGATCTGTAGGGAATATTATTAGTCTCGTAAATGATGCGAGAA 1017
QY 333 AlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
||| : : : : :
DB 1018 GCCACCGCTTCTGGCGCAATCAGAAAAATAGTCCCTGAAAAATACCTACACCTACGATTCC 1077
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
||| : : : : :
DB 1078 CTGTATCAGCTATCAGTCAACAGACGCTGAGATGCTTAACATCGGCCACGCAAGCAAC 1137
QY 373 GlnLeuProSerPro-----AlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThr 390
||| : : : : :
DB 1138 CAACTTCTTTCGCAATCATCTCTCTCTCTGATGAAACATCATATACCAATATATCT 1197
QY 391 ArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAla 410
||| : : : : :
DB 1198 CGCAGCTAATAATTACGATCGCGCGCAATTTGGTTCAATCCGACAGTTCCTCCCGCC 1257
QY 411 ThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnAsnArgSerAsnArgGlyValLeu 430
||| : : : : :
DB 1258 GCCCAAAATAACTTACACCAAGATATCACCGTTCGAATCGCAGTAACCGGCGAGTGTG 1317
QY 431 SerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGln 450
||| : : : : :
DB 1318 AGTTCCTTAACCTCAGACCCCAACAGGTGGAGGCACTGTTTGTATGCGCGGACATCAA 1377
QY 451 ThrSerLeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGluLeuLysGlnVal 470
||| : : : : :
DB 1378 ACMAAATTTGTACCGGGGCAAGAGCTGAGTTGGAATACAGAGGTGACACTAAAACAGGTA 1437
QY 471 -----AsnAsnGlyProGlyAsnGluTyrTyrArgTyrAspSerAsnGly 485
||| : : : : :
DB 1438 AGCCAGTCAGTCGCGAGAGCGCAGCGATCGGGAATGGTATCGTTACGCAACAGCGGC 1497
QY 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
||| : : : : :
DB 1498 ATGCGACGGTATAAAGTCACTGAGCAACAGACTGGCAACAGCAGCGACGACCAACAGTA 1557
QY 506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
||| : : : : :
DB 1558 ACTTATCTCCCGATCTGGAGCTACGTACAAACAAAATGGGACTACTACTACAGAAAGAC 1617
QY 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaValArgValLeuHisTyrGlu 545


```
Db 1618 CTGCATGCTATTACCGTGGAGCAGCAGCGCCACGCAACAGTGCAGTCTTACACTGGGAA 1677
Qy 546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuLe 565
Db 1678 ACTAGCCACACCGCGGTATCAATAACATCAGCTTCGCTATAGCTATGATAATTTGATT 1737
Qy 566 GlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnLeuLeuLeuLeuLeuLeu 585
Db 1738 GGTTCAGTCACTGAGTGAATACGAGGACAAATATCATCTCAGGAGAGATATAT 1797
Qy 586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db 1798 CCATTTGGCGCACAGCATTATGGCCAGCAAGAAACCAATAGAACGACGACTCAAAATC 1857
Qy 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyr 625
Db 1858 CTCGGTTACTCAGTAAAGAACGGGATGCTACCGGGCTCTATTATTACGGCTACCGCTAT 1917
Qy 626 TyrGlnProTrpAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TATCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATCTATACCGGATGGTGAGAAATAATCCGTCACACTGGTGTGATATTCTCGGGCTTGCA 2037
Qy 666 ProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeu 685
Db 2038 CCTACG-----AAATACAAATATTCCCGGATTTGACATTTGAT----- 2073
Qy 686 AlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerTyrThrLysAsn 705
Db 2074 -----GTAGAATAGATGAGCAAAAGATCTAAATTTAAACCA 2112
Qy 706 LysSerLeuLysValValArgValGlyAspSer-----AspProSerGlyTyr 721
Db 2113 -----ACGTTGATAAGAAATCAAGATGAATTTTACATTATGTCCTGTAGATAAG 2163
Qy 722 LeuLeuSerHisGluGluLeuLeuLysGlyGlyLeuLysSerGlnIleTyrSerArg 741
Db 2164 CTGTTA-----GAAGAAAAAACCAGCGCTCAATGTACACAGAGAGCTATTGTATAGA 2217
Qy 742 LeuGluGluAsnSerSerLeuSer 749
Db 2218 GGTCCATCCGGAATGGAGTGCTCA 2241
```

RESULT 11

```
US-10-262-794A-60
; Sequence 60, Application US/10262794A
; Publication No. US20030207806A1
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; APPLICANT: Sukhupinda, Kitisri
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
```

Alignment Scores:

Pred. No.:	1-35e-200	Length:	3132
Score:	2467.00	Matches:	470
Percent Similarity:	81.25%	Conservative:	89
Best Local Similarity:	68.31%	Mismatches:	111
Query Match:	52.05%	Indels:	18
DB:	6	Gaps:	5

US-10-647-956A-6 (1-915) x US-10-262-794A-60 (1-3132)

Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGAGTCCGTCGTGAGACTCTCTTTATACTCAAAACCCCAACAGTCAGCTGTAGATAAT	60
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	61	CGCGGCTCTGCCAATTCGTGATATTGTTTACCGCTATTGTAATTCGGGGGGGATCTGAC	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	ACCGCGCTACCCGTCACAGTATGATGCCCGTGGACACCTGAACTACAGTATTGACCCA	180
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	181	CGTTGTATGATGCAAAAGCAGGCTGATACTCAGTAAAGCCTAATTTTGTCTGCGACGAT	240


```

QY      643  AspGlyLeuAenLeuTyrArgMetValArgAsnAenProValSerLeuGlnAseGluAen 662
Db      1981  GATGGGTGAATTGTACCGAATGGTGAGGAATAACCCCATCAGATTGACCATGAC 2040
QY      663  GlyLeuAlaProGluLysGlyLys 670
Db      2041  GGATTAGCACCGTCTCCAAATAGA 2064

RESULT 13
US-10-754-115-25
; Sequence 25. Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 3132
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3132)
US-10-754-115-25

Alignment Scores:
Pred. No.:      1.35e-200      Length:      3132
Score:          2467.00      Matches:      470
Percent Similarity: 81.25%      Conservative: 89
Best Local Similarity: 68.31%      Mismatches: 111
Query Match:      52.05%      Indels:      18
DB:              8          Gaps:         5

US-10-647-956A-6 (1-915) x US-10-754-115-25 (1-3132)

QY      1  MetSerSerTyrAenSerAlaIleAseGlnLysThrProSerIleLysValLeuAseAen 20
Db      1  ATGAGTCCGCTGAGACTACTCTTTATTAACCAACCCCAACAGTCAGCGTGTAGATAAT 60
QY      21  ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAseGluAenSerAse 40
Db      61  CGCGGTCTGTCATTCGTGATTTGGTTTCCACCGTATTGTAATCGGGGGGATCTGAC 120
QY      41  GluLeuIleThrPheTyrGluPheAseAenIleProGlyPheGlnValLysSerThrAsePro 60
Db      121  ACCCGCTCACCCGTACACCATGATGATCCCGTGGACACCTGAACACTAGATTGACCCA 180
QY      61  Arg-----LysAseLysAseGlnSerGlyProAenPheIleArgValPhe 75
Db      181  CGCTTGATGATGCAAGCAGCGGTGATAACTCAGTAAAGCCTAATTTGTCTGCGCAT 240
QY      76  AsnLeuAlaGlyGlnValLeuArgGluSerValAseAlaGlyArgThrIleThrLeu 95
Db      241  GATCTGCCCGGTATGCGCCCTCGGACAGAGAGTGTGATGCTGCTGCTGCTGCTGCTG 300
QY      96  AsnAspIleGluSerArgProValLeuIleAseAlaThrGlyValArgGlnAseHis 115

```

```

Db      301  AATGATATTGAAGGTCTTCGGTAAATGACAAATGAATGCGACCGGTGTTCTGTCAGACCCGT 360
QY      116  ArgTyrGluAseAenThrLeuProGlyArgLeuLeuAlaIleThrGlnGlnVal----- 133
Db      361  CGCTATGAAGGCAACACCTTGCCTGCTGTTATCTGTGAGCGAGCAAGTTTCAAC 420
QY      134  GlnAlaGlyGluLysThrThrGluArgLeuIleThrAlaGlyAseAenThrProGlnGlnLys 153
Db      421  CAAGAGAGTGTAAAGTGAAGAGCGCTTTATCTGGGCTGGGAATACACCTCGGAGAAA 480
QY      154  AspTyrAseAenLeuAlaGlyGlnCysValArgHisTyrAseThrAlaGlyLeuThrGlnLeu 173
Db      481  GAGTATAACCTCTCCCGTCTGTGTATACGCCACTACACACCGGAGTGCACCGGTTG 540
QY      174  AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuLeuThrAseAen 193
Db      541  ATGAGTCAGTCAGTGGGGGGCCATGCTATCCCAATCTCACCAATGCTGGCGGAAGGG 600
QY      194  GlnAseAlaAseThrThrGlyGluAseGlnSerLeuThrGlnGlnLysLeuSerSerAse 213
Db      601  CAGGAGCTAACTGGAGCGGTGACGACGAACTGTCTGCGCAGGAAATGCTGGCAAGTGAG 660
QY      214  ValTyrIleThrGlnSerAenThrAseAlaThrGlyAlaLeuLeuThrGlnThrAseAla 233
Db      661  GTCATATACGACACAAAGTACCATAATGCCATCGCGGCTTACTGACCCCAACCGATGCG 720
QY      234  LysGlyAseAenIleGlnArgLeuAlaTyrAseValAlaGlyGlnLeuLysGlySerThrLeu 253
Db      721  AAAGGCAATATTCAGCGTCTGGCTTATGACATTCGCGGTCACTTAAAGGAGAGTGTGGTTG 780
QY      254  ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
Db      781  ACGGTGAAAGGCCAGAGTGAACAGGTGATTGTTAAGTCCCTGAGCTGGTCAGCGCAGGT 840
QY      274  GlnLysLeuArgGluGluHisGlyAseGlyIleValThrGluTyrSerTyrGluProGlu 293
Db      841  CATAAAATTCGCTGAAGACGACGCTTAACGGCGTGTACCGGAGTACAGTTATAGACCCGNA 900
QY      294  ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAseAlaLys 309
Db      901  ACTCAACGCTGATAGGTATCACCCCGCGTGGCGAAGGGAGTCAATCAGAGGCCAGA 960
QY      310  ValLeuGlnAseLeuArgTyrGlnTyrAseProValGlyAseValIleAseAenIleArgAse 329
Db      961  GTATTGCGAGATCTACGCTATAGTATGATCCGCTGGGGAATGTTATCAGTATCCATAAT 1020
QY      330  AseAlaGluAlaThrArgPheThrArgAseGlnLysValAlaProGluAseAenSerTyrThr 349
Db      1021  GATGCGAAGCTACCGCGCTTTTGGCGTAATCAGAAAAGTGGAGCGGAGAAATCGCTATGTT 1080
QY      350  TyrAseSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAseAenIleGlyGln 369
Db      1081  TATGATTCTCTGATCAGCTTATGAGTGCACAGGCGGTGAATGGCTAATATCGGTGAG 1140
QY      370  GlnAseAseGlnLeuProSerProAlaLeu-----ProSerAseAenAenThrTyrThr 387
Db      1141  CAAAGCAACCAACTTCCCTCACCGTTATACCTGTTCTTACTGACGACAGCACCTTATACC 1200
QY      388  AsnTyrThrArgSerTyrSerTyrAsePheHisSerGlyAseAenThrGlnIleArgHisSer 407
Db      1201  AATTACCTCGTACCTATCTTATGACCGTGGCGTAATTTGGTTCAAATCCGACACAGT 1260
QY      408  SerProAlaThrGlnAseAenTyrThrValAlaIleThrLeuSerAenAseAenArg 427
Db      1261  TCACCCGCGACTCAAATAGTTATACACACAGATATCACCGTTTCAAGCCGCGAGTAACCG 1320
QY      428  GlyValLeuSerThrLeuThrAseProAseGlnValAseThrLeuPheAseAlaGly 447
Db      1321  CGCGTATTGATGATACATTAACGACAGATCCAAACCCGAGTGGATCGGCTATTGATTCGGC 1380
QY      448  GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467

```

```
Db 1381 GGTCAATCAGAAAGATGTTAATACCGGGGCAAAATCTGGATTGGGAATATTCGGGGTGAATTG 1440
Qy 468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTrpTyrArgTyrAsp 482
Db 1441 CAACAGGATCACACCGGTGAGCCGTGAAATAAGCAGTGAATGGTATCGCTATAGC 1500
Qy 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db 1501 AGTATGCGCATCGCGTCTAAAGTGAAGTGAACAGCAGCGGGCAACAGTACTCAAGTA 1560
Qy 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
Db 1561 CAACGGGTGACTTATCTCCGGGATTAGAGCTACGGCAACACTGGGGTTGCAGATAAAACA 1620
Qy 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
Db 1621 ACCGAAGATTTCGAGGTGAATTACGGTAGGTGAACGGGTGCGCGACAGGTAAAGGGTATTG 1680
Qy 543 HisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAsp 562
Db 1681 CACTGGGAAGTGGTAGCCGACAGATATTGACAACTATCAGGTGCGCTACAGTACGAT 1740
Qy 563 AsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleSerGluGlu 582
Db 1741 AATCTGCTGGCTCCAGCCAGCTTGAACCTGGATAGCGAAGGGCAGATTCTCAGTCAGGAA 1800
Qy 583 GluTyrTrpProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSer 602
Db 1801 GAGTATTATCCGTATGCGGTACCGCGATATGGCGCGGAGAAATCAGACAGAAGCCAGC 1860
Qy 603 TyrLysThrIleAsrGlyTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGly 622
Db 1861 TACAAATTTATCTGTTACTCCGGTAAAGAGCGCGATGCCACTGGATTGTATTATTCGGC 1920
Qy 623 TyrArgTyrTrpGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIle 642
Db 1921 TACCGTTATTATCAACCTTGGGTGGTGCATGTTGAGTGTGATCCGGCGGGAACCGTG 1980
Qy 643 AspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn 662
Db 1981 GATCGGTGGAATTTGTACCGGAATGGTGAGGAATAACCCCATCACTTGACTGACCATGAC 2040
Qy 663 GlyLeuAlaProGluLysGlyLys 670
Db 2041 GGATTAGCACCGCTCTCCAAATAGA 2064

RESULT 14
US-10-754-115-50
; Sequence 50, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 2889
; TYPE: DNA
```

```
; ORGANISM: Xenorhabdus bovienii
US-10-754-115-50

Alignment Scores:
Pred. No.: 1,03e-176 Length: 2889
Score: 2187.50 Matches: 463
Percent Similarity: 67.30% Conservative: 140
Best Local Similarity: 51.67% Mismatches: 213
Query Match: 46.15% Indels: 81
DB: Gaps: 17

US-10-647-956A-6 (1-915) x US-10-754-115-50 (1-2889)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAATGTTTAAATCCAACCTTTATATGCGGTACACCGACTGTCCCGTCATGGACAAT 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGAGGGCTGTGCTGCGGGATATTGCTTATCACCGTACAACAGCAGGAGCAGGCTGAC 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACTCGCATCACCGCCCATCAATACAGTCCCATTAATTTTAAATCGAGACATTTGATCCA 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsn 76
Db 181 CGCTTTTGTGATTGCAATCTCAGACACCATAAACCTAATTTTACCTACTGCTCCTGCC 240
Qy 77 LeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsn 96
Db 241 TTGAAGGGTGATGCTCTACGACAGAGAGTGTGGATGCCGACAAACTGTCAATTTTGAGT 300
Qy 97 AspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArg 116
Db 301 GACATCGAAGGTGCTCGTTTACTGAATATCAGTCCGATGGGTGCTGCTCAAACTGTCGCA 360
Qy 117 TyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGly 136
Db 361 TATGAAGAGATGATACATTCGCGGGCGCTGCTCGTGTCTAGTGAA-----CGGAAGAAT 414
Qy 137 GluLysThrThr-----GluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
Db 415 GAGGCTTCAACACCCCAAAATTTATTGAACGGTTTTATTGGTCGGGAAATAGCCCATCAGAA 474
Qy 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
Db 475 AAAGATCACAAAATTTGGCGGAAATATCTTCGTCATTTATGATACCCGCGGATTAACACAG 534
Qy 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
Db 535 CTTAATGCTGTGCTCTGACACCGGTGGATCTCTCAACATCCCGTCAGTTATTTCAGGAT 594
Qy 193 AsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
Db 595 GATGTACACAGATTTGGAGCGGAAAGTGACGAATCCAGTGGGAAGACGCGACTGAGTAAC 654
Qy 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
Db 655 GACATATTCAACCCGAAATCAACCGCTGATGCGGTTGGCAATTTCTTGACTCAGAAATGAT 714
Qy 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
Db 715 GCCAAAAGCAACACGACCAACGATTGTCTATGATGTGGCAGGCGCATTAAGGCAAGCTGG 774
Qy 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
Db 775 CTGACGATAAAGCCAGAAATGACAGGTGATAGTAATCCCTGACTTACTCCGCGCGCA 834
Qy 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
Db 835 GGGCAGAAACTGGGTGAAGAGCAGGGGTAAACGGCGTTGTCTCACTGAATACTCTCTGAAGCA 894
```


! ORGANISM: Xenorhabdus bovienii
US-11-020-848-3

Alignment Scores:

Pred. No.: 1,03e-176 Length: 2889
Score: 2187.50 Matches: 463
Percent Similarity: 67.30% Conservative: 140
Best Local Similarity: 51.67% Mismatches: 213
Query Match: 46.15% Indels: 81
DB: 10 Gaps: 17

US-10-647-956A-6 (1-915) x US-11-020-848-3 (1-2889)

```
QY 1 MetSerTyrAenSerAlaIleAaspGlnLysThrProSerIleLysValLeuAaspAen 20
DB 1 ATGNATGTTTAAATCAACTTATATATGCGGTACACCGACTGTCCCGTCATGGCAAT 60
QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAasp 40
DB 61 CGAGGGTGTGAGTGGGATATTGCTTATCACCGTACAAACAGCAGGAGAGCGGCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAaspPro 60
DB 121 ACTGCATCACCCGCCATCAATACAGTCCCATTAATTTTAAATCGAGAGCATTTGATCCA 180
QY 61 Arg-----LysAenLysAenGlnSerGlyProAenPheIleArgValPheAen 76
DB 181 CGCCTTTTGTGTAATCTCAGAGCACCATAAACTTAATTTTCACTACTGTCTCTGCC 240
QY 77 LeuAlaGlyGlnValLeuArgGluSerValAaspAlaGlyArgThrIleThrLeuAen 96
DB 241 TTGAAGGTGATGCTTACGACAGAGAGTGTGATGCGGACAAACTGTCTATTTTGTGAT 300
QY 97 AspIleGluSerArgProValLeuIleAenAlaThrGlyValArgGlnAenHisArg 116
DB 301 GACATCAAGGTCTGCTGCTACTCAATATACGTCCGATGGTGTGCTCAAAACACTGGCAA 360
QY 117 TyrGluAaspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGly 136
DB 361 TATGAGAGAGTACATTTGCCGGGGCGCTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCT 414
QY 137 GluLysThrThr-----GluArgLeuIleTrpAlaGlyAenThrProGlnGlu 152
DB 415 GAGGCTTCAACACACCCCAATTTATTGAACGGTTTATTGTTGCGGAAATAGCCATCAGAA 474
QY 153 LysAspTyrAenLeuAlaGlyGlnCysValArgHisTyrAaspThrAlaGlyLeuThrGln 172
DB 475 AAAGATCACATTTGGCGGGAAATATCTTCGTCATTTATGATACCGCGGATTAACCCAG 534
QY 173 LeuAenSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAasp 192
DB 535 CTTAATGCTGTGCTGTGACACCGGTGATCTCTCAATCCCGTCAGTTATTCAGGAT 594
QY 193 AenGlnAaspAlaAaspTyrThrGlyLysGlnSerLeuTrpGlnLysLeuSerSer 212
DB 595 GATGTCACAGCAGATGGAGCGGAAGTGACCAATCCCAAGTGAAGACCGCACTGAGTAAC 654
QY 213 AspValTyrIleThrGlnSerAenThrAaspAlaThrGlyAlaLeuLeuThrGlnThrAasp 232
DB 655 GACATATTCAACACCGAAATCACCGCTGATCGGTTGGCAATTTCTTGACTCAGATGAT 714
QY 233 AlaLysGlyAenIleGlnArgLeuAlaTyrAaspValAlaGlyGlnLeuLysGlySerTrp 252
DB 715 GCCAAAACCAACAGCAACAGATTGCTTATGATGTGGCGGGCAGTTAAAGCGAAGCTGG 774
QY 253 LeuThrLeuLysGlyGlnAlaGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
DB 775 CTGACGATAAAGCCAGAAATGACGAGTATAGTTAACTCCCTGACTTACTCCGCCGCA 834
QY 273 GlyGlnLysLeuArgGluGluHi6LysAenGlyIleValThrGluTyrSerTyrGluPro 292
DB 835 GGGCAGAAATGCGGTGAAGAGCAGGGTAACGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 894
```

```
QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAaspAlaLysValLeuGln 312
DB 895 CAAACCTGGCGTTTGAATAGGTAAACGGCTTACCGCTCAGTCAGATAAAAAAGATTGCGAG 954
QY 313 AspLeuArgTyrGlnTyrAaspProValGlyAenValIleAenIleArgAenAaspAlaGlu 332
DB 955 GATCTTGTCTATAAATCTATGATCGGTCGGTATCTCTGAATATTCGCAATATGAGCAGAG 1014
QY 333 AlaThrArgPheTyrArgAenGlnLysValAlaProGluAenSerTyrThrTyrAaspSer 352
DB 1015 GCACCCGCTTCTGGCGTAAATCAGATAGTAGAACACAGACCACTATGCTTATGACTCG 1074
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGlnGlnAenAen 372
DB 1075 CTTTATCAATCATCATGCTAGTGTGTCAGAAATCGCCAGTATCGGTACAGCGGCGAGC 1134
QY 373 GlnLeuProSerPro-----AlaLeuProSerAaspAenThrTyrThrAenTyrThr 390
DB 1135 CGGCTGCTGTACCGAATATTCCTCTCTGCAATGACGATGTTTATCTCCTGCTACACC 1194
QY 391 ArgSerTyrSerTyrAspHisSerGlyAenLeuThrGlnIleArgHisSerProAla 410
DB 1195 CGCAGATATCACTATGATCGCGTGAATCTCTGCAGATCCGCGATTCGCGTCTCTGCT 1254
QY 411 ThrGlnAenAenTyrThrValAlaIleThrLeuSerAenArgSerAenArgGlyValLeu 430
DB 1255 ACAGATAATAAGTACACCAACAAAGATCAACCGTATCGAATCGTAGTAATCGTGCAGTATGG 1314
QY 431 SerThrIleuThrThrAaspProAenGlnValAaspThrLeuPheAaspAlaGlyGlyHisGln 450
DB 1315 GATACCTTGACACACATCCGCAAGTGGATACCCCTGTTTATCATGAGGGGCGATCAA 1374
QY 451 ThrSerLeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGluLeuLysGlnVal 470
DB 1375 CTTCAACTCAGTCAGCCAGACTTATGTTGGAATCTCGGGTGAATCTACAGCAATA 1434
QY 471 -----AenAenGlyProGlyAen---GluTyrTyrArgTyrAaspSerAen 484
DB 1435 ACAAGATACACGGGTGACGAAACCCGAGATAAAGAGCGGTATCGCTATGTTGTTGG 1494
QY 485 GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThrGlnGlnGlnArg 504
DB 1495 GCTGCGCGGTGCTGAAATTCAGCACACAGCAGCGGGGGAGAGCAGCCATGTGCGACGT 1554
QY 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAlaThrThrThrGlu 524
DB 1555 GTTGTATTATCGCGGGTTGGAATCTACGCAACACTCAGCATGATGCGACATTAATCGAA 1614
QY 525 GluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrp 544
DB 1615 GACTTACAGGTGATTATCATGGGTGAAGCAGGACGTGCTCAGGTACGCTACTTCATTGG 1674
QY 545 GluSerGlyLysProGluAaspValAenAenAenGlnLeuArgTyrSerTyrAaspAenLeu 564
DB 1675 GAAATACACACCGCGATATCTTAAATGACTCACTGCGTTACAGTACGATAGTTG 1734
QY 565 IleGlySerSerGlnLeuGluLeuAaspAenGlnGlyGlnIleIleSerGluGluGluTyr 584
DB 1735 ATGGGTTCCAGTCAGCTTGAATTTGGATGGAGCGGCGAGATTTATACGAGGAAGATAC 1794
QY 585 TyrProPheGlyGlyThrAlaLeuTrpAlaAenSerGlnThrGluAlaSerTyrLys 604
DB 1795 TACCCCTATGAGGTACAGCAATATGGCGGCAAGAAACCCAGACCGAAGCAATACAA 1854
QY 605 ThrIleArgTyrSerGlyLysGluArgAaspAlaThrGlyLeuTyrTyrTyrGlyArg 624
DB 1855 ACCATTGCTACTCCGCAAGAGCGGTGATGCGACGGGGCTTTTATTACTACGGGCACTG 1914
QY 625 TyrTyrGlnProTrpAlaGlyArgTyrLeuSerAlaAaspProAlaGlyThrIleAaspGly 644
DB 1915 TATTATCAGCGGTGCTAGGGCGCTGTTGAGCGCAGATCCCGCGGAACCGTGGACGGA 1974
QY 645 LeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAaspGluAenGlyLeu 664
```


This page blank (every)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 23:16:20 ; Search time 281 Seconds
(without alignments)
1596.057 Million cell updates/sec

Title: US-10-647-956A-6
Perfect score: 4740
Sequence: 1 MSYNSAIDQKPSIKVLN.....EAINRSAIAENLGMRTS 915

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlp
-Q=/cgn2_1/USPTO.spool.p/US10647956/runat 12122005 091822 29856/app query.fasta_1.1095
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINLEN=0
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ext -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10647956.CGN 1 184 @runat 12122005 091822 29856
-NCPU=6 -ICPU=3 -NO MAP -LARGESUB -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	4740	100.0	2745 6 US-10-647-956A-5
2	169	3.6	3840 6 US-10-793-626-3187
C	3	166.5	3.5 3543 6 US-10-793-626-4149
	4	166	3.5 3285 6 US-10-793-626-3153
	5	166	3.5 3730 6 US-10-793-626-3499
	6	163.5	3.4 3626 6 US-10-821-234-245
C	7	163.5	3.4 7786 9 US-11-096-051-3
	8	163.5	3.4 8362 9 US-11-096-051-1

9	163.5	3.4	8645	9	US-11-096-051-9	Sequence 9, Appli
10	163.5	3.4	8657	9	US-11-096-051-7	Sequence 7, Appli
C	11	144	3.0	3068	6	US-10-793-626-3824
	12	144	3.0	15071	6	US-10-793-626-2963
	13	143.5	3.0	8354	7	US-11-113-424-13
	14	136.5	2.9	3055	6	US-10-793-626-4075
C	15	135.5	2.9	6921	6	US-10-623-158-117
	16	132	2.8	3204	6	US-10-793-626-3940
	17	131.5	2.8	2307	7	US-11-055-557-17
	18	130.5	2.8	2796	6	US-10-793-626-4335
C	19	130.5	2.8	3520	6	US-10-793-626-4160
	20	130.5	2.8	7551	6	US-10-647-956A-1
	21	130	2.7	2305	6	US-10-485-517-389
	22	130	2.7	16792	6	US-10-995-561-262
C	23	130	2.7	17292	6	US-10-995-561-260
	24	130	2.7	17507	6	US-10-995-561-254
	25	130	2.7	17610	6	US-10-995-561-258
	26	130	2.7	17642	6	US-10-995-561-256
C	27	130	2.7	19023	6	US-10-995-561-259
	28	129.5	2.7	2947	6	US-10-793-626-3805
	29	129.5	2.7	3867	6	US-10-793-626-3769
	30	129.5	2.7	6159	7	US-11-013-759-8
C	31	129	2.7	2580	7	US-11-189-521-1
	32	129	2.7	3016	7	US-11-189-521-3
	33	129	2.7	4167	6	US-10-467-657-333
	34	129	2.7	11447	7	US-11-186-284-25
C	35	128.5	2.7	2307	7	US-11-055-557-5
	36	127.5	2.7	6942	7	US-11-013-759-10
	37	127	2.7	1752	6	US-10-793-626-1357
	38	127	2.7	2304	7	US-11-055-557-9
C	39	127	2.7	17436	6	US-10-995-561-257
	40	126.5	2.7	2307	7	US-11-055-557-3
	41	125.5	2.6	2307	7	US-11-055-557-7
	42	125.5	2.6	2820	6	US-10-510-386-9
C	43	125.5	2.6	4181	6	US-10-909-125-1738
	44	125	2.6	2304	7	US-11-055-557-1
	45	125	2.6	2304	7	US-11-055-557-13

ALIGNMENTS

RESULT 1
US-10-647-956A-5
; Sequence 5, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: french-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647, 956A
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817, 514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2745)
US-10-647-956A-5
Alignment Scores:
Pred. No.: 0 Length: 2745
Score: 4740.00 Matches: 915
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-647-956A-6 (1-915) x US-10-647-956A-5 (1-2745)			
Qy	1	MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGAGCAGTTACAAATCTGCANITGACCAAAAGACCCCTCGATTAAAGGTATTAGATPAC	60
Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Db	61	AGGAAATTAATGTACGTACTTTAGATAATCTACGCACCTCAAGCTGACGAAACAGTGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	GAATTAATACGTTCTATGAGTTCAATATTTCGCGGATTTTCAGGTAAAGACCCGATCCT	180
Qy	61	ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Db	181	CGTAAATAATAAACACAGACGCGCCCAATTTCAATTCGTGTCITTAATCTTTCGCGGTCAA	240
Qy	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Db	241	GTITTTACGTGAAGAAAGTGTGATGTCGCGTCCGACTATTACCTCAATGATATTGAAAGT	300
Qy	101	ArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAenAsn	120
Db	301	CGCCCGGTGTGATCATCAATGCAACCGGTGTCGCCAAACCAATCGTTATGAAAGATAAC	360
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
Db	361	ACCTTCCTCGGTGCTGCTCGCTATCACCAGAACAGTACAGGACGAGAGAAACGACC	420
Qy	141	GluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Db	421	GAACGTCTTATCTGGCGCGCAATACGCGCAAGAAAGATTACAACTTCGCGGTGCG	480
Qy	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Db	481	TGTCGCGCATACGATACGCGGGACTTACTCAACTCAATAGCCTTTCTCTGGCTGGC	540
Qy	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAspAlaAspTrpThrGly	200
Db	541	GTCTGTCTATCACAACTCTCAACAACCTGCTTACCGATTAACAGGATGCCAGTCGACAGGT	600
Qy	201	GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Db	601	GAAGACCAGACCTCTGGCAACAAAACCTGAGTAGTGTCTATATATACCCCAAGTAAC	660
Qy	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeu	240
Db	661	ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGCAACATTCAGCGGCTG	720
Qy	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db	721	GCCATATGATGGCGGGCAGCTAAAGGGAGTTGGTTAACTCAAGGTCGACGCGGAA	780
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis	280
Db	781	CAGGTGATTATCAATCGCTAACCTACTCCGCGCGGGCAAAAATTAACGTGAAGAGCAC	840
Qy	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	841	GGTAACGGGATGTCTACTGAATACAGCTPACGAACCGGAAACCCACCGCTTATCGGCATT	900
Qy	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Db	901	ACCACTCGCGGTCCATACAGACCGCAAGGTGTGAAGACCTTACGCTATCAATATGACCCA	960
Qy	321	ValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArgPheTrpArgAenGln	340
Db	961	GTAGGCAATGTCAITTAATATCCGTAAATGATGCGGNAGCCACTCGCTTTTGGCGCAATCAG	1020

Qy	341	LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Db	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCAC	1080
Qy	361	GlyArgGluMetAlaAsnIleGlyGlnGlnAenAsnGlnLeuProSerProAlaLeuPro	380
Db	1081	GGGCGGGAATGGCCAATATCGGTACGAAAAACAACCAACTTCCCTCCCTCGGTACCT	1140
Qy	381	SerAspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAen	400
Db	1141	TCTGACAAACAATACCTACACTAACTATCTCGCAGCTACAGCTATGATCACAGTGTAAAT	1200
Qy	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr	420
Db	1201	CTACGCCAAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCAC	1260
Qy	421	LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Db	1261	CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCAACCGATCCAAATCAAGTG	1320
Qy	441	AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db	1321	GATACGTTGTTGATCGCGTGTGTCACCAAAACCACTTATATACCCGACAGACACTATC	1380
Qy	461	TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg	480
Db	1381	TGACACACCGAGAGAGTTAAAGCAGGTTAATAATGGCCGGGAAATAGTGTGTACCG	1440
Qy	481	TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Db	1441	TACGACAGCAACCGCATGAGCAACTGAAAGTGAGTGAACAGCAACCCAGATACTACG	1500
Qy	501	GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla	520
Db	1501	CAGCAACAACCGGTAAATCTATTTGCGGGACTGAGCTACGCAACAACCCAGAGCAACGC	1560
Qy	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db	1561	ACAACAACGGAAGATTACACGTTATCACACTCGGTGAAGCCGTCGCGCACAGGTACGG	1620
Qy	541	ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAsnGlnLeuArgTyrSer	560
Db	1621	GTCTTGCACTGGGAGAGCGGTAAAGCAGCAAGATGTCAACAATAATCAACTACGTTACG	1680
Qy	561	TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer	580
Db	1681	TACGATAATCTGATCGCTCCAGCCAGCTTGAACCTGACAAACCAAGSACAAATTTATCAG	1740
Qy	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Db	1741	GAGGAAGAGTATTATTCATTTCGCGGACAGCCCTGTGGCAGCAAAACACCAACAGAA	1800
Qy	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Db	1801	GCCAGCTATAAAACGATTCCGTATTCGCAAAAGAACGAGATGCCACCGGTTGTTAT	1860
Qy	621	TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly	640
Db	1861	TACGTTATCGTTATTACCAACCGTGGCGCGCAGATGGTTAAGCGCGGACCCCGCAGGA	1920
Qy	641	ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp	660
Db	1921	ACCATTTGATGGGTGAATCTATACCGGAATGGTAAAGAAATAATCTGTGAGTTTACAAGAT	1980
Qy	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPhePheAspGlu	680
Db	1981	GAATAATGATTAGCGCCAGAAAAAGGAATATACCAAGAGGTAAATTTCTTTTGTATGAA	2040
Qy	681	LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Db	2041	TTAAAAATTCAAATGGCAGCCAAAAAGTTTCACTGTTGTCAATGGAACGAGAAAGAGAGC	2100

QY 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
 DB 2101 AGTTATACAAAATAAATCAATGAAAGGTGTCGTGCGTGAATCCGATCCGTCGGGT 2160
 QY 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
 DB 2161 TATTGCTAAGCCACGAGAGTACTAAAGGTATAGAAAAAGTCAATCATATATAGC 2220
 QY 741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
 DB 2221 CGACTTGAAGAAAAACAGCTCCCTTTTCAGAAAAATCAAAAAAGCAATCTTCTTAGGATCT 2280
 QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
 DB 2281 GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAAATATGCCGAGAG 2340
 QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
 DB 2341 CATAAATATAGAGTAAATCAACCTGATTTTATTCAGAAACCGATTTCTTGGCTTAATG 2400
 QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
 DB 2401 GATAAAGTGAATAAATAATGATTATCCGGTGAAGAAAAAATTTATCGGCAATGGAGGTT 2460
 QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
 DB 2461 AAGGTTTATCATGATTATTAATAAATAAACAATCAAGATTAATCATGCAATGCAATGGCC 2520
 QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
 DB 2521 CATCCCTATACGCAATGAGTATAGAAAGAGCGCTGTTGCAAGAACAGAACCCGCT 2580
 QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
 DB 2581 ATTGCAATAGATAGAGATATAATTTCAAAGGTGTTGGCAATTCCTGCAATGAAAGCA 2640
 QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
 DB 2641 ATTAATAAATCATTTGAAGGACATAAATAATTAATAGGATATCAACAGAGGCTATTATATT 2700
 QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
 DB 2701 CGCTCTGGCGCTATCGCTGAGAAATTTAGGAATCGGAGAACTTCA 2745

RESULT 2

US-10-793-626-3187
 ; Sequence 3187, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3187
 ; LENGTH: 3840
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-3187

Alignment Scores:

Pred. No.: 0.000275 Length: 3840
 Score: 169.00 Matches: 175
 Percent Similarity: 36.34% Conservative: 175
 Best Local Similarity: 18.17% Mismatches: 369
 Query Match: 3.57% Indels: 244

DB: 6 Gaps: 42
 US-10-647-956A-6 (1-915) x US-10-793-626-3187 (1-3840)
 QY 9 AspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAsnValArgThrLeu 28
 DB 871 GATGCAAAACCTGAGCTATAGATACGATACTATATTCACGCAATATTGTCAAAAAAA 930
 QY 29 GluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPhe 48
 DB 931 CCATCCGCTCGAGTGGAAATTAGATTCAAAGTTTGAGGATTTAAAGCGT----- 978
 QY 49 AsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGly 68
 DB 979 -----CAAATCAATGCAACG-----CCCAATGCTACACAAGAAAGAAACAACAA 1020
 QY 69 ProAsnPheIleArg-----ValPheAsnLeuAlaGlyGlnVal 81
 DB 1021 GATGCAATTCAAAGATTGAATGGTAAAGAGATGAAGTTAAGNATCTAATAATCAAGAT 1080
 QY 82 LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArg 101
 DB 1081 AGACGTGCAATGCAAGTTGCAACAGCACAAAAATATTGGACTTCACGAATTAGAAACG-- 1137
 QY 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
 DB 1138 -----ATTCATGCTAATCCAACTAGAAAATCTGATCGCTCCAAGAG----- 1179
 QY 122 LeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGlu 141
 DB 1180 TTACAACCTAAATTTATTTTCAACAACAGAGTTAATTAATAATAACAAGATGCACTAAT 1239
 QY 142 ArgLeuIleThrPalaglyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
 DB 1240 -----GAAGAAAAAGATGAA-----GCCAAACGACTT 1266
 QY 162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
 DB 1267 CTTGAGATTAGTAAAAATAAACTATACAAATATCAAT----- 1305
 QY 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGlu 201
 DB 1306 -----CHAGGCCAATTAATAATCAA---GTTGAT---AATGCTAA 1341
 QY 202 AspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr 221
 DB 1342 GATAACGGCATG-----AATGAGATTGCTACCAATAATACCAGCAACAACAATTAAACA 1395
 QY 222 AspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAla 241
 DB 1396 GATGCAAAACCGCTATTGATAAAAAAGCTGAGCAACAAGTTACATCATCAATGGTAAC 1455
 QY 242 TyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGluGln 261
 DB 1456 AACGATGCAACAGATGAAGAAAAAGCAGAGGCTAGAAAGCTGTTGAAAAGCGAAAT 1515
 QY 262 ValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHisGly 281
 DB 1516 GAAGCCAAATCTAATATTACAATAGTATCTGAAGGGAAGTCAATGGTGTCAAAACC 1575
 QY 282 AsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIleThr 301
 DB 1576 AATGGGTTAGAAAAATAAAACAATATTCACCTCACTCAA----- 1617
 QY 302 ThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProVal 321
 DB 1618 ACTAAACCAAAATGCTAAGCAAGAAATAAATGACAAAGCTCAAGAACAA----- 1665
 QY 322 GlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLys 341
 DB 1666 -----TTAATCCAAATTAATACAGCGCTGATGCACCGAAGAAAGCAAGAG--- 1716
 QY 342 ValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGly 361


```
Db 1717 -----GCAACAAT 1725
Qy 362 ArgGluMetAlaAenIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuProSer 381
Db 1726 AGATCAATGCTGATTAGACAA-----GCAATACAAAT 1761
Qy 382 AspAenAenThrTyThrAenTyThrArgSerTyThrArgSerTyThrArgSerGlyAsnLeu 401
Db 1762 ATTAATATGCACATAGT-----ACTCAAGAAGTAATGAATCTAAACAATAGTATT 1815
Qy 402 ThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyThrValAlaIleThrLeu 421
Db 1816 GCTACATCAAGAGTGATACACCCCAATGTGATCAAAAACCGACT----- 1860
Qy 422 SerAenArgSerAenAArgGlyValLeuSerThrLeuThrThrAenProAenGlnValAsp 441
Db 1861 -----GCTATAAATAGTTTGACTCAAGAAGCTAATAATCAAAAG 1899
Qy 442 ThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrp 461
Db 1900 ACGTTAATAGTAATGATGTAATGCTACTGAT----- 1932
Qy 462 ThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyArgTy 481
Db 1933 GATCAAAAAGAGGCTGCAGAACATATTAGTACCCCAAAAATAATGAACAATTCAA-- 1989
Qy 482 AspSerAenGlyMetAArgGlnLeuLysValSerGluGlnProThrGlnAenThrThrGln 501
Db 1990 -----AAAATTCATGAAAGTACACAAGATCAAGTTGAT 2025
Qy 502 GlnGlnArgValIleTyLeuProGlyLeuGluLeuAArgThrGlnSerAsnAlaThr 521
Db 2026 AACGTAAAGCACAAAGCTATCACTGCAATTAATG-----ATTAATGCAATGACAT 2079
Qy 522 ThrThrGluGlu-----LeuHisValIleThr--LeuGlyGluAlaGlyAArgAlaGlnVal 539
Db 2080 AAAAGACAGATGCATTAATATTGCTACTTAATCTAGCTGAAGTAATAAATCATCATATA 2139
Qy 540 ArgValLeuHisTrpGluSerGlyLysProGluAspValAen----- 553
Db 2140 AGAGCCAAT-----CAAGATGCAACTACTGAAGAAAAAATACGGCAATCAATCTATA 2193
Qy 554 AsnAenGlnLeuAArgTyThrSerTyAspAenLeuIleGlySerSerGlnLeuLeuAsp 573
Db 2194 GATGATAGCTTAGCACAGCAGTAAACAATTAATGCTGCA----- 2235
Qy 574 AsnGlnGlyGlnIleIleSerGlu-----GluGluTyTyThrProPheGlyGlyThrAla 591
Db 2236 AATACAAATGCTTAGTGATGAGAAATTTAGAGATGGTAGCAAAAAGTTACACGTTATT 2295
Qy 592 LeuTrpAlaAenSerGlnThrGluAlaSerTyLysThrIleAArgTySerGlyLys 611
Db 2296 GTGTTGTCAACTCAAACTAAAACACAGCTAAAGCAGACATTTGCTCAAGCAATAGGTCAA 2355
Qy 612 GluArgAspAlaThrGlyLeuTyTyTyThrGlyTyArgTyTyThrGlnProTrpAlaGly 631
Db 2356 CAAAGG----- 2361
Qy 632 ArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAenLeuTyArgMetVal 651
Db 2362 -----TCGACATAGAC----- 2373
Qy 652 ArgAenAenProValSerLeuGlnAspGluAenGlyLeuAlaProGluLysGlyLysTy 671
Db 2374 -----CAGAAATCAAAATGCTACACAGAGAAAAACAAGAGCC 2412
Qy 672 ThrLysGluValAen-----PhePheAspGluLeuLysPheLysLeuAla 686
Db 2413 CTTGAGAGACTTAATCAAGAAACAAATGGAGTCAATGATAGAAATACAGCAGCTTTAGCA 2472
Qy 687 AlalysSerSerHisValValLysTrpAenGluLysGluSer----- 700
```

```
Db 2473 AATCAAAAATGTTACAGCAGAAAAAATAATATATTAGAAACAATAAGAAATGTTGAACCT 2532
Qy 701 ---SerTyThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSer 719
Db 2533 ATTGTAAATTGTAAACCAAAGCTAATGAAATAATATTAGAAAAAAAAGCTGGGAAACACG 2592
Qy 720 GlyTyLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTy 739
Db 2593 ACTTTAATAAATCAAAATCAAGATGCGACA-----CTAGAAGAAAAACAATAGCATT 2646
Qy 740 SerArgLeuGluGlu-----AenSerSerLeuSerGluLysSerTyThrAsnLeuSer 757
Db 2647 GCGAAATTAGAAGAGTAAAGAGTGAAGCGTTAAATCAAGTATCATCAGGACACAC- 2700
Qy 758 LeuGlySerGluIleSerGlyTyMetAlaArgThrIleGlnAenThr 773
Db 2701 -----TCAATAATGATGCAAAATTTGTGAAAAAATAATGGAATGCTAAA 2745
Qy 774 IleSerGluTyThrAlaGluGluHisLysTyArgSerAsn-----HisPro 788
Db 2746 ATTCTGAGGTCCATCCTGAGACTATAATTAACGTAATGCTAAACAAGAAATGAACAA 2805
Qy 789 AspPheTySerGluThrAspPheAlaLeuMetAspLysSerGluLysAsnAspTy 808
Db 2806 GATCGCAAGTCAAATGATACTATCAATGCAATAATAATAATCAACTAATGAAGAAAA 2865
Qy 809 SerGlyGlu-----ArgLysIleTyAla 816
Db 2866 TCAGCGCTATAGATAGATTAAATGAGCTAAAATTTGATGCTATTAAACAATATTACTAAT 2925
Qy 817 AlaMetGluValLysValTyHisAspLeuLysAsnLys----- 829
Db 2926 GCTACAACACTACACAATAGTTAATGATGCTAAAATAGTGGTAACACGAGTATTAGCCAA 2985
Qy 830 -----GlnSerGluLeuHisValAsnTyAlaLeuAlaHisProTyThrGlnLeu 846
Db 2986 ATATTACCAAGTACAGCAGTCAAAACTAAT---GCATTAGCAGCTCTAGCTAGCGAAGCT 3042
Qy 847 SerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspAspGlu 866
Db 3043 AAAAAT---AAAAACGCTAATAGATCAAAACACCAAAATCGCAGACGAGAGAAAAAGAA 3099
Qy 867 TyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLys 886
Db 3100 GAAGCAATAATAAAGTTGATGCT---CTTCAAGAGAGACGAGTGTCTAATATCTTAAAA 3156
Qy 887 GlyHis-----LysIleAenAArgIleSerThrGluAlaIle---AsnIleArgSer 902
Db 3157 GCACACACTACTGATGAAGTTAATAATATTAAAAATCAAGCTGTTCAAAATATTAAAGCT 3216
Qy 903 AlaAlaIle 905
Db 3217 GTTCAAGTT 3225
RESULT 3
US-10-793-626-4149/c
; Sequence 4149, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4149
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

! OTHER INFORMATION: Description of Artificial Sequence: synthetic
! OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4149

Alignment Scores:

Pred. No.: 0.000408 Length: 3543
Score: 166.50 Matches: 173
Percent Similarity: 36.23% Conservative: 173
Best Local Similarity: 18.12% Mismatches: 366
Query Match: 3.51% Indels: 243
Gaps: 6

US-10-647-956A-6 (1-915) x US-10-793-626-4149 (1-3543)

QY 9 AspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAsnValArgThrLeu 28
DB 2344 GATGCAAACTGAGGCTATAGATACGATACTAATATTCAACCAATGTTGCAAAAAA 2285
QY 29 GluTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPhe 48
DB 2284 CCATCGCTCGAGTGAATTAGATTCAAAGTTTGAGGATTTAAAGCGT----- 2237
QY 49 AsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGly 68
DB 2236 -----CAATCAATGCAACG-----CCCAATGCTACAGAAGAAACAA 2195
QY 69 ProAsnPheIleArg-----ValPheAsnLeuAlaGlyGlnVal 81
DB 2194 GATGCAATCAAGATTGAATGCTAAAGAGATGAAGTTAAGATCTAATAATCAAGAT 2135
QY 82 LeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArg 101
DB 2134 AGACGTGACAATGAAGTTGAACAGCACAAAAATATTGCACTTCAAGAAATTAGAAACG-- 2078
QY 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
DB 2077 -----ATTGATGCTAATCAACTAGTAAATCTGATCGCTCCAAAGAG----- 2036
QY 122 LeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGlu 141
DB 2035 TTACAACTAAATTTATTTACAAACAGAGTTAATTAAATAAACAAGATGCACTAAT 1976
QY 142 ArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
DB 1975 -----GAAGAAAGAGATGAA-----GCCAAACGACTT 1949
QY 162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuLeuAlaGlyVal 181
DB 1948 CTTGAGATTAGTAAAAATAAACTATAACAAATATCAAT----- 1910
QY 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGlu 201
DB 1909 -----CAAGCGCAACTAATAATCAA-----ATTGAT---AATGCTAAA 1874
QY 202 AspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr 221
DB 1873 GATAACGGCATG-----AATGAGATTGCTACCATTAATACCAACAACAATTAACAA 1820
QY 222 AspaIleThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAla 241
DB 1819 GATGCAAAACGGCTATTGATATAAAAGCTGACCAACAGTTTCAATCATCAATGGTAAAC 1760
QY 242 TyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGluGln 261
DB 1759 AACGATGCAACAGATGAAGAAAGACGAGGCTAGAAAGCTGGTTGAAAAGGCGAAAT 1700
QY 262 ValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHisGly 281
DB 1699 GAAGCCAAATCTAATATTACAAATAGTGATACTGAAAGGGAAGTCAATGGTGTGTAAC 1640
QY 282 AsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleThr 301
DB 1639 AATGGGTTAGAAAAATAAACAAATATTCAACCACTCACTCA----- 1598

QY 302 ThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspProVal 321
DB 1597 ACTAAACCAATGCTAAGCAAGAAATAAATGCAAAAGCTCAAGACAA----- 1550
QY 322 GlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLys 341
DB 1549 -----TTAATCCAAATTAATACACGCTGACCAAGCAAGAAAGCAAGAG--- 1499
QY 342 ValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThrGly 361
DB 1498 -----GCACCAAT 1490
QY 362 ArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuProSer 381
DB 1489 AGAGTCAATGCTGGATTAGCACAA-----GCAATACAAAT 1454
QY 382 AspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeu 401
DB 1453 ATTAATAATGCCATAGT-----ACTCAAGAGTAATGAATCTAAACAAATAGTATT 1400
QY 402 ThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeu 421
DB 1399 GCTACATCAAGAGTGACACCAATGCTGATCAAAAAACCGACT----- 1355
QY 422 SerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAsp 441
DB 1354 -----GCTATAATAGTTGACTCAAGAGCTAATATCAAAAG 1316
QY 442 ThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleTrp 461
DB 1315 ACGTTTAATAGGTAATGATGCTACTGAT----- 1283
QY 462 ThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArgTyr 481
DB 1282 GATGAAAAAGAGCTGCAAGCAATTAGTGACCAAAATTAATGAACAAATTCAA--- 1226
QY 482 AspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrGln 501
DB 1225 -----AAATTCATGAAGTACACAAAGTAAATCAAGTTGAT 1190
QY 502 GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThr 521
DB 1189 AACGTAACAGCACACAGCTATCCTGCAATTAATG-----ATTAATGCAATGCACAT 1136
QY 522 ThrThrGluGlu---LeuHisValIleThr---LeuGlyGluAlaGlyArgAlaGlnVal 539
DB 1135 AAAGACAAAGATGCCATTAATATTTGACTAATCTAGCTGNAAGTAATAAATCAGATATA 1076
QY 540 ArgValLeuHisTrpGluSerGlyLysProGluAspValAsn----- 553
DB 1075 AGAGCCAAT-----CAAGATGCAACTACTGAAGAGAAAAATACGGCAATACATCTATA 1022
QY 554 AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp 573
DB 1021 GATGATACGTTTACCAACAGCAGCTAACAATTAATGTTGTCGA----- 980
QY 574 AsnGlnGlyGlnIleIleSerGlu-----GluGluTyrTyrProPheGlyGlyThrAla 591
DB 979 AATACAAATCGGTTAGTGGATGAGATTTAGAGATGGTAAGCAAAAGTTACACGCTATT 920
QY 592 LeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLys 611
DB 919 GTGTTGCTCAACTCAAACTAAACACAAAGCTAAAGCAGACATTGCTCAAGCAATAGTCAA 860
QY 612 GluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGly 631
DB 859 CAAAG-----TCACATAGAC----- 842
QY 632 ArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetVal 651
DB 853 -----TCACATAGAC----- 842

```
Qy 652 ArgAsnAenProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyr 671
Db 841 -----CAGAAATCAAAATGCTACACAGAGAGAGAGAGAGAGAGAGCC 803
Qy 672 ThrLysGluValAen-----PhePheAspGluLeuLysPheLysLeuAla 686
Db 802 CTTGAGAGACTTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
Qy 687 AlalysSerSerHisValValLysTyrAsnGluLysGluSer----- 700
Db 742 AATCAAAATGTTACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683
Qy 701 ---SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSer 719
Db 682 ATTGTAATTGTAAACCAAGAGCTTAATGAATAATTAAGAGAGAGAGAGAGAGAG 623
Qy 720 GlyTyrLeuLeuSerHisGluGluLeuLysGlyLeuGluLysSerGlnLeuLys 739
Db 622 ACTTTAATAAATAAATCAAGATGCGACA-----CTAGAAGAGAGAGAGAGAG 569
Qy 740 SerArgLeuGluGlu-----AenSerSerLeuSerGluLysSerLysThrAsnLeuSer 757
Db 568 GGCAGAAATTAGAGAGAGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 515
Qy 758 LeuGlySerGluLysSerGlyTyrMetAlaArgThrIleGlnAspThr----- 773
Db 514 -----TCAATAATGATGTGAATAATGTTGGAATAATATGGAATGTCTAAA 470
Qy 774 IleSerGluTyrAlaGluGluHisLysTyrArgSerAen-----HisPro 788
Db 469 ATTTCTGAGGTCCTCCTGAGACTATAATTAAGAGCTAATGCTAAACAGAGAAAT 410
Qy 789 AspPheTyrSerGluThrAspPhePheAlaLeuMetAspLysSerGluLysAenAspTyr 808
Db 409 GATCGCAAGTCAAAATGATCTATCAATGCAAAATAATAATACTAATGAAGAGAAA 350
Qy 809 SerGlyGlu-----ArgLysIleTyrAla 816
Db 349 TCAGCCGCTATAGATAGATTAAATGCTAGCTAAATGATGCTATTAACTAATTA 290
Qy 817 AlaMetGluValLysValTyrHisAspLeuLysAenLys----- 829
Db 289 GCTACAACTACACAAATAGTTAATGATGCTAAAAATAGTGGTAAACAGAGATT 230
Qy 830 -----GlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeu 846
Db 229 ATATTACCAAGTACAGCAGTCAAAACTAAT---GCATTAGCAGCTCTAGCTAGC 173
Qy 847 SerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArgGlu 866
Db 172 AAAAAAT---AAAAACGCTTAAATAGTCAACACCAAAATGCGACGAGAGAGAGAA 116
Qy 867 TyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLys 886
Db 115 GAAGCAAAATAATAAGTTGATCGT---CTTCAAGAGAGAGAGAGAGAGAGAGAG 59
Qy 887 GlyHis-----LysIleAsnArgIleSerThrGluAlaIle 898
Db 58 GCACACACTACTGATGAAGTTTAATAATAATAATAATAATAATAATAAGCTGTT 14
RESULT 4
US-10-793-626-3153
; Sequence 3153, Application US/10793626
; Publication No. US20050253478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3153
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3153
```

```
Alignment Scores:
Pred. No.: 0.000407 Length: 3285
Score: 166.00 Matches: 204
Percent Similarity: 35.50% Conservative: 151
Best Local Similarity: 20.40% Mismatches: 413
Query Match: 3.50% Indels: 232
DB: 6 Gaps: 45
```

US-10-647-956A-6 (1-915) x US-10-793-626-3153 (1-3285)

```
Qy 8 IleAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeuAenValArgThr 27
Db 331 TTTAAAGAGCAAAATCCAAGTGTAGCTGATGTCAACAATGCACATAAATAAGTAAGAGAA 390
Qy 28 LeuGluTyrLeuArgThrGlnAla-----AspGluAenSerAsp 40
Db 391 GTACACAAAAATTAACGAGCCAGACGACCTTTACAAAAATAAGAGATAATAGTGCA 450
Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db 451 CTAGTTGCGAGCCAAAGAACAACTTCAACAGCGCAGTTGACCAAGTCCCTTCCACAGAGAGT 510
Qy 61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80
Db 511 ATGACGCAACAACTAAAGATGAT-----TACAAATTCAAAACAACAA 552
Qy 81 ValLeuArgGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer 100
Db 553 GCTGCTCAACAGAGAAATATCAAAAGCACAACAGTTATCGATAATGCGGATGCGACTACA 612
Qy 101 ArgProValLeuIleIleAenAla---ThrGlyValArgGlnAenHisArgTyrGluAsp 119
Db 613 CAACAA-----ATTTCTAACGCCAAACAAATGTTGAACGCGCTTTTAGAAGCATTAAT 666
Qy 120 AsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGln---AlaGlyGluLys 138
Db 667 AATGCAAAACTGGT---TTAAGAGCAGATAAAGAGAACTTCAAAATGCTATATATCA 723
Qy 139 ThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGlu---LysAspTyrAsnLeu 157
Db 724 TTAACCTCAAAATATTGATACGCGGTAAACGCGCTGCAAGTATCAGAGAAATACAATGAA 783
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSer 177
Db 784 GCTAAGTCAGCTATTCAA-----ACTCAAATTGATTACGTAGCTAAA 822
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThr---AspAen---GlnAsp 195
Db 823 -----AATAAGCAACAAACAGTATTTTAAACAATGAACATCTCCTCAAGTA 864
Qy 196 AlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyr 215
Db 865 TCACAGTGACTGCTGCGTTAAACAAAAATAAAGCTGTTCAACCTGATTAATAGATAAAGCG 924
Qy 216 IleThrGln---SerAenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLys 234
Db 925 ATAGCAATGCTTAAAAATAAGAGATAATAATATGCTATGTT-----CAAGCGAAA 975
Qy 235 GlyAsnIleGlnArgLeuAlaTyrAspVal-----AlaGlyGlnLeu 248
Db 976 CAACAACCTTCAACAATTTGTAATGATAGATAGATCCACACAGGCATGACACAGATACT 1035
Qy 249 LysGlySerTrpLeuThrLysGlyGlnAlaGluGlnValIleLysSerLeuThr 268
```

Db 1036 GCTAATAACTATATAAATCAAAAAACGCTGAAGCTGAAGATGAATAA 1080
QY TyzSerAlaAlaGlyGlnLysLeuArgGluHisGlyAsnGlyValThrGluTyr 288
Db 1081 -----CAAAAGCTCAACAATCATTAACCAATGGCGATGCGCATGAGCAA 1125
QY SerTyGluProGluThrGlnArgLeuLeuGlyLeuThrArgArgProSerAspAla 308
Db 1126 CAAATTAATAACGAAAACAAATAGA----- 1149
QY LysValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValLeuAsnLeuArg 328
Db 1150 -----GTAATCAACGCGATTAAATGAATA 1173
QY AsnAspAlaGluAlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsnSerTyr 348
Db 1174 AAC-----AAAGCAAAAACGATTACGCTGCTGATTAAGTCTCAATTTGGAAATGCT--- 1224
QY ThrTyAspSerLeuTyrGlnLeuLeuSerAlaThrGlyArgGluMetAlaAsnLeuGly 368
Db 1225 ---TATAACCAATTAATACAAATGTTGATACAAATGGTAAAAAACCTGCTAGTATT--- 1278
QY GlnGlnAsnAsnGlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsn 388
Db 1279 ---CAACAATACCAAGCTGCTCGACAAGCTATTGAG-----ACGCAA 1317
QY TyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnLeuArgHisSerSer 408
Db 1318 TACAATTAACGCTAATTAACAGAGCACAT-----CAATTTCTTGAATAATAGT 1362
QY ProAlaThrGlnAsnAsnTyrThrValAlaLeu----- 419
Db 1363 AACCCCTTCAGTTAATGAAGTAGCACAGCATTTACAAAAAGTTGAAGCTGTACAACTTAA 1422
QY 420 -----ThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeu 433
Db 1423 GTTAATGACCGATTATCATATGCTTCAAAATTAAGAGAAATAT-----AGTGCACCTT 1473
QY ThrThrAspProAsnGlnVal-----AspThrLeuPheAspAlaGlyGly 448
Db 1474 GTCACAGCTAAAATCACTTCAGCAAGCAGTTAATGATCAACCAATTAACACAGGTATG 1533
QY HisGlnThrSerLeu-----LeuProGlyGlnThrLeuLeuTyr 461
Db 1534 ACTCAAGATTCTATTAATAACTATGCTAGCTAAGAGAAATCAGGCTCAAAAGTCTATC--- 1590
QY ThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArgTyr 481
Db 1591 -----AGAAATGCAGAAGCTGCTATCAACAATGGCGATGCAACTGCMAAACAAATTTCA 1644
QY AspSerAsnGlyMetArgGlnLeuLysValSer-----GluGlnPro 495
Db 1645 GACGAGAAATCTAAAGTTGAACAGCNCCTAGCACATTTGATGATGCTAAACAGCAATTA 1704
QY ThrGlnAsnThrThrGlnGlnGlnArgValLeuTyr----- 507
Db 1705 ACTGCAGATACTACTGAATTAACAAACAGCAGTTCAACAATTAACAGAGCGGATACA 1764
QY 508 -----LeuProGlyLeuGluLeu 513
Db 1765 AATAATAAAAAAGCAAGATATCAATGATATATAATAAAGCAATTTCAATCATTAGAACA 1824
QY ArgThrThr-----GlnSerAsnAlaThrThrThrGluGluLeuHisValLeuThrLeu 531
Db 1825 CAAATTAATCTCTGCTAAAGATATATGCCAACGCTGTGTATACAAAACCTATACGTACTGTT 1884
QY GlyGluAlaGlyArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGluAsp 551
Db 1885 CAAGAGGTAAATTAATGATTACAAACAGTA----- 1914
QY ValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuLeuGlySerSerGlnLeu--- 570
Db 1915 -----AATCAGTTG-----AATCAACAATTAAC 1938
QY GluLeuAspAsnGlnGlyGlnLeuLeuSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 1939 GAAGCAATTAATCAACTTCAACCGCTATCAAAATTAATGAT----- 1977
QY AlaLeuTyrAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrLeuArgTyrSer 609
Db 1978 GCATTAAGAGCTGCAAGATTAATTTAGAAAAATAAAATTAATCAAACTGTACAACTGAT 2037
QY GlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyr 629
Db 2038 GGTATGACACAAACATCTATAGAGGCTTATCAAAACGCTTAACCGCTGCCCAAAATGAA 2097
QY AlaGlyArgTyrLeuSerAlaAspProAlaGlyThrLeuAspGlyLeuAsnLeuTyr--- 648
Db 2098 TCTAACACTGCTTTAGCATTAATTAATAACGGCGATGCGATGAACAAACAATTAACA 2157
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2158 GAAACAGACCGAGTCAATCAGCAAACTTAACCTCAAGCAATTAACCGGTTAACA 2217
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2218 GTTAATAAAGAACCATTAGAAACCGCTAAACAGCGTTACAAATTAACATCGACCGTA 2277
QY LysPheLysLeuAlaLysSerSerHisValValLysTyrAsnGluLysGluSerSer 701
Db 2278 CCTAGTACAGATGTTAGTACAGCAATCTGTTGCAAAATTAATTAATCAAAAA----- 2328
QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyr 721
Db 2329 -----CTACAAATAGCTAAA---AACGAAATTAACACAAATTAATAAC 2367
QY 722 LeuLeuSerHisGluGluLeuLysGlyLeuGluLysSerGlnLeuLeuTyrSerArg 741
Db 2368 GTTTTAGAACCAACAATCTAGATGTTAATGCAATCAAAACCAATTAACAGCAGCGGAACGA 2427
QY 742 LeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGlu 761
Db 2428 ATCAGTAACGATTTAACA-----CAAGCTAAGAATAACTTACAGTTGATCTACAA 2478
QY 762 IleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHis 781
Db 2479 CCTTTAGAAAAATAAAAGACAACTTCAAGATGAAATTCATCAAGCTACTAACACAGAT 2538
QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMetAsp 801
Db 2539 GGAATGACTCAAGATTCAGTGGATTAATTACATGATAGCTTAAGTCAGCAATTTATAGAA 2598
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
Db 2599 AAAGGCANAGTAATAAATAATTAATAACGTAATCCGACAGTAGAACAGTTAAAGAGAGC 2658
QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 2659 GTTGTCTAATGCAACAACAGTCATACAAGATTTACAAATGCTCGAACT----- 2706
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
Db 2707 -----TCACTTTTCCAGACAAAACCTCAACTCAAGAGCTTAAATAATAGATTAGAAAC 2760
QY 852 AlaLeuLeuGlnGluThrGlu---ProAlaIleAlaIleAsp-----ArgGluTyrAsn 868
Db 2761 AGTATTAACCAACAACAGATACTGACGCGATGACTCAAGATTCGCTTAACAATTAAT 2820
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLysGlyHis 888
Db 2821 GATAAATTAGCAAAAGCTAGACAAAACCTTGAAAAAATATCTAAAGTTTTAGGTGCTCAA 2880
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 2881 CCTACTGTAGTGAATTAAGACAAAATACAGATGAAGCAAAATGCACATAAACCAAGCATTA 2940

Db 1915 -----AATCAGTTG-----AATCAACAATTAAC 1938
QY 571 GluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 1939 GAAGCAATTAATCAACTTCAACCGCTATCAAAATTAATGAT----- 1977
QY 591 AlaLeuTyrAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrLeuArgTyrSer 609
Db 1978 GCATTAAGAGCTGCAAGATTAATTTAGAAAAATAAAATTAATCAAACTGTACAACTGAT 2037
QY 610 GlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyr 629
Db 2038 GGTATGACACAAACATCTATAGAGGCTTATCAAAACGCTTAACCGCTGCCCAAAATGAA 2097
QY 630 AlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr--- 648
Db 2098 TCTAACACTGCTTTAGCATTAATTAATAACGGCGATGCGATGAACAAACAATTAACA 2157
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2158 GAAACAGACCGAGTCAATCAGCAAACTTAACCTCAAGCAATTAACCGGTTAACA 2217
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2218 GTTAATAAAGAACCATTAGAAACCGCTAAACAGCGTTACAAATTAACATCGACCGTA 2277
QY 682 LysPheLysLeuAlaLysSerSerHisValValLysTyrAsnGluLysGluSerSer 701
Db 2278 CCTAGTACAGATGTTAGTACAGCAATCTGTTGCAAAATTAATTAATCAAAAA----- 2328
QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyr 721
Db 2329 -----CTACAAATAGCTAAA---AACGAAATTAACACAAATTAATAAC 2367
QY 722 LeuLeuSerHisGluGluLeuLysGlyLeuGluLysSerGlnLeuLeuTyrSerArg 741
Db 2368 GTTTTAGAACCAACAATCTAGATGTTAATGCAATCAAAACCAATTAACAGCAGCGGAACGA 2427
QY 742 LeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGlu 761
Db 2428 ATCAGTAACGATTTAACA-----CAAGCTAAGAATAACTTACAGTTGATCTACAA 2478
QY 762 IleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHis 781
Db 2479 CCTTTAGAAAAATAAAAGACAACTTCAAGATGAAATTCATCAAGCTACTAACACAGAT 2538
QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMetAsp 801
Db 2539 GGAATGACTCAAGATTCAGTGGATTAATTACATGATAGCTTAAGTCAGCAATTTATAGAA 2598
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
Db 2599 AAAGGCANAGTAATAAATAATTAATAACGTAATCCGACAGTAGAACAGTTAAAGAGAGC 2658
QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 2659 GTTGTCTAATGCAACAACAGTCATACAAGATTTACAAATGCTCGAACT----- 2706
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
Db 2707 -----TCACTTTTCCAGACAAAACCTCAACTCAAGAGCTTAAATAATAGATTAGAAAC 2760
QY 852 AlaLeuLeuGlnGluThrGlu---ProAlaIleAlaIleAsp-----ArgGluTyrAsn 868
Db 2761 AGTATTAACCAACAACAGATACTGACGCGATGACTCAAGATTCGCTTAACAATTAAT 2820
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLysGlyHis 888
Db 2821 GATAAATTAGCAAAAGCTAGACAAAACCTTGAAAAAATATCTAAAGTTTTAGGTGCTCAA 2880
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 2881 CCTACTGTAGTGAATTAAGACAAAATACAGATGAAGCAAAATGCACATAAACCAAGCATTA 2940


```
QY 508 -----LeuProGlyLeuGluLeu 513
Db 2210 AATAATAAAGCCAGAGATATCAATGATATAATAAGCAATTCATCAATAGAAACA 2269
QY 514 ArgThrThr-----GlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeu 531
Db 2270 CAATTAATCTCTGCTAAAGATAATGCGACGCTGTGATACAAAACCTATACGTACTGTT 2329
QY 532 GlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAsp 551
Db 2330 CAAGAGGTAAATAATGCTTACCAACAAGTA----- 2359
QY 552 ValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeu--- 570
Db 2360 -----AATCAGTTG-----AATCAACAATTAAC 2383
QY 571 GluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThr 590
Db 2384 GAAGCAATTATCACTTCACCGCTATCAATAATGAT----- 2422
QY 591 AlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyr---LysThrIleArgTyrSer 609
Db 2423 GCATTAAAGCTCGAAGTAAATTTAGAAATAAATAATTAATCAAACTGTACAACTGAT 2482
QY 610 GlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrp 629
Db 2483 GGTATGACACAACAATCTATAGAGGCTTATCAAAACGCTAAACGCTAGCCCAAAATGAA 2542
QY 630 AlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyr--- 648
Db 2543 TCTAAACACTGCTTTAGCATTAATTAACGGCGATGCCGATGAACAACAATAATTACAACT 2602
QY 649 -----ArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 2603 GAAACAGACCGAGTCAATCAGCAAACTACAACTTAACCAACCAATTAACGGTTAACA 2662
QY 666 -----ProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeu 681
Db 2663 GTTAATAAAGAACCAATAGAAACCGCTAAACCGCTTACAAAATAAATCAACATCGACCGTA 2722
QY 682 LysPheLysLeuAlaLysSerSerHisValValIleValTrpAsnGluLysGluSer 701
Db 2723 CCTAGTACAGATGGTATGATCTAGCAATCTGTGCAAAATTAATCAAAA----- 2773
QY 702 TyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerProSerGlyTyr 721
Db 2774 -----CTCAAAATAGCTAAA-----AACGAAATTAACACAATAATTAAC 2812
QY 722 LeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
Db 2813 GTTTAGCGAAACAATCTAGATGTTAATGCAATCAAAACGAATAAAGCAGAACGGAACGA 2872
QY 742 LeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGlu 761
Db 2873 ATCAGTAACGATTTAACA-----CAAGCTAAGAATAAATCAACGTTGATCTCA 2923
QY 762 IleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHis 781
Db 2924 CCTTAGAAAAATAAAGACAACTTCAGATGAAATTCATCAAGTACTACACAGAT 2983
QY 782 LysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMetAsp 801
Db 2984 GGAATGACTCAAGATTTCAGTGGATTAATTAATGATAGCTTAAGTGCAGCAATATATAGAA 3043
QY 802 LysSer-----GluLysAsnAspTyrSerGlyGluArgLysIleTyr 815
Db 3044 AAAGGCAAGTAATAAATTAATTAACGTAATCCGACAGTGAACAAGTAAGAAGAGAC 3103
QY 816 AlaAlaMetGluValLysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisVal 835
Db 3104 GTTGCTAATGCACAACANGTCATACAGATTTACAAATCTCGAACT----- 3151
QY 836 AsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGlu-----GluArg 851
```

```
Db 3152 -----TCACTGTGTTCCAGACAAAACTCAACTCAAGAAAGCTAAAAATAGATTAGAAAC 3205
QY 852 AlaLeuLeuGlnGluThrGlu---ProAlaIleAlaIleAsp-----ArgGluTyrAsn 868
Db 3206 AGTATTAAACCAACAACAGATACTACGCGCATGACTCAAGATTCGCTTAACAATTATAT 3265
QY 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysSerLeuLysGlyHis 888
Db 3266 GATAAATTAGCAAAAGCTAGACAAAACCTTGAATAAATATCTAAAGCTTTAGGTGCTCAA 3325
QY 889 LysIle-----AsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAlaIle 905
Db 3326 CCTACTGTAGTGAATTAGACAAATACAGATGAAGCAATGCACATAAACCAAGCATTA 3385

RESULT 6
US-10-821-234-245/c
; Sequence 245, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 245
; LENGTH: 3626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-821-234-245

Alignment Scores:
Pred. No.: 0.000772 Length: 3626
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 6 Gaps: 44

US-10-647-956A-6 (1-915) x US-10-821-234-245 (1-3626)

QY 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIle 50
Db 3592 TTAGCCACTAAAGTGTGAACTGGA-----TGGACAAACGTTTTTTGACTATGACAGT 3539
QY 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 3538 GAAGGT-----CGTCTGACAAATGTTAGTTTCCAAC 3506
QY 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 3505 GGAGTG---GTCAACAACCTGCGATGGGACATGGACAGGCTATCACAGTGGACATTGAG 3449
QY 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 3448 TCATCTAGCCGAGAGAGAA-----GATGTGAGCATCACTTCAATCTGTCTCGATCGAT 3395
QY 100 Ser----- 101
Db 3394 TCTTCTACACCATTGTTCAAGATCAGTTAAGAAACAGCTACAGATTGTTATGACGGC 3335
QY 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
Db 3334 TCCTCAGAAATTATCTACGCCAGTGGCCCTGAGCTACATACCAACACAGCGCAGGTT 3275
QY 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
```


3274	Db	CTGGCTGGCACCGCTAAATCCGACGGTTGGCCAAAAGAAACATGACTTTGGCTGGCGAGAAC	3215
139	Qy	ThrThrGluArgLeuLeuIleTrrAlaGlyAsnThrProGln--GluLysAspTyrAsnLeu	157
3214	Db	GGTCAAAACTGGTGGGAATGGAGATTCGAAAGAGCAAGCCCAAGGAAGTCAATGTC	3155
158	Qy	AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer	177
3154	Db	TTTGGCCGCAAGCTCAGG-----GTTAATGGCAGAAACCTCTTTC	3113
178	Qy	LeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp-----	195
3112	Db	GTTGACTTTGATCGAACAAACAGACAGAAAGATCTATGACGACCACCCGTAATTTCTA	3053
196	Qy	-----AlaAspTrrThrGlyLysAspGlnSerLeuTrrp-----GlnGlnLysLeu	210
3052	Db	CTGAGGATCGCCTACGACACCTCTGGGACCCGACTCTCTGGCTGCGCAAGCAGCAAGCTG	2993
211	Qy	SerSerAspValTrrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln	230
2992	Db	ATGGCC---GTCAATGTCACTTATTCACACAGTCAATATGGCAGCATCCAGCAGGC	2936
231	Qy	ThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----	248
2935	Db	ACCACTAGC-----GAGAAAGTAGATTATGACGACAGGGGAGGATCGTGTCT	2888
249	Qy	-----LysGlySerTrrpLeu	253
2887	Db	CGGCTCTTGTGTGATGGTAAACATGGAGTTTACACATATTAGAAAAAGTCCATGGTTC	2828
254	Qy	ThrLeuLysGlyGlnAlaGluGlnValIle-----IleLysSer	266
2827	Db	CTGCTTCATAGCAGCGCAGTACATCTTCGAATACGATATGTGGGACCGCTGTCTGCC	2768
267	Qy	LeuThrTrrSerAlaAlaGly-----GlnLysLeuArgGlu-----	278
2767	Db	ATCACCATGCCAGTGGCTCGGCACACACCATGACAGCATCCGATCCATTTGGCTACTAC	2708
279	Qy	-----GluHisGlyAsnGlyIleValThrGluTrrSerTrrpGlu	291
2707	Db	CGCAACATATACACCCCGGAAGCAACGCCCTCCATCATCAGGACTACAAGAGGAA	2648
292	Qy	-----ProGluThrGlnArgLeuIleGlyIleThrThr	302
2647	Db	GGGCTGCTTCTACAAACAGCTTTCTGGGTACAGTCGGAGGGTCTTATTCAAAATACAGA	2588
303	Qy	ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTrrGlnTrrAsp	319
2587	Db	AGGCAGACTAGGCTCTCAGAAATTTATATGATAGCACACAGAGTCAGTTTTACCTATGAT	2528
320	Qy	ProValGlyAsnValIleAsnIleArgAsn-----	329
2527	Db	GAACAGCAGGAGTCTTAAAGACACAGTAAACCTCCAGAGTGATGTTTTATTGGCACCAT	2468
330	Qy	-----AspAlaGluAlaThrArgPheTrrpArgAsnGln	340
2467	Db	AGATACAGGCCAAATGGTCCCTGATTTGACAGGCAGATTTCCGCTTTAGTGAAGATGGG	2408
341	Qy	LysValAlaProGluAsnSerTrrThrTrrAspSer-----	352
2407	Db	ATGGTAAATGCAAGATTGACTATAGCTATGATGATATATATGATATATACCATGATCTTCT	2228
353	Qy	-----LeuTrrGlnLeuIleSerAlaThrGly	361
2347	Db	GGTGTGATCAATGAACGCCACTGCCTATGATCTGTATCATCTGTTGATGACATTTCTGGC	2288
362	Qy	Arg-----GluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSer	376
2287	Db	AAAGTTGACAGTTGGAAAGTTGGAGTTATATATATGATATATACCATGATCTTCT	2228
377	Qy	ProAlaLeuProSerAspAsnAsnThrTrrThrAsn-----	388

Db	2227	ACAGCTGTA-----ATGACCTATACGAAGCATTCTTGATGCTCATGCCGCTATC	218
Qy	389	-----TyrThrArgSerTyrSerTyrAsp	396
Db	2179	AAGGAGATTCAATATAGATATTTCAGGTGCGTCTCATGTACTGGATTACAATTCAGTATGAT	2120
Qy	397	HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProIalaThrGlnAsnAsn	414
Db	2119	AACATGGTGGGTAACTAACAGAGAGAGATTAAATAAGGGCCCTTGCCAAACACCCAAA	2060
Qy	415	TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValleuSerThrLeuThr	434
Db	2059	TATGCTTTATGAATATAGATTGTAT-----GGACAGCTCCAAACAGATTAC	2015
Qy	435	ThrAspProAsnGlnValAspThrLeu-----PheAspAlaGlyGlyHisGlnThrSerLeu	453
Db	2014	CTCATGAAAGATATATGTGGCGGTACACTAGATCTGATGAGTGAACCTCCATTACTTG	1955
Qy	454	LeuProGlyGlnThrLeuIleTrrpThrPro---ArgGlyGluLeuIysGlnValAsnAsn	472
Db	1954	AACCCAGTAACAGTGGCGCTCTGACACCCCTTCGTATGACCTGGCAGACAGAATCACT	1895
Qy	473	GlyProGlyAsnGluTrrpTyrArgTyrAspSerAsnGly---MetArgGlnLeuIysVal	491
Db	1894	CGACTGGGTGATGTTCAATATCGGTTGGATGAAGATGGTTCTCTACGTCAA-----	1844
Qy	492	SerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeu	511
Db	1843	-----AGGGGACG	1835
Qy	512	GluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu	531
Db	1834	GAATCTTCGAATATAGCTCCAAGGGCTCTTAAC-----CGAGTTTACAGTAAA	1784
Qy	532	GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTrrpGluSer-----GlyIys	548
Db	1783	GGCAGTGGCTGGCAGCATGATCTACCGTTATGACGGCTGGGAAGGGCGTGTTCTAGCAAA	1724
Qy	548	sProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle-----	565
Db	1723	ACCA-----GTCTA-CGACAGCACCTGCAGTTTTTTTATGCTGACTTAACTTATCCAC	1671
Qy	566	-----GlySerSerGln-----LeuGluLeuAspAs	574
Db	1670	TAGGATTACTCATGCTTACAACCATTCGAGTTCAGAAATTAACCTCCCTGATTATGATCT	1611
Qy	574	nGlnGly-----GlnIleIleSerGluGluGluTyrTyrProPheGly--	588
Db	1610	CCAAAGGACATCTTTTGGCCATGGAAATCAACGATGGGGATGAATTCATTATGTCATCGGA	1551
Qy	589	-----GlyThrAlaLeuTrrpAlaAlaAsnSerGlnThrGluAlaSerTyrIysThrIle	606
Db	1550	TAACACAGGACACCACTG---GCTGTGTTCAAGTACCAATGGGCTTATGCTGAACACAGAT	1494
Qy	606	eArgTyrSer-----	609
Db	1493	TCAGTACACTGCATATGGGAAATCTATTTTGACTCTAATATTGACTTTCAACTGGTAAT	1434
Qy	610	-----GlyIysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr	625
Db	1433	TGGATTTTCATGGTGGCCCTGTATGACCCACATCACCATAATTAATCCACTTTGGAGAAAGAGA	1374
Qy	625	rTyrGlnProTrrpAlaGlyArgTrrp-----LeuSe	635
Db	1373	TTATGACATTTTGGCAGACGGTGGACACACCTGCATAGAAATCTGGAAAGAATTGG	1314
Qy	635	rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr	655
Db	1313	GAAGGACCCAGCT-----CCTTTTAACTTGTCATGTTTAGGAATAACAACCC	1266
Qy	655	oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluIysGlyIysTyrThrIysGln	674
Db	1265	TGCAAGGAAAATTCATACGCTGGAAGATTACATCACAGATGTTTAAACAGCTGGCTGGTGAC	1206


```
Qy 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn----- 388
Db 5720 ACAGCTGTA-----ATGACCTATACGAAGCACCTTTGTGCTCATGCGCGTATC 5767
Qy 389 -----TyrThrArgSerTyrSerTyrAsp 396
Db 5768 AAGGAGATTCAATATGAGATATTACAGGTGCTCATGCTACTGATTACAAATTCAGTATGAT 5827
Qy 397 HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAsnAsn 414
Db 5828 AACATGGGTGGGTAACCAAGAGAGAGATTAAATAAGGGCCCTTTGGCAACACACCACAA 5887
Qy 415 TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThr 434
Db 5888 TATCTCTTATGATATGATGTTGAT-----GGACAGCTCCAAACAGTTTAC 5932
Qy 435 ThrAspProAsnGlnValAspThrLeu-----PheAspAlaGlyGlyHisGlnThrSerLeu 453
Db 5933 CTCAATGAAGAAGATAATGTGGCGGTACAACTACGATCTGAATGGAAACCTCCATTACTG 5992
Qy 454 LeuProGlyGlnThrLeuIleThrPro-----ArgGlyGluLeuLysGlnValAsnAsn 472
Db 5993 AACCAAGTAACAGTGGCGGTCTGACACCCCTTCGCTATGACCTGCGAGACAGAACTCACT 6052
Qy 473 GlyProGlyAsnGluTyrTyrArgTyrAspSerAsnGly---MetArgGlnLeuLysVal 491
Db 6053 CGACTGGGTGATGTTCAATATCGGTGGATGAAGATGGTTCTCTACGTCAA----- 6103
Qy 492 SerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db 6104 -----AGGGGCACG 6112
Qy 512 GluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu 531
Db 6113 GAAATCTTTGAATATAGTCTCCAAAGGGGCTTCTAACT-----COCGTTTACAGTAAA 6163
Qy 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTyrGluSer-----GlyLy 548
Db 6164 GGCAGTGGCTGGACAGTATCTACCGTTATGACGGCTGGAGAGCGGTGTTCTAGCAAA 6223
Qy 548 sProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle----- 565
Db 6224 ACCA-----GTCTA-GGACAGCACCTGCAGTGTCTTATGCTGCTAACTTAATCCAC 6276
Qy 566 -----GlySerSerGln-----LeuGluLeuAspAs 574
Db 6277 TAGGATTACTCATGTCTCAACCAATTCAGTTCAGAAATTAACCTCCCTGTTATGATGCT 6336
Qy 574 nGlnGly-----GlnIleIleSerGluGluGluTyrTyrProPheGly-- 588
Db 6337 CCAAGGACATCTTTTGGCATGGGAATCAGCAGTGGGGATGAATCTATATGTCATCGGA 6396
Qy 589 -----GlyThrAlaLeuThrPalAalaAsnSerGlnThrGluAlaSerTyrLysThrIl 606
Db 6397 TAACACAGGGACACCACTG---GCTGTGTTTCAGTAGCAATGGGCTTATGCTGGAACAGAT 6453
Qy 606 eArgTyrSer----- 609
Db 6454 TCAGTACATCGCATATGGGGAAATCTATTTTGACTCTAATATGACTTTCACTTCACTGTAAT 6513
Qy 610 -----GlyLysGluAuaGspAlaThrGlyLeuTyrTyrGlyTyrArgTyr 625
Db 6514 TGGATTTTCATGGTGGCCGTGTATGACCCACTCACCAAAATTAATCCACTTTGGAGAAAGAGA 6573
Qy 625 rTyrGlnProThrAlaGlyArgTyr-----LeuSe 635
Db 6574 TTATGACATTTTGGCAGGACGGTGGCAACACCTGCACATAGAAATCTCGAAAAAGAAATGG 6633
Qy 635 rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
Db 6634 GAAGGACCCAGCT-----CCTTTTAACTTTGTACATGTTTGAAGATAACACCC 6681
Qy 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG1 674
```

```
Db 6682 TGCACGCAAAATCCATGACGTGAAAGATTACATCAGAGATTTAACAGCTGGCTGTGTGAC 6741
Qy 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
Db 6742 ATTTGGTTTCCATCTGCACAAATGCTATCTCTGATTCCTGTTCCTCCAAATTTGATTTAAC 6801
Qy 686 aAlaLysSerSerHisValValLys-----TrpAsnGlu 697
Db 6802 AGAACCTTCTTAGCAACTTGTGAAGAGTCAGCAGTCGGATGAT 6844

RESULT 8
US-11-096-051-1
; Sequence 1, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1
; LENGTH: 8362
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(8215)
US-11-096-051-1

Alignment Scores:
Pred. No.: 0.00243 Length: 8362
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44

US-10-647-956A-6 (1-915) x US-11-096-051-1 (1-8362)
Qy 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIle 50
Db 4967 TTAGCCACTAAAAGTGTGAAGAACTGGA-----TGCACAAACGTTTTTTGATGATGACAGT 5020
Qy 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 5021 GAAGGT-----CGTCTGACAAATGTTACGTTTCCAACT 5053
Qy 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 5054 GGAGTG---GTCACAAACCTTCATGGGACATGACCAAGGCTATCAGATGGACATTGAG 5110
Qy 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 5111 TCATCTACCGCAGAGAA-----GATGTGAGCATCACTTCAAATCTGTCTCTCGATCGAT 5164
Qy 100 Ser-----Arg 101
Db 5165 TCTTTTACACCATGGTTCAGATCAGTTAAGAAACAGCTACACGATTGTTATGACGGC 5224
Qy 102 ProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
```



```
Qy 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG1 674
Db 7294 TGMAGCAAAATCCATGAGCTGAAAGATTACATACAGATGTTAAACAGCTGGCTGGTGAC 7353
Qy 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuA1 686
Db 7354 ATTGGTTTCCATCTGCACAAATGCTATTCTCTGGATTCCCTGTTCCCAAATTTGATTAAAC 7413
Qy 686 aAlaLysSerSerHisValVallys-----TTPAsnGlu 697
Db 7414 AGAACCTTCTTACCAACTTGTGAAGACTGAGCAGCTGGGATGAT 7456

RESULT 9
US-11-096-051-9
; Sequence 9, Application US/11096051
; Publication NO. US20050244869A1
; GENERAL INFORMATION:
; APPLICANT: Keku, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Eitenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 9
; LENGTH: 8645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(8313)
US-11-096-051-9

Alignment Scores:
Pred. No.: 0.00254 Length: 8645
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44

US-10-647-956A-6 (1-915) x US-11-096-051-9 (1-8645)
Qy 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuThrPheTyrGluPheAsnIle 50
Db 5065 TTAGCCCTAAAGTAGTGAACCTGGA-----TGGACACGTTTTTTTGATGATGACAGT 5118
Qy 51 ProGlyPheGlnVallysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 5119 GAAGGT-----CGTCTGACAAATGTTACGTTTCCAAC 5151
Qy 71 PheLeuArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 5152 GGAGTG---GTCAAAACCTCATGGGACATGGACAGGCTATCACAGTGGACATTGAG 5208
Qy 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 5209 TCATCTAGCCGAGAAGAA-----GATGTACGATCACTTCAAAATCTGTCTCTCGATCAT 5262
Qy 100 Ser-----Arg 101
Db 5263 TCTTCTACACCATGGTTTCAAGATCAGTTTAAGAAACAGCTACCAGATTGGTTTATGACGGC 5322
```

```
Qy 102 ProValLeuIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThr 121
Db 5323 TCCTCAGAAATTATCTACGCCAGTGGCTGACACTACACTACCAACAGAGCCGACGTT 5382
Qy 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
Db 5383 CTGGCTGGCAGCGCTAATCCGACGGTTGCCAAAAGAAACATGACTTTGCTCGCGAGAAC 5442
Qy 139 ThrThrGluArgLeuIleTrpAlaGlyAsnThrProGln---GluLysAspTyrAsnLeu 157
Db 5443 GGTCAAAACCTTGGTGAATGGAGATTCCGAAAAGACAGCAACCCAGGGGAAAAGTCAATGTC 5502
Qy 158 AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer 177
Db 5503 TTTGGCCGCAAGCTCAGG-----GTTAATGGCAGAAAACCTCTCTTCA 5544
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp----- 195
Db 5545 GTTGACTTTGATCGAACACAAAGACAGAAAAGATCTATGACGACCACCGTAAATTTCTA 5604
Qy 196 -----AlaAspTrpThrGlyGluAspGlnSerLeuTrp-----GlnGlnLysLeu 210
Db 5605 CTGAGGATCGCTTACGACAGCTCTGGGCACCCGACTCTCTGGCTGCCAAGCAGCAAGCTG 5664
Qy 211 SerSerAspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln 230
Db 5665 ATGCCC---GTCAATGTCCACTATTTCACACAGGTCAAAATGCCAGCATCCAGCAGGC 5721
Qy 231 ThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeu----- 248
Db 5722 ACCACTAGC-----GAGAAAGTAGATTATGACGACAGGGGAGGAGCTGTCT 5769
Qy 249 -----LysGlySerTrpLeu 253
Db 5770 CGGGTCTTTGCTGATGGTAAACATGGAGTTACACATATTTAGAAAAGTCCATGGTCTTT 5829
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValIle-----IleLysSer 266
Db 5830 CTGCTTCATAGCCAGCGGCAGTACATCTTCGAATAGATATGTTGGACCGCCTGTCTGCC 5889
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
Db 5890 ATCACCATGCCAGTGTGGCTGCCACACCATCCAGACCATCCGATCCATTTGCTACTAC 5949
Qy 279 -----GluHisGlyAsnGlyIleValThrGluTyrSerTyrGlu 291
Db 5950 CGCAACATATACAAACCCCGGAAAGCAACGCTCCATCATCATCGGACTACACGAGGAA 6009
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThrThr 302
Db 6010 GGGCTGCTTCTACAAACAGCTTCTTGGGTGACAGTCCGAGGGTCTTTATTAATAACAGA 6069
Qy 303 ArgArgProSerAspAlaLysValLeuGlnAsp-----LeuArgTyrGlnTyrAsp 319
Db 6070 AGCAGACTAGGCTCTCAGAAATTTATATGATAGCACAGAGTCACTTTTACCTATGAT 6129
Qy 320 ProValGlyAsnValIleAsnIleArgAsn----- 329
Db 6130 GAAACACAGCAGGAGTCTCTAAAGACAGATAAACCTCCAGAGTGTGTTTATTGACCACT 6189
Qy 330 -----AspAlaGluAlaThrArgPheTrpArgAsnGln 340
Db 6190 AGATACAGGCAAAATGGTCCCTGATGTTGACGAGGATTTTCGCTTTTAGTGAAGATGG 6249
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSer----- 352
Db 6250 ATGTTAAATCAAGATTGACTATAGCTATAGTATGACACAGCTTTCGAGTGACCATGCAG 6309
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361
Db 6310 GGTGTGATCAATGAAACGCCACTGCCTATTGATCTGTATCAGTTGTATGATCATTTCTGCG 6369
```

```
QY 362 Arg-----GluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSer 376
Db 6370 AAAAGTTGACGAGTTTGGAAAGTTTGGAGTTATATATATATGATATTAAACGAGTCAATTTCT 6429
QY 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn----- 388
Db 6430 ACAGCTGTA-----ATGACCTATACGAGCATTTCATGCTCATGCGCGGTATC 6477
QY 389 -----TyrThrArgSerTyrSerTyrAsp 396
Db 6478 AAGGAGATTCAATATGAGATATTTCAGTCTCATGTACTGGATTACAATTCAGTATGAT 6537
QY 397 HisSerGlyAsnLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAsnAsn 414
Db 6538 AACATGGTGGGTAAACCAAGAGAGAGATTAAATAGGGCCCTTTGCCAACACCAACAA 6597
QY 415 TyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThr 434
Db 6598 TATGCTTATGAATATGATGTTGAT-----GGACAGCTCCMAACAGTTTAC 6642
QY 435 ThrAspProAsnGlnValAspThrLeu---PheAspAlaGlyGlyHisGlnThrSerLeu 453
Db 6643 CTCAATGAAAGATAATGTGGCGGTACAACCTACGATCTGAATGGAACCTCCATTTACTG 6702
QY 454 LeuProGlyGlnThrLeuIleThrPro---ArgGlyGluLeuLysGlnValAsnAsn 472
Db 6703 AACCCCAAGTAACAGTGGCGCTCTGCACACCCCTTCGTATGACCTGGCAGCAGAACTCACT 6762
QY 473 GlyProGlyAsnGlnTrpTyrArgTyrAspSerAsnGly---MetArgGlnLeuLysVal 491
Db 6763 CGACTGGGTGATGTTCAATATCGTTGGATGGAAGATGGTTCTCTAGCTCAA----- 6813
QY 492 SerGluGlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db 6814 -----AGGGGCAGC 6822
QY 512 GluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeu 531
Db 6823 GAAATCTTGAATATAGTCCAAAGGGCTTCTAACT-----CGAGTTTACAGTAAA 6873
QY 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTrpGluSer-----GlyIly 548
Db 6874 GGCAGTGGCTGGACAGTGAATCTACCGTTATGACGGCTGGGAAGGCGTGTCTTAGCAAA 6933
QY 548 sProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle----- 565
Db 6934 ACCA-----GTCTA--GGACAGCACCCTGCAGTGTCTTTTATGCTGACTTAATCTATCCCAC 6986
QY 566 -----GlySerSerGln-----LeuGluLeuAspAs 574
Db 6987 TAGGATTACTCATGTCTACAACCATTCGAGTTTCAGAAATTTACCTCCTGTATTATGATCT 7046
QY 574 nGlnGly-----GlnIleLeSerGluGluGluTyrTyrProPheGly-- 588
Db 7047 CCAAGGACATCTTTTGGCCATGGAAATCAGCAGTGGGATGAATCTATATATGTCATCGGA 7106
QY 589 -----GlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIle 606
Db 7107 TAACACAGGACACCACTG---GCTGTGTTCTAGTACCAATGGCGCTTATGCTGAAACAGAT 7163
QY 606 eArgTyrSer----- 609
Db 7164 TCAGTACACTGCATATGGGGAATCTATTTTGACTCTAATATTGACTTTTCAACTGGTAAT 7223
QY 610 -----GlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTy 625
Db 7224 TGGATTTCATGGTGGCTGTATGACCCACTCACCACAAATTAATCCACTTTGGAGAAAGAGA 7283
QY 625 rTyrGlnProTrpAlaGlyArgTrp-----LeuSe 635
Db 7284 TTATGACATTTTGGCAGGAGCGTGGACACACCTGCATAGAAATCTGGAAAGAAATGG 7343
QY 635 rAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
```

```
Db 7344 GAAGGACCCAGCT-----CCTTTTAACTTGTACATGTTTAGGAATAACAACCC 7391
QY 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysG 674
Db 7392 TGCAGCAAAATCCATGACGTGAAGAGATTACATCAGATGTTTAAACAGCTGGCTGGTAC 7451
QY 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
Db 7452 ATTGTGTTTCCATCTGCACAATGCTATTCTCGATTCCCTGTTCCCAATTTGATTAAAC 7511
QY 686 aAlaLysSerSerHisValValLys-----TrpAsnGlu 697
Db 7512 AGAACCTTCTACGAACTTGTGAAGAGTCAGCAGTGGGATGAT 7554

RESULT 10
US-11-096-051-7
; Sequence 7, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CurSeqList version 0.1
; SEQ ID NO 7
; LENGTH: 8657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(8325)
US-11-096-051-7

Alignment Scores:
Pred. No.: 0.00254 Length: 8657
Score: 163.50 Matches: 183
Percent Similarity: 33.41% Conservative: 116
Best Local Similarity: 20.45% Mismatches: 304
Query Match: 3.45% Indels: 293
DB: 9 Gaps: 44

US-10-647-956A-6 (1-915) x US-11-096-051-7 (1-8657)
QY 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsnIle 50
Db 5077 TTAGCCACTAAAGATGATGAAGTGA-----TGCACAACTGTTTTCATGATGACAGT 5130
QY 51 ProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGlnSerGlyProAsn 70
Db 5131 GAAGGT-----CGTCTGACAAATGTTTACGTTTCCAAC 5163
QY 71 PheIleArgValPheAsnLeuAlaGlyGlnVal----- 81
Db 5164 GGAGTG---GTCCACAAACCTGTCATGGGACATGGGACATGACAGCTATCATGAGATTGAG 5220
QY 82 -----LeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 5221 TCATCTAGCCGAGAGAGAA-----GATGTCAGCATCACTTCAATCTGCTCGATCGAT 5274
QY 100 Ser-----Arg 101
```


Db 5275 TCITTTACACCATGGTTCAAGATCAGTTAAGAAACAGCTACACGATTTGGTTATGACGGC 5334
Qy 102 ProValLeuIlelleAenAlaThrGlyValArgGlnAenHisArgTyrGluAenAenThr 121
Db 5335 TCCTCAGAATTATCTACGGCAGTGGCTGGAGCTCACACTACCAACACGCGCACGTT 5394
Qy 122 LeuProGlyArg-----LeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLys 138
Db 5395 CTGGCTGGCAGCGTAACTCCGACGGTTGCCAAAAGAAACATGACTTTGGCTGGCGAAGC 5454
Qy 139 ThrThrGluArgLeuIleThrAlaGlyAenThrProGln---GluLysAenPtyrAenLeu 157
Db 5455 GGTCAAAACCTTGGTGAATGGAGATTCGGAAGAGCAAGCCCAAGGAAAGTCAATGTC 5514
Qy 158 AlaGlyGlnCysValArgHisTyrAenThrAlaGlyLeuThrGlnLeuAenSerLeuSer 177
Db 5515 TTTGGCGCAAGCTCAGG-----GTTAATGGCAGAAACCTCTTTCA 5556
Qy 178 LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAenGlnAenP----- 195
Db 5557 GTTGACTTTGATCGAACAACAAAGACAGAAAGATCTATGACGACCAACCGTAAATTTCTA 5616
Qy 196 -----AlaAenPtpThrGlyGluAenPtnSerLeuTrp-----GlnGlnLysLeu 210
Db 5617 CTGAGGATCGCTACGACAGCTCTGGGACCCGACTCTCTGGCTGCCAAGCAGCAAGCTG 5676
Qy 211 SerSerAenPValTyrIleThrGlnSerAenThrAenAlaThrGlyAlaLeuLeuThrGln 230
Db 5677 ATGGCC---GTCAATGTCACTTATTCACAGGTCAAATTTGCCAGCTCCAGCAGGAGC 5733
Qy 231 ThrAenPAlaLysGlyAenIleGlnArgLeuAlaTyrAenValAlaGlyGlnLeu----- 248
Db 5734 ACCACTAGC-----GAGAAAGTATGATCAGGACAGGGAGGATCGTGTCT 5781
Qy 249 -----LysGlySerTrpLeu 253
Db 5782 CGGCTCTTGTGATGGTAAACATGGAGTTACACATATTTAGAAAGTCCATGGTCTT 5841
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValle-----IleLysSer 266
Db 5842 CTGCTTCATACCCAGCGCATACATCTTCGAATACGATATGTGGACCGCTCTCTGCC 5901
Qy 267 LeuThrTyrSerAlaAlaGly-----GlnLysLeuArgGlu----- 278
Db 5902 ATCACCATGCCAGTGTGGCTGGCCACACCATGACAGACCATCCATCCATGGCTACTAC 5961
Qy 279 -----GluHisGlyAenGlyIleValThrGluTyrSerTyrGlu 291
Db 5962 CGCAACATATACACCCCGGAAAGCAACGCTCCATCATCATCAGGACTACACAGAGAA 6021
Qy 292 -----ProGluThrGlnArgLeuIleGlyIleThr 302
Db 6022 GGGCTGCTTCTACAAACAGCTTCTTGGTTACAAGTCGAGGGTCTTATTCAAAATACAGA 6081
Qy 303 ArgArgProSerAenAlaLysValLeuGlnAenP-----LeuAenTyrGlnTyrAenP 319
Db 6082 AGGCAGACTAGGCTCTCAGAAATTTATATATAGCACAGAGATGAGTGTTCACCTATGAT 6141
Qy 320 ProValGlyAenValIleAenIleArgAen----- 329
Db 6142 GAAACAGCAGGATCTCTAAGACAGTAAACCTCCAGAGTGTGGTTTATTTCACCATTT 6201
Qy 330 -----AenPAlaGluAlaThrArgPheTrpArgAenGln 340
Db 6202 AGATACAGGCAAAATGGTCCCTGATTCAGAGGAGATTTTCGCTTTAGTGAAGATGGG 6261
Qy 341 LysValAlaProGluAenSerTyrThrAenP----- 352
Db 6262 ATGTAAATGCAAGATTTGACTATAGCTATGACAAACAGCTTTTCGAGTGACCATGTCAG 6321
Qy 353 -----LeuTyrGlnLeuIleSerAlaThrGly 361

Db 6322 GGTGTGATCAATGAAAGCCGCACTGCCTATTGATCTGTATCAGTTTGTATGACATTTCTGGC 6381
Qy 362 Arg-----GluMetAlaAenIleGlyGlnAenAenGlnLeuProSer 376
Db 6382 AAAGTTGACAGTTTGGAAAGTTTGGAGTTATATATATATATATATATATATATATATAT 6441
Qy 377 ProAlaLeuProSerAenAenAenThrTyrAen----- 388
Db 6442 ACAGCTGTA-----ATGACCTATACGAGCACTTTTGATGCTCATGSCCGCTATC 6489
Qy 389 -----TyrThrArgSerTyrSerTyrAenP 396
Db 6490 AAGGAGATTCAATATGAGATATTTCAGTCCGCTCATCTGATGGAATTAATTCAGATGAT 6549
Qy 397 HisSerGlyAenLeuThr-----GlnIleArgHisSerSerProAlaThrGlnAenAen 414
Db 6550 AACATGGTGGGTAAACCAAGAGAGATATAAATAGGGCCCTTCCCAACACCAACAAA 6609
Qy 415 TyrThrValAlaIleThrLeuSerAenArgSerAenArgGlyValLeuSerThrLeuThr 434
Db 6610 TATGCTTATGAATATATGTTGAT-----GGACAGCTCCCAACAGTTTAC 6654
Qy 435 ThrAenPProAenGlnValAenPThrLeu-----PheAenPAlaGlyGlyHisGlnThrSerLeu 453
Db 6655 CTCAATGAAAGATAATGTGGCGGTACAACTACGATCTGAATGGAACCTCCATTTACTG 6714
Qy 454 LeuProGlyGlnThrLeuIleThrPro---ArgGlyGluLeuLysGlnValAenAen 472
Db 6715 AACCCAGTAACAGTGGCGTCTGACACCCCTTCGCTATGACCTGGAGAGACAGAACTACT 6774
Qy 473 GlyProGlyAenGluTrpTyrArgTyrAenPserAenGly---MetArgGlnLeuLysVal 491
Db 6775 CGACTGGGTGATGTTCAATATCGTTGGATGAAGATGGTTTCTCTACGTCAA----- 6825
Qy 492 SerGluGlnProThrGlnAenThrThrGlnGlnArgValIleTyrLeuProGlyLeu 511
Db 6826 -----AGGGGCGACG 6834
Qy 512 GluLeuArgThrThrGlnSerAenAlaThrThrGluGluLeuHisValIleThrLeu 531
Db 6835 GAAATCTTTGAATATAGTCCCAAGGGCTTCTAACT-----CGAGTTTACAGTAA 6885
Qy 532 GlyGlu-AlaGlyArgAlaGlnValArgValLeuHisTrpGluSer-----GlyLys 548
Db 5886 GGCAAGTGGCTGGACAGTATCTACCTTATGACGGCTGGAGGGCTGTTCTAGCAAA 6945
Qy 548 sProGluAenPValAenAenGlnLeuArgTyrSerTyrAenAenLeu----- 565
Db 6946 ACCA-----GTCTA-GGACAGCACCTGCAGTGTGTTTATGCTGACTTAATCCCAT 6998
Qy 566 -----GlySerSerGln-----LeuGluLeuAenPAs 574
Db 6999 TAGGATTTACTGCTCTACAAACATTCGAGTTGAGAAATTAACCTCCCTGATTTATGATCT 7058
Qy 574 nGlnGly-----GlnIleIleSerGluGluGluTyrTrpProPheGly-- 588
Db 7059 CCAAGGACATCTTTTGGCCATGGAATCAGCACTGGGATGATTTCTATATTCATCGGA 7118
Qy 589 -----GlyThrAlaLeuTrpAlaAlaAenSerGlnThrGluAlaSerTyrLysThrI 606
Db 7119 TAACACAGGGACCACTG--GCTGTGTTTCTAGTAGCAATGGGCTTATGCTGAAACAGAT 7175
Qy 606 eArgTyrSer----- 609
Db 7176 TCAGTACACTGCATATGGGAAATCTATTTTGACTCTAATATTCGACTTTCACTGGTAAT 7235
Qy 610 -----GlyLysGluAenPAlaThrGlyLeuTyrTyrGlyTyrArgTy 625
Db 7236 TGGATTTTCATGGTGGCTGTGATGCCACTCACCAATTAATCCACTTTGAGAGAAAGAGA 7295
Qy 625 rTyrGlnProTrpAlaGlyArgTrp-----LeuSe 635
Db 7296 TTATGACATTTTGGCAGGACGGTGGACACACCTGACATAGAAATCTGGAAAGAAATGG 7355

QY 635 rLaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPr 655
Db 7356 GAAGGACCAGCT-----CCTTTAACTTGTACATGTTTAGGAATAACAACCC 7403
QY 655 oValSer---LeuGlnAspGluAsnGlyLeuAlaProGluLysGlyIleTyrThrIle 674
Db 7404 TCGAAGCAAAATCCATGACGTGAAGATTACATCACAGATGTTTAAACAGCTGGCTGTGAC 7463
QY 674 uValAsnPhe-----PheAspGluLeuLysPheLysLeuAl 686
Db 7464 ATTGGTTTCCATCTGCACATGCTATTCTCTGATTCCCTGTTCCCAAAATTGATTAAAC 7523
QY 686 aLaLysSerSerHisValValLys-----TyrAsnGlu 697
Db 7524 AGAACCTTCTTACGAACCTTGTGAAGATCAGCAGTGGGATGAT 7566

RESULT 11
US-10-793-626-3824/c
; Sequence 3824, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3824
; LENGTH: 3068
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3824

Alignment Scores:
Pred. No.: 0.0314 Length: 3068
Score: 144.00 Matches: 194
Percent Similarity: 36.29% Conservative: 174
Best Local Similarity: 19.13% Mismatches: 389
Query Match: 3.04% Indels: 258
DB: 6 Gaps: 53

US-10-647-956A-6 (1-915) x US-10-793-626-3824 (1-3068)

QY 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 2929 GCGTAAATAATGACATTAAACAAGCGGAGACATTAATTAACAGCTCAATCTCTAAC 2870
QY 23 LeuAsnValArgThrLeuArgTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeu 42
Db 2869 TTTAAATGCACAGACATT-----ACTAATGCTTTAAATAAT----- 2834
QY 43 IleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLys 62
Db 2833 ATTAACAACAGCACAGATAACCTTCATGGAGCTCA-----AAATTACAGCAAGCAAAAAAT 2777
QY 63 AsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeu 82
Db 2776 ACAACTNATCAGCCATTGTTAC-----TTAATCATCTTAATCAACCTCAA 2729
QY 83 ArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgPro 102
Db 2728 AAAGATCGCTTATACAGCT-----ATTAATGGAGCTACATCTAGGAC 2684
QY 103 ValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeu 122
Db 2683 CAAGTT-----GCAGAAAACTTAAAGAGCGCCGAGCGCTT 2648

QY 123 ProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArg 142
Db 2647 GATGAAGCTATCAAAACAACCTTGAAGATCAAGTGAATCAAGATGATCAAAATTTCAATAGC 2588
QY 143 LeuIleTyrAlaGly---AsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys 161
Db 2587 AGCCCAATTCATAATGAAGACTCAGACAACAAAATACTTATAAT----- 2543
QY 162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal 181
Db 2542 -----GATAAAATCCAAGCTGCAAAAGAA 2519
QY 182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThrGlyGlu 201
Db 2518 ATAATTAATCAAAACATCTAATCAACCTTAGATAAACAATAAATTGCTGATACACTTCAA 2459
QY 202 AspGlnSerLeuTyrGlnGlnLysLeuSerAspValTyrIleThrGlnSerAsnThr 221
Db 2458 AATATTAAGATGCTAGTGAATATTACATGGTGATCAAAAATTGCTCAATCTAAACAA 2399
QY 222 AspAlaThrGly----- 225
Db 2398 GACGCTAATAATCAATTAATCATTTAGATGACTTAACCGAAGACAAAACCACTTTT 2339
QY 226 ---AlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspVal 244
Db 2338 AAACCGTTAATAATAATGCTGATCTCGAGATGAGTAAATAA---CAACTAGAGATT 2282
QY 245 AlaGlyGlnLysGlySerTyrLeuThrLeu-----LysGlyGln 258
Db 2281 GCTAAACAATAATGCTGATGATGAGTACACTTATAAAGTCAATAATGATAAAGATCAA 2222
QY 259 AlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu 278
Db 2221 ATCAACATTTA-----AGCAATTACATTAAATGCTGATTAATGATAAATAACAA 2174
QY 279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIle 298
Db 2173 AATTATGATAATGCTATT-----AAAGAAGCTGAGGATTTAATT 2135
QY 299 GlyIleThrThrArgArgProSer-----AspAlaLysValLeuGlnAspLeuArgTyr 316
Db 2134 -----CATAATCATCATAGATCATAGATCATATAAAGCATTAAGAATTTATTAAAC 2084
QY 317 GlnTyrAspProValGlyAsnValIle----- 325
Db 2083 AAGATAGACCAAGCGCATACGNAATTAATGGAGATCCAGATTTAAACAGCGCTTTAGAC 2024
QY 326 AsnIleArgAsnAspAlaGluAlaThrArgPheTyrArgAsnGlnLysValAlaProGlu 345
Db 2023 AATGCTTTAAACGACATAGATAGCTTA-----AACAGTCTCAATGTTCACAA 1976
QY 346 AsnSerTyrThrTyrAspSerLeuTyrGlnLeu-----IleSerAlaThrGlyArgGlu 363
Db 1975 CGTCAAACTGTTAAGGATAACATCAACCATGTGCAACACTCTAGAAGCTTTAGCTCAAGAA 1916
QY 364 MetAlaAsnIleGlyGlnGlnAsn-----AsnGlnLeuProSer 376
Db 1915 TTCACAAAGCAAAAGAGCTTAATGATGCTATCAAGCAATGAGAGATAGCATTTGAAT 1856
QY 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsn-----TyrThrArgSerTyrSer 394
Db 1855 CAAGACAAATTCGTAATAAATAGCAATTAATCAATGAAGACTTAGCTCAACAAATGCC 1796
QY 395 TyrAspHisSer---GlyAsnLeuThrGlnIleArgHisSerSerProAlaThr----- 411
Db 1795 TATAATCATGCGATAGATAATAATAACATATTGTTGGTAAGACAAATGCGAGCATGGAT 1736
QY 412 -----GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsn 426
Db 1735 CCTCAATAATCAACAACGCACTCAAGATATAAATACAGCTATAAATGATTAATGGA 1676

Qy 427 ArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValaAspThrLeuPheAspAla 446
Db 1675 GATCAAAACTTCNAGATGCAAGACAGAGTCTAAACAAACAATTAACATT- 1622
Qy 447 GlyGlyHisGlnThrSerLeuLeuProGlyGln-----ThrLeuIle--- 460
Db 1621 -----ACTGTTTAACTGAACCAACAAACAAAGCATTTGGAAAAACATCATTAAC 1574
Qy 461 ---TrrPThrProArgGlyGluLeu---LysGlnValAsnAsnGlyProGlyAsnGluTrrP 478
Db 1573 CAACAAAGTAGAGCAAAATGTTGCTAAACAGTTAAGTCAATGCT- 1529
Qy 479 TyrArgTyrAspSerAsnGlyMetArgGlnLeuLysVal----- 491
Db 1528 ---AAATCTTAATGGAAGAAATGGAAGAAATTAAGTTGCAGTAGCCAAAGCGTCATTA 1472
Qy 492 -----SerGlnGlnProThrGlnAsnThrThrGlnGlnGln 503
Db 1471 GTAAGACAAAATAGTATATATTAATGAAGATGCTCTGAAAAAGAGCATATGAACAA 1412
Qy 504 ArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 523
Db 1411 GCTATT-----GCCAAAGGTGAGNAATTAATTAATTCAGAAATAATCCAAACATTAAGT 1358
Qy 524 GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValaArgValLeuHis 543
Db 1357 AGTACTGATCAATCGTACCATTCAGAAATTAATGATGCTGAA---CAAAATCTTCAT 1301
Qy 544 TrpGluSer-----GlyLysProGluAspValAsnAsnGlnGlnLeuArgTyrSerTyr 561
Db 1300 GGTGAAAATAAATTAAGACACAGACAGAAATTCGAAAGAAATGAATAACAA- 1250
Qy 562 AspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGlu 581
Db 1249 ---AATCTAGACGGATTAATTTACGTCAAAATCAACAAATTAATCCAGATATAGGCAGA 1193
Qy 582 GluGluTyrTyrProPheGlyGlyThrAlaLeuTrrPAlaAlaAsnSerGlnThrGluAla 601
Db 1192 ACAACAATAAATCGAGTACTCAGAACTCAGAACTAGAAAGCAAGCAATAAACAAGCT 1133
Qy 602 SerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 621
Db 1132 ---ATGCAACAACTTAACAAAGTATAGCCGATAGGATGCTACT----- 1091
Qy 622 GlyTyrArgTyrTyrGlnProTrrPAlaGlyArgTrrPLeuSerAlaAspProAlaGlyThr 641
Db 1090 -----CTAAATTCAGTAACTATCTCAATGAAGAT----- 1061
Qy 642 IleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGlu 661
Db 1060 -----TCTGAGAAAAGTTAGCGTACGATATGCTGTAGCCAGCTGAACAA 1013
Qy 662 AsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeu 681
Db 1012 -----CTCATAATCAACTTAACGCCCACTATGATATAAGTAAATTAATCAAGCTATT 959
Qy 682 LysPheLys---LeuAlaAlaLysSerSer-----HisValValLysTrrPAsn 696
Db 958 ACTCAAAAGGTTCATTCAAGCAAAAAGATTCAATGCGGTGCGAATAAATTCGACAAAAT 899
Qy 697 GluLysGluSerSerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSer 716
Db 898 CAACGATTCAAATTTAATAATAATCAATCA-----ACAAATTTAATGATATAA 848
Qy 717 AspProSerGlyTyr-----LeuLeuSerHisGluGluLeuLysGlyIleGluLys 734
Db 847 CAAAAGCAAGCATTAATGACTTAATTAATCATGCTCAA-----ACTAAA 803
Qy 735 SerGlnIleIleTyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThr 754
Db 802 CAGCAAGTGGCA-----GAAATAATTTGACCAAGCTTAATAGTTA 764
Qy 755 AsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIle 774

Db 763 AATAACGAATGGGCACA-----CTAAAAACACTCGTAGAAGAACAG 722
Qy 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisPro-----AspPheTyr 791
Db 721 TCAACAGTTTCATCAACAAAGTAAATATATTAATGAAGATCCCGCAAGTTCAAAATATTAT 662
Qy 792 SerGlu-----ThrAspPhePheAlaLeu 799
Db 661 AATGACTCCATTCAAAAAGTCGAGAAATATTAAACGGCAGCTACAGATGATGTTTTAAAC 602
Qy 800 MetAspLys-----SerGluLysAsnAspTyrSerGly 810
Db 601 AACATAAATAATAGCAGATGCCATTCAAAACATTCATTAACTAAAAACGATTTACATGCT 542
Qy 811 GluArgGlyValIleTyrAlaAlaMet-----GluValLysValTyrHisAsp 825
Db 541 GATCAAAAATTTACAAAAGCACAACAGATGCAACCAATGAATTAACATTTAAACAAAT 482
Qy 826 LeuLysAsn-----LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 481 CTAACAAATCTCAAGACAAAGCGAG---CATGATGAGATTAACTCTGCTCCTTCAGA 425
Qy 844 ThrGlnLeuSerAsnGlu-----GluArgAlaLeu-----LeuGlnGluThr 857
Db 424 ACTGAAGTTTCTAATGATTTAAATCATGCTAAAGCACTTAATGAAGCTATGCGTCAACTT 365
Qy 858 GluProAlaIleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThr 877
Db 364 GAGAAATCAAGTTGCTCTT-----GAAACAGAGTTTAAAAAATTAAGCGACTTTATCA-- 313
Qy 878 MetLysAlaIleLysLysSerLeuLysGlyHisLysIleAsn 891
Db 312 ATGAAG-----ATGAAGCGGCACAAAATGAAT 286
RESULT 12
US-10-793-626-2963
; Sequence 2963, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2963
; LENGTH: 15071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2963
Alignment Scores:
Pred. No.: 0.278 Length: 15071
Score: 144.00 Matches: 194
Percent Similarity: 36.29% Conservative: 174
Best Local Similarity: 19.13% Mismatches: 389
Query Match: 3.04% Indels: 258
DB: 6 Gaps: 53
US-10-647-956A-6 (1-915) x US-10-793-626-2963 (1-15071)
Qy 3 SerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLys 22
Db 4240 CGGTATTAATTAATGACTTAAACCAAGCGGAGAGACATTATTAACTAACAGCTCAATCTTAAC 4299
Qy 23 LeuAsnValArgThrLeuArgTyrLeuArgThrGlnAlaAspGluAsnSerAspGluLeu 42

Db		: : : :	4300 TTAATGCACAGACATT-----ACTAATGCTTTAAATAAT-----	4335
Qy	43 IleThrPheTyrGluPheAsnIleProGlyPheClnValLysSerThrAspProArgLys	: : : : :	62	
Db	4336 ATTAACAACGACCAAGATAACCTTCATGGAGCTCAA---AAATACAGCAGACAAAAT	: : : : :	4392	
Qy	63 AsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeu	: : : :	82	
Db	4393 ACACTAATCAAGCCATTGTGAAC-----TTAATCATCTTAATCAACTCAA	: : : : :	4440	
Qy	83 ArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgPro	: : : : :	102	
Db	4441 AAAGATCGCTTATACAAGCT-----ATTAAATCGAGTACATCTAGGAC	: : : : :	4485	
Qy	103 ValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeu	: : : : :	122	
Db	4486 CAAGTT-----GCAGAAAAACTTAAAGAGGCCGAGCGCTT	: : : : :	4521	
Qy	123 ProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThrGluArg	: : : : :	142	
Db	4522 GATGAAGCTATGAACAACTTGAAGATCAATGAATCAAGATGATCAAAATTTCAAATAGC	: : : : :	4581	
Qy	143 LeuIleTrpAlaGly----AsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCys	: : : : :	161	
Db	4582 AGCCATTCTATAAATGAAGACTCAGACAAACAAAACCTTATAAT-----	: : : : :	4626	
Qy	162 ValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGlyVal	: : : : :	181	
Db	4627 -----GATAAATCCNAGCTGC AAAAGAA	: : : : :	4650	
Qy	182 ValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGlyGlu	: : : : :	201	
Db	4651 ATAATTAATCAAAACATCTAATCCAACCTTAGATAAACAAAAAATTCGTGATACACTTCAA	: : : : :	4710	
Qy	202 AspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThr	: : : : :	221	
Db	4711 AATATTAAAGATGCAGTGAATATTTACATGGTGATCAAAAAATTTAGCTCAATCTATAACAA	: : : : :	4770	
Qy	222 AspAlaThrGly-----	: : : : :	225	
Db	4771 GACCTAATATCAATTAATATCATTTAGATGACTTAACCGAAGAACAAAAACCATT	: : : : :	4830	
Qy	226 ---AlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAspVal	: : : : :	244	
Db	4831 AACCGTTAATTAATAATGCTGATFACTCGAGATGAGGTAAATAAA---CAACTAGAGATT	: : : : :	4887	
Qy	245 AlaGlyGlnLeuLysGlySerTrpLeuThrLeu-----LysGlyGln	: : : : :	258	
Db	4888 GCTAAACAATTAATGCTGTATGATGATACACTTCATAAAGTCAATAATGATAAAGATCAA	: : : : :	4947	
Qy	259 AlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGlu	: : : : :	278	
Db	4948 ATTCAACATTTA-----AGCAATTACATTAACTGCTGATATGATGATAAACAACAA	: : : : :	4995	
Qy	279 GluHisGlyAsnGlyIleValThrGluTy-SerTyrGluProGluThrGlnArgLeuIle	: : : : :	298	
Db	4996 AATTATGATAATGCTATT-----AAAGAAGCTGAGGATTTAATT	: : : : :	5034	
Qy	299 GlyIleThrThrArgArgProSer-----AspAlaLysValLeuGlnAspLeuArgTyr	: : : : :	316	
Db	5035 -----CATATCATCTCCAGATACATTAAGATCATTAAGANTTTACAAGATTTTATAAAC	: : : : :	5085	
Qy	317 GlnTyrAspProValGlyAsnValIle-----	: : : : :	325	
Db	5086 AAGATACCAAGCGCATTAACGAATTAATGAGAGATCCAGATTAAACAGGCTTTAGAC	: : : : :	5145	
Qy	326 AsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGlu	: : : : :	345	
Db	5146 AATGCTTTAAACGACATAGTAGCTTA-----AACAGTCTCAATGTGCCACAA	: : : : :	5193	
Qy	346 AsnSerTyrThrTyrAspSerLeuTyrGlnLeu-----IleSerAlaThrGlyArgGlu	: : : : :	363	

5194	CGTCAAACTGTTAAGGATTAACATCAACCATGTGACAACTCTAGAAAGTTT	AGCTCAAGAA	5255
364	MetAlaAsnIleGlyGlnGlnAsn-----	AsnGlnLeuProSer	376
5254	TTGCAGAAACCAAAAGAGCTTAATGATGCTATGAAAGCAATGAGAGATAGCATATGAAAT	5313	
377	ProAlaLeuProSerAspAsnAsnThrThrAsn-----	TyrThrArgSerTyrSer	394
5314	CAAGAGCAAAATTCGTAAAAATAGCAAAATTAATCAATTAATGAAGACTTAGCTCAACAAAATGCC	5373	
395	TyrAspHisSer--GlyAsnLeuThrGlnIleArgHisSerProAlaThr-----	411	
5374	TATAATCATGCAGTAGATAATATAATAACATTTATTGGTGAAGACAAATGGCAGCATGGAT	5433	
412	-----GlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsn	426	
5434	CCTCAAAATAATCAACCAAGCAACTCAAGATATAATAATACAGCTATAAAATGGATTAAATGGA	5493	
427	ArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAla	446	
5494	GATCAAAAACCTTCAAGATGCAAAAGACAGATGCTAAACAACAAAATTACTAATCTTT-----	5547	
447	GlyGlyHisGlnThrSerLeuLeuProGlyGln-----	ThrLeuIle--	460
5548	-----ACTGGTTTAACTGAACCAACCAAAACAGCATTTGGNAACATCATTTAAC	5595	
461	---TrpThrProArgGlyGluLeu---LysGlnValAsnAsnGlyProGlyAsnGluTrp	478	
5596	CAACAAACAGTAGAGCAAAATGTTGCTAAACAGTTAAGTCATGCT-----	5640	
479	TyrArgTyrAspSerAsnGlyMetArgGlnLeuIleVal-----	491	
5641	---AAATTCTTAAATGCAAAAATGGAAGAAATTAAGATTTCAGTAGCCAAAGCGTCAATTA	5697	
492	-----SerGluGlnProThrGlnAsnThrThrGlnGlnGln	503	
5698	GTAAGACAAAAATAGTAACATAATTAATGAAGATGCTCTGGAAAGAGCATATGAACAA	5757	
504	ArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThr	523	
5758	GCTATT-----GCAAAAGCTCAGGAAATAATTAATTCAGAAAAATATCAACAATAAAGT	5811	
524	GluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHis	543	
5812	AGTACTGATATCAATCGTACCATTTCAGAAATAATTAATGATGCTGAA---CAAAATCTTCTCAT	5868	
544	TrpGluSer-----GlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyr	561	
5869	GGTGAAATTAATTAAGACAGGACAGCAAGAAATTCGAAAGAAATGAATATACAA-----	5919	
562	AspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGlu	581	
5920	---AATCTAGACGATTAATATTCAGCTCAAAATAACAAAATTAATCCAAAGATATAGGCAGA	5976	
582	GluGluTyrTyrProPheGlyGlyThrAlaIleLeuTrpAlaIleAsnSerGlnThrGluAla	601	
5977	ACAACAACTAAACCTGCAGTAACCTCAGAAACTAGAAAGCAAAAGCAATAAACCAAGCT	6036	
602	SerTyrIlysthrlleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	621	
6037	---ATGCAACAACTTAAACAAAGATATAGCCGTAAGGATGCTACT-----	6078	
622	GlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThr	641	
6079	-----CTAAATTCCTAGTAACATATCTCAATGAAGAT-----	6108	
642	IleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGlu	661	
6109	-----TCTGAGAAAAAGTTAGCCGTACGATAATGCTGTGAAGCCCAAGCTGTAACAA	6156	
662	AsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeu	681	
6157	-----CTCATTAATCAACTTAACGCCCAACTATGATATAGTAATATATCAAGCTATT	6210	

```
Qy 682 LysPheLys---LeuAlaAlaLysSerSer-----HisValValLysTrpAsn 696
Db 6211 ACTCAAAAGGTCAATCAAGCAAAAGATTCATGTCACGGTGGCAATAAACTTGCACAAAAT 6270
Qy 697 GluLysGluSerSerTyrThrLysAsnLysSerLysLysValValArgValGlyAspSer 716
Db 6271 CAAGCAGATTCAAATTTAATAATAATCAATCA-----ACAAATTTAATGATATAA 6321
Qy 717 AspProSerGlyTyr-----LeuLeuSerHisGluLysLysGlyIleGluLys 734
Db 6322 CAAAAGCAAGCATTAATAATGACTTAATAATCATGCTCAA-----ACTAAA 6366
Qy 735 SerGlnIleIleTyrSerArgLeuGluLysSerSerLysSerGluLysSerLysThr 754
Db 6367 CAGCAAGTGGCA-----GAAATAATTGCACCAAGCTAATAAGTTA 6405
Qy 755 AsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIle 774
Db 6406 AATAACGAATGGGCACA-----CTAAAAACACTCGTAGAAGACAG 6447
Qy 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisPro-----AspPheTyr 791
Db 6448 TCAAAACGTTTCATCAACAAAGTAATATATTAATGAAGATCGCAAGTTCAAAAATATTTAT 6507
Qy 792 SerGlu-----ThrAspPhePheAlaLeu 799
Db 6508 AATGACTCCATTCAAAAAGGTGCGAGAAATATTAACCGCAGCTACAGATGATGTTTTAAAC 6567
Qy 800 MetAspLys-----SerGluLysAsnAspTyrSerGly 810
Db 6568 AACATAAATAGCAGATGCCATTCAAACACATTTCATTAACTAAACGATTTACATGGT 6627
Qy 811 GluArgLysIleTyrAlaAlaMet-----GluValLysValTyrHisAsp 825
Db 6628 GATCAAAAATATCAAAAAGCAACAAGATGCAACCAATGAATTAATAACTATTTAACAAAT 6687
Qy 826 LeuLysAsn-----LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 6688 CTAAACAACTCTCAAGACAAAGCGAG---CATGATGAGATTAACCTCTGCTCTCTTCAAGA 6744
Qy 844 ThrGlnLeuSerAsnGlu-----GluArgAlaLeu-----LeuGlnGluThr 857
Db 6745 ACTGAAGTTCTATGATGTTAATAATCATGCTAAAGCAGCTTAATGAAGCTATGCGTCAACTT 6804
Qy 858 GluProAlaIleAlaAlaAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThr 877
Db 6805 GAGAAATGAAGTTGCTCTT-----GAAAACAGTGTAAAAAATAAAGCGAGCTTTATCA-- 6856
Qy 878 MetLysAlaIleLysLysSerLysLysGlyHisLysIleAsn 891
Db 6857 ATGAAG-----ATGAAGCGGCACAAAATGAAT 6883

RESULT 13
US-11-113-424-13
; Sequence 13, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-113-424-13

Alignment Scores:
Pred. No.: 0.137 Length: 8354
Score: 143.50 Matches: 219
Percent Similarity: 31.19% Conservative: 126
Best Local Similarity: 19.80% Mismatches: 392
Query Match: 3.03% Indels: 373
DB: 7 Gaps: 55

US-10-647-956A-6 (1-915) x US-11-113-424-13 (1-8354)
Qy 31 LeuArgThrGlnAlaAspGluAsnSerAspGluLeuIleThrPheTyrGluPheAsn--- 49
Db 5078 CTGGCAACCAAAAGCAATGAAACGGA-----TGGACAACATTTATGATAGCAGACG 5131
Qy 50 -----IleProGlyPheGlnValLysSer----- 57
Db 5132 TTGGCGCGCTGACAAATGTGACCTTCCCTACTGGCAGGTGAGCAGTTTCCGAAGTGAT 5191
Qy 58 ThrAspPro-----Arg 61
Db 5192 ACAGACAGTTTCAGTGCATGTCCAGGTAGACACCTCCAGCAAGGATGATGTCAACATAACC 5251
Qy 62 LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnVal 81
Db 5252 ACCAACTGTCTGCCTCAGCGCGCTTCTACACACTG-----CTGCAAGACCAAGTC 5302
Qy 82 LeuArgGluGluSerValAspAlaGly-----ArgThrIleThrLeuAsnAspIle 98
Db 5303 CGGAACAGCTACTACATCGGGCGCGATGGCTCTTGGCGTGTCTGGCCAGCGCATG 5362
Qy 99 Glu-----SerArgProValLeuIleAlaAsnAlaThrGlyValArgGlnAsn 114
Db 5363 GAGGTGGCGCTGCAGACTGAGCCCACTTGTCTG-----GCTGGCAC-CGTCAACCC 5412
Qy 115 HisArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGlnGlnValGln 134
Db 5413 CACCGTGGGCAA-----GAGGAATGTAC 5436
Qy 135 AlaGlyGluLysThrThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu----- 152
Db 5437 GCTGCCCA-TCGACAACGGCTCAACTGTGGAGTGGCCCGCAGCGCAAGAGCAGGCTC 5495
Qy 153 -----LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeu 170
Db 5496 GGGGCCAGGTCACTGTCTTTGGCGCGCGTGC-----GGGTGC 5534
Qy 171 ThrGlnLeuAsnSerSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeu 190
Db 5535 ACAACCGA-AATCTCTATCTCTGGACTTTGATCGCGTAAACGACGACAGAGAATCTAT 5593
Qy 191 ThrAspAsnGlnAsp-----AlaAspTrpThrGlyGluAspGlnSer 204
Db 5594 GATGACCAACGCAAGTTCACCTTCGGATTCGTGTACGACCGCGCGGGCGG---CCCGAGC 5650
Qy 205 LeuTrpGln---GlnLysLeuSerSerAspValTyrIleThrGlnSerAsnThrAspAla 223
Db 5651 CTCTGGTCACCCAGCAGCGCTGAATGGTGTCAACGTGACATACTCC----- 5698
```

224 ThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeuAlaTyrAsp 243
|||
:::
5699 CTTGGGGGTTACATTGCTGCATCCAGAGGGCATCATGCTCTGAAGAATGGAATACGAC 5758
|||
:::
244 ValAlaGlyGlnLeu----- 248
|||
:::
5759 CAGCGGGCGGCATACATCCAGATCTTCGCTGATGGGAAGACATGGAGCTACACATAC 5818
|||
:::
249 -----LysGlySerTrpLeuThrLeuLysGlyGlnAlaGlnValIle----- 263
|||
:::
5819 TTAGAGAGTCCATGGTGTCTACTACAGCAGGCGAGTATATCTTTGATGTTGAC 5878
|||
:::
264 -----IleLysSerLeuThrTyr---SerAlaAlaGlyGlnLysLeuArgGlu 278
|||
:::
5879 AAGAATGACCGCTCTCTCTGTGAGCATGCCCAAGCTGGCGGCGAGACACTAGAGACC 5938
|||
:::
279 GluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlnThrGlnArgLeuIle 298
|||
:::
5939 ATCCGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAG----- 5983
|||
:::
299 GlyIleThrThrArgProSerAspAlaLysValLeuGlnAspLeuArg----- 315
|||
:::
5984 -----GSCAATGCCTCAGTCATACAGACCTTCACTGAGGATGGG 6022
|||
:::
316 -----TyrGlnTyrAspPro 320
|||
:::
6023 CACCTCTTCCACACCTTCTACCTGGGCAGCTGGCGAGGTGATATACAAATGTCGAAA 6082
|||
:::
321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln 340
|||
:::
6083 CTCTAAAGCTG-----GCAGACGCTCTTATGACACCAACC 6118
|||
:::
341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
|||
:::
6119 AAGGTC-----AGTTCCACTATGACAG-----ACG 6145
|||
:::
361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuPro----- 375
|||
:::
6146 GCAGGCGATGCTGAAGACCATCAACCTACAGAAATGAGGGCTTCACTGCACCATCCGCTAC 6205
|||
:::
376 -----SerProAlaLeuProSerAspAsnAsnThrTyrThr----- 387
|||
:::
6206 CGTCAGATTGGGCGCTGATTGACCGACAGATCTCCGCTTCACTGAGGAAGCATGGTC 6265
|||
:::
388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArg----- 405
|||
:::
6266 AACCCCGTTTGACTACAACTATGACACAGCTTCCGGGTGACACGATGCGAGCTGTG 6325
|||
:::
406 ---HisSerProAlaThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArg 424
|||
:::
6326 ATCAACGAGACCCCACTGCCCATTTGATCTCTATCGCTATGATGTCAGGCAAGACA 6385
|||
:::
425 SerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeu--- 443
|||
:::
6386 GAGCAGTTTGGGAAGTTGGTGTCTATTACTATGACATTAACACAGATCATCACCAGCT 6445
|||
:::
444 -----PheAspAlaGlyHisGln----- 450
|||
:::
6446 GTCATGACCCACCAAGCATTTTGTGTCATATGGCAGGATGAAGGAGTGCAGATGAG 6505
|||
:::
451 -----ThrSerLeuLeuProGlyGlnThrLeuIleTrpThrProArgGlyGluLeu--- 467
|||
:::
6506 ATCTTCGCTCGCTACTGATGATGATCGCTCCAGTATGATTAACATGGGCGGAGTAGTG 6565
|||
:::
468 ---LysGlnValAsnAsnGlyPro-----GlyAsnGluTrpTyrArgTyrAsp 482
|||
:::
6566 AAGAAGGAGCTGAAGGTAGGACCCCTACGCCAATACCACTCGCTACTCTCTATGATGATGAT 6625
|||
:::
483 SerAsnGlyMetArgGln---LeuLysValSerGluGlnPro----- 495
|||
:::
6626 GCTGACGGCGAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTAC 6685
|||
:::

496 -----ThrGlnAsnThrThrGln----- 501
|||
:::
6686 GACCTCAATGGAACTGTCACATTCTAGACCTCGGAACAGTCGACGGCTCACACCACCTA 6745
|||
:::
502 -----GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGln 517
|||
:::
6746 CGGTATGACATCCGGACCGCATCACTCGCTGGGTGAGCTGCAATACAAAGATGGATGAG 6805
|||
:::
518 SerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly----- 535
|||
:::
6806 GATGGCTTCTCAGGCGAGCGGGCGGTGATATCTTTGAGTACAACCTCAGCTGCGCTGCTC 6865
|||
:::
536 ---ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 554
|||
:::
6866 ATCAAGGCTTACAACCGGCTGGCAGCTGG----- 6895
|||
:::
555 AsnGlnLeuArgTyrSerTyrAspAsnLeu-----IleGlySer----- 567
|||
:::
6896 ---AGTGTCAAGTACCGCTACCGTGGCGGCGGTGTCCAGCAAGACAGCAGCCAC 6952
|||
:::
567 ----- 567
|||
:::
6953 AGCCACCACCTGCAAGTTCTTCTATGCAGACCTGACCAACCCCAACAGGTACCCACCTG 7012
|||
:::
568 -----SerGlnLeuGluLeuAspAsnGlnGly----- 576
|||
:::
7013 TACAACCACTCCAGCTCTGAGATCACTCCCTCTACTACGACTTGAAGGACACCTCTTT 7072
|||
:::
577 -----GlnIleIleSerGluGluTyrTyr----- 585
|||
:::
7073 GCCATGGAGCTGAGCAGTGTGTGATGATTTTACATAGCTTGTGACAACATCGGAGCCCT 7132
|||
:::
586 ---ProPheGlyGlyThrAlaLeuTrpAlaAlaAsn----- 596
|||
:::
7133 CTTGTCTCTTTAGTGGAAACAGGTTTGTATGATCAAGCAAAATCTGTACACAGCCTATGGG 7192
|||
:::
597 -----SerGlnThrGluAlaSerTyrLysThrIle-----ArgTyrSerGlyLys 611
|||
:::
7193 GAGATCTACATGGATACCAACCCCACTTTCAGATCATCATAGCTTACCATGTGGCGCTC 7252
|||
:::
612 GluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGly 631
|||
:::
7253 TATGATCCACTACCAAGCTTGTCCACATGGCGCGGAGATTATGATGTGTGGCGGA 7312
|||
:::
632 ArgTrpLeuSerAlaAsp-----ProAlaGlyThrIleAspGly 644
|||
:::
7313 CGCTGGAGTAGCCACACCAAGCTGTGGAAGCACCTTAGTAGCAGCAACGTATGCTCCT 7372
|||
:::
645 LeuAsnLeuTyrArgMetValArgAsnAsnProValSer----- 657
|||
:::
7373 TTTAATCTCTATATGTTCAAAAACAACACCCCATCAGCAACTCCAGGACATCAAGTGC 7432
|||
:::
658 ---LeuGlnAspGluAsn---GlyLeuAlaProGluLysGlyLysTyrThrLysGluVal 675
|||
:::
7433 TTCATGACAGATGTTAAACAGCTGGCTGCACCTTTGGATTCCAGCTACACA----- 7484
|||
:::
675 lAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLysTrp 695
|||
:::
7485 -----ACGTGATCCCTGGTTATATCCCAACACAGACATGGATGCCATG 7525
|||
:::
695 pAsnGluLysGluSerSerTyrThr-----LysAsnLysSerLeuLysValValArg 712
|||
:::
7526 GAACCCCTCTACGAGCTATCCACACACAGATGAAAACCGCAGAGTGGGACAAACAGCAAG 7585
|||
:::
712 gValGlyAspSerAspProSerGlyTyrLeuLeuSerHisGluGlu----- 727
|||
:::
7586 TCTATCC-----TCGGGGTACAGTGTGAAGATACAGAAAGCAGCTCAAGGCCCTTT 7633
|||
:::
728 -----LeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
|||
:::
7634 GTCACCTTAGAACGGTTTGACAGCTCTATGGCTCCACAATCACCAGCTGCCAGAGCT 7693
|||
:::
742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluI 762
|||
:::


```
Db 7694 CCAAGACCAAGAGTTTGCATCCAGCGCTCAG---TCITGGCAAGGGGTCAAGTTT 7750
Qy 762 eSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHisLy 782
Db 7751 GCCTTGAAGATGCC-CGAGTGACACACAGACATCATCAGTGTGGCCAATGAGGATGGCG 7809
Qy 782 sTyrArgSer-----AsnHisProAspPheTyrSer----- 792
Db 7810 AAGGTTGCTGCCCATCTTGAAACCAATGCCCACTACTAGAGAACTCGCACTTCCACCATGA 7869
Qy 793 -----GluThrAspPheAlaLeuMetAspLysSerGluLysAsnAspTyrSer-- 809
Db 7870 TGGGTTGGATACCATTAATCTTGTGAACACGAGACCTTCAGAA---CGTGACCTGGCCAT 7926
Qy 810 -----GlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHi 824
Db 7927 CCTGGGCTCAGTGGGGGGCGGCGAACCCTGGAGAATGGGGTCAACGCTCACTGTG----- 7981
Qy 824 sAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeu-----AlaHi 841
Db 7982 -----TCCAGATCAACACACAGTACTTAATGGCAGGACTAG 8016
Qy 841 sProTyrThrGlnLeuSerAsnGluAlaGluLeuGlnGluThrGluProAlaI 861
Db 8017 ACGTACACACACATCCAGCTCCAGTAGCGGGCACTGTCTTGACACACGCTACGGGAC 8076
Qy 861 eAlaIleAspArgGlu 866
Db 8077 AACGTTGGATGAGGAG 8092

RESULT 14
US-10-793-626-4075
; Sequence 4075, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4075
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4075

Alignment Scores:
Pred. No.: 0.142 Length: 3055
Score: 136.50 Matches: 127
Percent Similarity: 35.28% Conservative: 121
Best Local Similarity: 18.07% Mismatches: 254
Query Match: 2.88% Indels: 201
DB: 6 Gaps: 27

US-10-647-956A-6 (1-915) x US-10-793-626-4075 (1-3055)
Qy 251 SerTrpLeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSer 270
Db 1022 AGCATGTTGAATCAAAAACACAGATGATCAGACAATATAGAAAATTTTATAAAAT 1081
Qy 271 AlaAlaGlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyr 290
Db 1082 ATGACAGATCAACATCTGAGTCAAGTTCAATCAGACAAAATAAAGCACTTGTAAAGTTT 1141
Qy 291 GluProGluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysVal 310
```

```
Db 1142 -----ATATTGATAGGAGGGGTAAAGATTTTGAAGCCT 1174
Qy 311 LeuGlnAspLeuArgTyrGlnTyrAspPro---ValGlyAsnValIleAsnIleArgAsn 329
Db 1175 TTACATATATAGTTATGGAGAACTTTGGCCCTTTTATTAAAGAAACTATGATTTTGAGCAA 1234
Qy 330 AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThr 349
Db 1235 GTTGAACACTGATCAACTCTTTTAAATGTTGGTAAAAACCTGGATCTCGTAAACAACTGATT 1294
Qy 350 TyrAsp-----SerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAla 365
Db 1295 TTTGATGCTATAGTATACGCAATTATACGCTATGCTTCGACCAAACTAGAAAAAGAGGA 1354
Qy 366 AsnIleGlyGlnGlnAsnAsnGlnLeuProSerPro-----AlaLeuPro 380
Db 1355 GATTTAAGAAGTCAATTTTGCAGACGCGTAAATCGCCAATGCTGTAAATTTATCAATTTAAA 1414
Qy 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 1415 GTTAAATAATCAAACTTTTAAATTCAT---AGAGAAGCCCACTTTTATAAGAGGGGAAT 1471
Qy 401 LeuThrGlnIleArg-----HisSerSerProAlaThrGlnAsnAsnTyrThrVal 417
Db 1472 ATAACTAAACACACACCAAGTTAAATATATATATGATTAATGATTAATCAATTTGAATTA 1531
Qy 418 AlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspPro 437
Db 1532 AGAGAAAGTAAAGTGAATCAAGGTAATCAATTTATCGTCAATTTATAGCGTAAATGCT 1591
Qy 438 AsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGln 457
Db 1592 GAACAATTTTCGTCAATTAATTT----- 1612
Qy 458 ThrLeuIleTrpTrpProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGlu 477
Db 1613 -----ATTTTGCTCAAGAGAAATTTAAAGTTT----- 1642
Qy 478 TrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGln 497
Db 1643 -----CTTCAG 1648
Qy 498 AsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuLuleuArgThrThrGln 517
Db 1649 TCAAATAGTAAAGACAAACAACTCGATT-----CTTAGAACCTTTT 1690
Qy 518 SerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAla 537
Db 1691 AATAGTCAGCGATTTCATGAGATTGACATCTACTTGTGA----- 1729
Qy 538 GlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeu 557
Db 1730 -----GAAAATGTAAAGCAAGAAAAGTA-----CAAATT 1759
Qy 558 ArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGln 577
Db 1760 GAAAAATAGATATAC-----ACTCAAAATTTGAA----- 1783
Qy 578 IleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrp----- 593
Db 1784 -----AATTATGGAATGATATAGAT 1804
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg 613
Db 1805 ACATTTAAATAATGATCAATTTGGCCCTTATATAAAGAAATTAGAGAGTTCTCAGACAGATAAA 1864
Qy 614 AspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrp 633
Db 1864 ----- 1864
Qy 634 LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
```

```
Db 1865 -----ATGATTGAAAAATTCACCAATTT 1888
Qy 654 AsnProValSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyrThrLys 673
Db 1889 AATGATTATGATGCAAAATTCCTCAAGTCATTTGAAGACGCTAAGATAATAAATACTAAG 1948
Qy 674 GluValAsnPhePheAspGluLeuLysPheLysLeuAlaLysSerHisValVal 693
Db 1949 GAATTA-----GATGATTTA-----AATCATAAATAT 1975
Qy 694 LysTrpAsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLysValValArgVal 713
Db 1976 AAAGTGAATTTGAATTAAGTAGAATACTATAAAATTTAAACGGGAAAAATCAATTT 2035
Qy 714 GlyAsp---SerAspProSerGlyTyrLeuLeuSerHisGluLeuLysGlyIle 732
Db 2036 GACGATTTGAAAAAAGAACAAATTTATTTGATAAATTTAAAGCAAGATTTAAANATGATT 2095
Qy 733 GluLysSerGlnIlelle-----TyrSerArgLeu----- 742
Db 2096 CAGGAATCTAAGATTAATTAATCACTATTATTTACTAGTTTACAAAGTTTAAAAAAGATAAA 2155
Qy 743 GluLysAsnSerSerLeuSerGluLysSerLysThrAsn---LeuSerLeuGlySerGlu 761
Db 2156 GATGAATTTAGTGCCTCTATGAGCAATCAAAATTTAAACGAAACAACTATCAATGAA 2215
Qy 762 IleSerGlyTyrMetAlaArg-----ThrIleGlnAspThrIleSerGlu 776
Db 2216 ATTAAAGTTTTCAAAACAACTCGAACATTTATCAACACGAGAAATGAATTAATCTCAA 2275
Qy 777 TyrAlaGluHisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhe 796
Db 2276 TTT-----AATCAGTATCTAGAAAAAAACCAAGTTTCTTCAATCAATTAGAT--- 2323
Qy 797 PheAlaLeuMetAspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAla 816
Db 2324 -----AAGATTATTAGTAGTTTATCAACAAAAACCGGTAATT 2359
Qy 817 AlaMetGluValLys-----ValTyrHisAspLeuLysAsnLysGlnSerGlu 832
Db 2360 GAAGAAGAAATATAAAGATTATACAGTGAATATAATGATTTTATACCAAAAAAGAGAA 2419
Qy 833 Leu-----HisValAsnTyrAlaLeuAlaHisProTyrThrGln 845
Db 2420 TTGACGAAAGAAATGAACAAACAAAGAAAGATTTTGCAATTTATGAACATTAACCTGAA 2479
Qy 846 LeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArg 865
Db 2480 GAGATTTTAAAGCTGAAAGAAATATATAGATGAATCTCGAAAGACAAAAAAGGATGAGAAA 2539
Qy 866 GluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeu 885
Db 2540 TTATTTGATAAATTACAACTAGATAAATCATCTTATCTTAGCAAAATTTAAAGAG----- 2593
Qy 886 LysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaIle 905
Db 2594 AAGAAACACAGTTAATGAATTAATGATCATCAATCAATCAATATATAGATGCGCTTAATT 2653
Qy 906 AlaGluAsn 908
Db 2654 GATTTGAAT 2662
```

RESULT 15

US-10-623-155-117

; Sequence 117, Application US/10623155

; Publication No. US20050261166A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Peckham, David W.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

```
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 6921
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-155-117

Alignment Scores:
Pred. No.: 0.531 Length: 6921
Score: 135.50 Matches: 220
Percent Similarity: 34.29% Conservative: 151
Best Local Similarity: 20.33% Mismatches: 395
Query Match: 2.86% Indels: 317
Db: 6 Gaps: 51
```

US-10-647-956A-6 (1-915) x US-10-623-155-117 (1-6921)

```
Qy 4 TyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsnArgLysLeu 23
Db 932 TATGAACCTAAACTGTGTCAGAGAGAGCAGTTATAGCTCACAAGATAATATTGAGAAT 991
Qy 24 AsnValArgThrIleuGluTyrLeuArgThrGlnAlaAspGluAsn----- 38
Db 992 CTAATAAGTACTTTAAAGCAATGGAGATCTGAAGTAGATCAAAAGACAGAGGTATTCAT 1051
Qy 39 -----SerAspGluLeuIleThrPheTyr 46
Db 1052 GCCTTAGAGATGAGTTGTCAGAAAGCTAAAGCCATCAGTATGAAATGTTTAAACGTAT 1111
Qy 47 GluPheAsnIleProGlyPheGlnValLysSerThrAspProArgLysAsnLysAsnGln 66
Db 1112 AAAGAACGGGACCTTGATTT-----GACTGGCACAAGAAAA----- 1150
Qy 67 SerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGlnValLeu---ArgGluGlu 85
Db 1151 -----GCAGATCAATTAGTTGAAGAGTGGCAA 1177
Qy 86 SerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSerArgProValLeuIle 105
Db 1178 AATGTTTCATGTCAGATTGCAACACAGGTTCACGGGACTTAG----- 1219
Qy 106 IleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsnThrLeuProGlyArg 125
Db 1220 -----GGCATTGGCAAAATCCTGAAGTACTACAGACACTTACCAT----- 1261
Qy 126 LeuLeuAlaIleThrGluGlnValGlnAlaGlyLysIleThrGluArgLeuIleTrp 145
Db 1262 -----CCTTTAGATGATCGATCCAGCAGGTTGAA---ACTACTCAGACAAAGATT--- 1309
Qy 146 AlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyr 165
Db 1310 CAGGAAAAATCAGCCT---GAAAAATAGTAAAAACCTAGCCACACAGTGAATCAACAGAA- 1365
Qy 166 AspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly----- 180
Db 1366 GAT---GCTGGTGTCCGAATAGAAATGAACACAGACAAATGGACGAGTGTCAANAATA 1422
Qy 181 -----ValValLeuSerGlnSerGlnLeuThrAspAsnGlnAspAlaAspTrp 198
Db 1423 TGCAGAACAGTACTCAGCTACAGTGAAGGACTATGAATTAACAACAAATGACCTACCGGGC 1482
Qy 199 ThrGlyGluAspGlnSerLeuTrpGlnGlnLysSerSerAspVal-TyrIleThrGln 218
Db 1483 CATGGTAGA-----TTCAACAACAAAAATCTCCAGTGAAGACCGCGAAGAAATGCA 1530
Qy 218 nSerAsnThrAspAlaThrGlyAlaLeuLeuThrGln-----ThrAspAlaLysGlyAs 236
Db 1531 GAGTTTCAGCAGAT-----CTCATTTTCAAGAGTTTCATGACCTAAGGACTCG 1578
```

Qy 236 nileGlnArgLeuAlaTyAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLy 256
Db 1579 ATATACTGCCCTGCTCACTCTCATGACACACATATATTAAATTTGCTGGTGCATTGAA 1638
Qy 256 sGlyGlnAlaGluGlnValIleLeuLysSerLeuThrTySerAlaAlaGlyGlnLysLe 276
Db 1639 GAGGCTGGAGAGGAGGAGATTAAAGGTGT-----AAGGA 1674
Qy 276 uArgGluGluHisGly-----AsnGlyIleValThrG1 287
Db 1675 GACTTCTGAACATGGGGCATANTCAGATCTGCTTCAGCGTCAGAGGCAACAGGCTTGA 1734
Qy 287 uTySer-----TyGluProGluThrGlnArgLeuIleGlyIleThrThrAr 303
Db 1735 GAATAGCAAACTTACAGGAAGATAAGTGAGTTGGAAAGATGTAGCTGACTAAAGAA 1794
Qy 303 gArgProSerAspAla-----LysValLeuGln-----AspLe 314
Db 1795 ACAAAAGTCCCGAGTAGAGGAAGAACTTCCGAAGGTCAGGGAGGCTGCAGAAAAATGAAT 1854
Qy 314 uArgTyGlnTyAspProValGlyAsnValIle-----AsnIleArgAsnAspAlaG1 332
Db 1855 GAGAAACAGCAGAGAAATGTAGAAGATATCTCTCGCAGAAAGATAGGGCTGAAAGTGA 1914
Qy 332 uAlaThrArgPheTrpArg-----AsnGlnLysValAlaProGluAs 346
Db 1915 AGCCAGCAGTACCGCAGGAGACTTGAACCATTTGTGAGAGAAAGAGCCGCTGAAG 1974
Qy 346 nSerTyThrTyAspSerLeuTyGlnLeu-----IleSerAlaThrGlyArgGluMetal 365
Db 1975 AGAA-----CTGGAGCGGGTGAGCGAGCTCACCATAGAGCGCGCTAAAGAGCTGC 2028
Qy 365 a-----AsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuProSerAs 382
Db 2029 CGTGAAGAGAACCTCTCGAATTTTCGCAATTCAGTTG-----GA 2067
Qy 382 pAsnAsnThrTyThrAsnTyThrArgSerTyThrAspHis----- 397
Db 2068 GGAATAACACCTTTACAGACGAAACACTGGAA-----GATCATCTTAAAGAAAGA 2118
Qy 398 -----SerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAnty 415
Db 2119 TTTAAGTCTCAATGATTGGAGCAA-----CAAAAAAATAA 2154
Qy 415 rThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrTh 435
Db 2155 ATTAATGGAAGAAATTAAGAAAGAAAGAGAGACAATGAGGAAGAACTTTGAAAGCTGATAA 2214
Qy 435 rAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPr 455
Db 2215 GCAGATGGAAMAAA-----GACCTTGCAATTCAGAAACAGGTAGCAGAGAAACAGTTGAAAGA 2271
Qy 455 oGlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProG1 475
Db 2272 AAAGCAGAAAAATTCGAATTTGGAAGCAAGAGAAAGAAATAACTGAATTCAG----- 2320
Qy 475 yAsnGluTrpTyArgTyAspSerAsn----- 484
Db 2321 -----TATACATGTAGAGAAAAATGCAATTCGCCAGTGTGTCGCATCACACAGGCTAC 2370
Qy 485 -----GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAs 498
Db 2371 ATCATGCGGCGCACTAACGGGTCTCCAGCAA-----GAACATGCAAGCAGAA 2418
Qy 498 nThrThrGln-----GlnGlnArgValIleTyThrLeuProGlyLeuGluLeuArgThrThrG1 517
Db 2419 AGCAGAAAGAACTCAACAGCAGGCTAGATGAACACTACAGCTGCCAATAGAAAGGCTGAACA 2478
Qy 517 nSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGlu-----AlaGlyAr 536
Db 2479 AGACATGAGAGAGCTGACATAGAACTTAATGCGCTCCAGCTTGAAAAAAACGTCTCTGA 2538
Qy 536 gAlaGlnValArgValLeuHisTrpGluSerGlyTyAspProGluAspValAsnAsnGln 556

Db 2539 GGAAGAGGCTCGTTTCTGTAATA-----GATAAACTAGATCAAAACAAATAATAC 2586
Qy 556 nLeuA9TySerTyAspAsnLeuIleGlySerSerGlnLeuLeuLeuAspAsnGlnG1 576
Db 2587 ACTCAGA-----TGCCTTAAAGTTGGAGCTGGAAAGGAGGA 2622
Qy 576 yGlnIleIleSerGluGluGluTyTrpPheGlyGlyThrAlaLeuTrpAlaAs 596
Db 2623 TCAG-----GCGAGAAAGGGTAT-----TCTCA 2646
Qy 596 nSerGlnThrGluAlaSerTyTrpLeuArgTySerGlyLysGluArgAspAlaTh 616
Db 2647 ACAACTCAGAGACTTGGTAGGCAATTAATCAACACAGGTAAGCTGAAGAGCCAT 2706
Qy 616 rGlyLeuTyTyTrpGlyTyArgTyTrpGlnProTrpAlaGlyArgTrpLeuSerAl 636
Db 2707 GCAA----- 2710
Qy 636 aAspProAlaGlyThrIleAspGlyLeuAsnLeuTyArgMetValArgAsnProVa 656
Db 2711 -----GAAGCTAGTGTCTCAAGAAATTAAGCGCAATTTATCAGTT 2751
Qy 656 lSerLeuGlnAspGluAsnGlyLeuAlaProGluLysGlyLysTyThrLysGluValAs 676
Db 2752 AGAATTAGAACTCTCTTAAT-----CATGAAAAGGAAACTACAAGAGAGTA-- 2800
Qy 676 nPhePheAspGluLeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAs 696
Db 2801 -----GACAGAATCACAGGCGACATGCTGTAGCTGAGAAAGATATTACAGCATTTAA 2853
Qy 696 nGluLysGluSerSerTyThrLysAsnLysSerLeuLysValValArgVal----- 713
Db 2854 TTCACAAATTCATCTCTTTTCGAGATGAGAAAGAAATTAGAAAGACTCAAAATCTGCCAGAG 2913
Qy 714 ---GlyAspSerAspProSerGlyTyThrLeuLeuSerHisGluGluLeuLysGlyI1 732
Db 2914 AAAATCAGATCATCTAAAGAACAAATTTGAGAAAGCCATGACGAGTTGCTTCAAAATAT 2973
Qy 732 e-----GluLysSerGlnIleIleTySerArgLeuGluGluAs 745
Db 2974 CAAAGCTGAAAAAGAAATAATATGATAAAATCCAAGGCTCAATGAAAGAAATTTGAGAAAA 3033
Qy 745 nSerSerLeuSerGluLysSerLys-----ThrAsnLeuSerLeuGlySerGluI1 762
Db 3034 TAATAGTGTGCAGAGATGCTAAAAACAAAAGTAGAGGAGCTTACTAGGCAGAAATATGA 3093
Qy 762 eSerGlyTyTrpMetAlaArgThrIleGln-----As 772
Db 3094 AACCAAAATTAATGATGCAGAGAAATTCAGGCAGAAATCAGAGAAATATAGTTTAGAGAAACA 3153
Qy 772 pThrIleSerGluTyAlaGluGluHisLysTyArgSerAsn----- 786
Db 3154 AACTATCCAGCAAAAGATGTGAAGCACTGMAAAATTCAGGCAGATCGTTTTTAAGATCAGCT 3213
Qy 787 -----HisProAspPheTySerGluThrAspPhe----- 796
Db 3214 ACGCAGCAAAATGAACACTTGTCATAACACAGCAAAACACAGACGAGGATTTTCAAAGAAA 3273
Qy 796 ----- 796
Db 3274 AATTAAATGCTAGAGAGACCTGGCGAAAAGTCAAAATTTGGTAAGTGAATTTAAGCA 3333
Qy 797 -----Ph 797
Db 3334 AAAGTGTGACCAACAGAACATTTATCATCCAGAAATACCAAGAAAGAAAGTTAGAAATCTGAA 3393
Qy 797 eAlaLeuMetAspLysSerGluLysAsnAspTySerGlyGluArgLysIle-----Ty 815
Db 3394 TGCAGAACTGAATGCTTCCAAAGAGAGAGCGACCGCGGGGAGCAGAAAGTTCCAGCTACA 3453
Qy 815 rAlaAlaMetGluValLysValTyThrHisAspLeuLysAsnLysGlnSerGluLeuHisVa 835

```
Db 3454 ACAGCTCAGGTGCAAGAGTTAATAACAGGTTCAAAAAAGTACAGACGAATTACAC-- 3511
Qy 835 lAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGl 855
Db 3512 -----TTAAAGACCATAGAGGAGCAGATGACCCACAGAAAGATGGTTCTGTTTCA 3561
Qy 855 nGluThrGluProAlaIleAlaIleAspArgGluTyrAsnPheIysGlyValGlyLysPh 875
Db 3562 GGAAGAATCTGGTAAATTCAACCAATCAGCAGAGGAGGTTTCGGGAAGAAGATGGAAAAAATT 3621
Qy 875 eLeuThrMetIysAlaIle---LysLysSerLeuLysGlyHisLysIleAsnArgIleSe 894
Db 3622 AATGGAGTCCAAAGTCATCACTGAAATGATATTTCAGGCATTAGGCTTGACTTGTGTC 3681
Qy 894 rThrGluAlaIleAsnIleArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgTh 914
Db 3682 TCITCAACAAGAAAACTCTAGAGCC-----CAAGAAATGCTAAGCTTTGTGAAC 3732
Qy 914 rSer 915
Db 3733 AAAC 3736
```

Search completed: December 14, 2005, 23:52:11
Job time : 420 secs

This Page Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: December 14, 2005, 10:30:03 ; Search time 10168 Seconds
(without alignments)
5115.240 Million cell updates/sec

Title: US-10-647-956A-6

Perfect score: 4740

Sequence: 1 MSYNSAIDQKTPSIKVLND.....EAINIRSAIAENLGMRRTS 915

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2.1/USPTO spool_p/US10647956/runat 12122005 091817 29585/app_query.fasta_1.1095
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1 7780 @runat 12122005 091817 29585 -NCPU=6 -ICPU=3
-NO MNAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

ALIGNMENTS

RESULT 1
AR427909 LOCUS
DEFINITION Sequence 5 from patent US 6639129.
ACCESSION AR427909
VERSION AR427909.1 GI:40186940
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2745)
AUTHORS ffrench-Constant,R.H., Bowen,D.J., Rocheleau,T.A. and
TITLE DNA sequences from photorhabdus luminescens
JOURNAL Patent: US 6639129-A 5 28-OCT-2003;
Wisconsin Alumni Research Foundation and University of Bath;
Madison, WI
FEATURES Location/Qualifiers
source 1..2745
/organism="unknown"
/mol_type="genomic DNA"

linear PAT 18-DEC-2003

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4740	100.0	2745	6	AR427909 Sequence
2	4686	98.9	127816	1	AF346500 Photorhab
3	4429	93.4	349519	1	BX571862 Photorhab

Alignment Scores:
Pred. No.: 2,50-248 Length: 2745
Score: 4740.00 Matches: 915
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-647-956A-6 (1-915) x AR427909 (1-2745)			
QY	1	MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAenAsn	20
DB	1	ATGAGCAGTTACAAATCTGCAATGTACCAAAAGACCCCTCGATTAAAGTATTAGATAAC	60
QY	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAepGluAenSerAsp	40
DB	61	ACGAAATTAATAGTACGTACTTTAGATAATCTACGCACCTCAAGCTGACGAAACAGTGAT	120
QY	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro	60
DB	121	GAATTAATTAAGTCTATGATGTTCAATATTCCGGGATTTTCAGGTAAAGACACCGATCCT	180
QY	61	ArgLysAenLysAenGlnSerGlyProAsnPheIleArgValPheAenLeuAlaGlyGln	80
DB	181	CGTAAAAATAAAAACACAGAGCGGCCCAATTTCAATCGTGTCTTTAATCTTGGCGGTCAA	240
QY	81	ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
DB	241	GTTTTACGTGAAGAAAGTGTGATGCGCGTCCGACTATTACCTCAATGATATTGAAAGT	300
QY	101	ArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAenAsn	120
DB	301	CGCCCGGTGTGTATCATCAATGCAACCGGTGTCGCCAACAACCATCGTTATGAAGATAAC	360
QY	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
DB	361	ACCTTCCCGGTGTGTCTGCTCGTATCCAGACACAGTACAGCAGAGAGAAAAACGACC	420
QY	141	GluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
DB	421	GAAGCTCTTATCTGGGCGCGCAATACGCCGCAAGAAAAAGATTACAACTTCGCCGCTCAG	480
QY	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuLeuAlaGly	180
DB	481	TGTGTCCGCTATTACGATACCGGGGACTTACTCACTCAATAGCCTTCTCTGGCTGGC	540
QY	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAenAlaAspTrpThrGly	200
DB	541	GTGGTGTATACAACTCTCAACACTCTTACCGATTAACAGATGCGACTGGACAGGT	600
QY	201	GluAenGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
DB	601	GAAGACCAGAGCCTCTGGCAACAAAAACTGAGTAGTGATGTCTATATACCCAAAGTAAAC	660
QY	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeu	240
DB	661	ACTGATGCCACCGGGCTTTTACTGACCACAGACCGATGCCAAAGGCAACATTTACAGCGCTG	720
QY	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
DB	721	GCCTATGATGTGGCCGGCAGCTAAAGGGAGTTGGTTTACACTCAAAAGGTACGGCCGAA	780
QY	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLysLeuArgGluHis	280
DB	781	CAGGTGATTATCAATCGCTAACTACTCCGCCCGCGGCAAAAAATTTACGTGAAGACAC	840
QY	281	GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
DB	841	GGTAACGGGATTTGTCACTGAATACAGCTACGAAACCGGAAACCCCAACCGGCTTATCGGCATT	900
QY	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAenAspLeuArgTyrGlnTyrAspPro	320
DB	901	ACCACTCCCGCTCCATCAGACGCCCAAGGTGTGCAACACCTACGCTATCAATATGACCCA	960
QY	321	ValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArgPheTrpArgAenGln	340
DB	961	GTAGGCAATGTCTAATTAATATCCGTAAATGATGCGGAAGCCACTCGCTTTTGGCGCAATCAG	1020
QY	341	LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
DB	1021	AAAGTAGCCCCGGAGAAATAGCTATACCTACGATTCCCTGTATCAGCTTATCAGCGCCACC	1080
QY	361	GlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuProSerProAlaLeuPro	380
DB	1081	GGCGCGAAATGGCCAATATCGGTACGAAACCAACAACTTCCCTCCCTCGGCTACCT	1140
QY	381	SerAspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAsn	400
DB	1141	TCTGACAAACAATACCTACATACTACTCGCAGCTACAGCTATGATCACAGTGGTAAT	1200
QY	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr	420
DB	1201	CTGACGCAAAATTCGGCACAGCTCCGACGACTACCAGAACAACTACACCGTGGGTATCACC	1260
QY	421	LeuSerAsnArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
DB	1261	CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGTAAACCAACCGATCCAAATCAAGTG	1320
QY	441	AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
DB	1321	GATACGTTGTTGATCCGCTGGTCCACCAACCAAGTTTATTACCGGACAGACACTTATC	1380
QY	461	TrpThrProArgGlyGluLeuLysGlnValAsnAenGlyProGlyAenGluTyrTyrArg	480
DB	1381	TGACACACAGAGAGAGTTAAAGCAGGTTAATATGCGCCGGGAAATGAGTGGTACCGC	1440
QY	481	TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
DB	1441	TACGACAGCAACCGCATGAGACAACTGAAAGTCAGTGAACAGCAACCCAGAAATACTACG	1500
QY	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
DB	1501	CAGCAAAACGGGTAAATCTATTTCGCGGACTGAGCTACGCAACACCCAGAGCAACGCC	1560
QY	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
DB	1561	ACAAACACGGAAGATTACAGTTATCACTCGGTGAAGCCGTCGCGCAGAGTACGG	1620
QY	541	ValLeuHisTrpGluSerGlyLysProGluAspValAsnAenAenGlnLeuArgTyrSer	560
DB	1621	GTGTTGCACCTGGGAGAGCGGTAAAGTCAGTGAACAGCAATTAATCAACTACGTTACAGC	1680
QY	561	TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer	580
DB	1681	TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGACAAACCAAGGACAAATTTATCAGC	1740
QY	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
DB	1741	GAGAAAGATTATTTATTCATTTGGCGGACAGCCGCTGTGGCAGCAACACAGCCAAACAGAA	1800
QY	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
DB	1801	GCCAGCTATAAAACGATTCGCTATTCCGCAAAAGAACAGAGATGCCACCGGTTGTTAT	1860
QY	621	TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly	640
DB	1861	TACGGTTATCGTTATTACCAACCGTGGCGGAGATGGTTAAGCGCGGACCCCGGACGGA	1920
QY	641	ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp	660
DB	1921	ACCATTTGATGGGTGAAATCTATACCGAATGAGTAAGAAATTAATCTGTGAGTTTACAAGAT	1980
QY	661	GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu	680
DB	1981	GAATATGATTACGGCCAGAAAAAGGAAATATACCAACAGAGGTAAATTTCTTTGTATGAA	2040
QY	681	LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
DB	2041	TTAAAAATTCAAATGGCAGCCAAAAGTTTCATGTTGTCAAAATGGAAACGAGAAAGAGC	2100

Qy	701	SerTyrThrIysAsnIysSerLeuLysValValArgValGlyAspSerAspProSerGly	720
Db	2101	AGTTATACAAAAATAAATCATTCAGAAAGTGTTTCGTGCGTGATTCAGATCCGTCGGT	2160
Qy	721	TyrLeuLeuSerHisGluGluLeuLeuLysGlyLeuGlySerGlnIleIleTyrSer	740
Db	2161	TATTTGCTAAGCCACCAAGAGTTACTAAAGGTTATAGAAAAAGTCAAATCATATATAGC	2220
Qy	741	ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer	760
Db	2221	CGACTTGAGAAAAACAGCTCCCTTCAGAAAAATCAAAAACGATCTTCTTTAGGATCT	2280
Qy	761	GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu	780
Db	2281	GAATAATCCGGTTATATGCGAAGAACCATACAGATACGATATCAGATATGCGAAGAG	2340
Qy	781	HisIysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet	800
Db	2341	CATAAATATAGAAGTAATACCTCGATTTTATTCAGAAACCGATTTCTTTGCGTTAATG	2400
Qy	801	AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal	820
Db	2401	GATAAAGTGAAAAAATGATTATTCGGTGAAAGAAAAATTTATGCGCAATGAGGTT	2460
Qy	821	LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla	840
Db	2461	AAGGTTTATCATGATTATAAAAAATAAACAATCAGAAATCATGTCACATGCAATGGCC	2520
Qy	841	HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla	860
Db	2521	CATCCCTTATACGAATTTAGTAATATGAGAAAGACGCGTGTTCAGAGAAACAGAACCGCT	2580
Qy	861	IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla	880
Db	2581	ATTGCAATAGATGAGAAATATATTTTCAAGAGTGTGGCAATTCCTGACAAATGAAAGCA	2640
Qy	881	IleLysLysSerLeuLysGlyHisLysAlaAsnArgIleSerThrGluAlaIleAsnIle	900
Db	2641	ATTAATAAATCATTTGAAAGACATATAAAATTAATAGGATATCAACAGAGGCTATTATATT	2700
Qy	901	ArgSerAlaIleAlaGluAsnLeuGlyMetArgArgThrSer	915
Db	2701	CGCTCTCGCGTATCGCTGAGAATTTAGGAATCGGAGAACTTCA	2745
RESULT 2			
LOCUS	AF346500	127816 bp	DNA linear BCT 17-JUL-2003
DEFINITION	Photorhabdus luminescens strain W14 toxin complex pathogenicity island 1, partial sequence.		
ACCESSION	AF346500	AY144119	
VERSION	AF346500.2	GI:27479637	
KEYWORDS	Photorhabdus luminescens		
SOURCE	Photorhabdus luminescens		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.		
REFERENCE	1 (bases 1 to 127816)		
AUTHORS	Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and french-Constant,R.H.		
TITLE	The tc genes of Photorhabdus: a growing family		
JOURNAL	Trends Microbiol. 9 (4), 185-191 (2001)		
PUBMED	11286884		
REFERENCE	2 (bases 1 to 127816)		
AUTHORS	Waterfield,N.R., Daborn,P.J. and french-Constant,R.H.		
TITLE	Genomic islands in Photorhabdus		
JOURNAL	Trends Microbiol. 10 (12), 541-545 (2002)		
PUBMED	12564983		
REFERENCE	3 (bases 1 to 127816)		
AUTHORS	french-Constant,R.H., Bowen,D.J. and Waterfield,N.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JAN-2001) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK		
REFERENCE	4 (bases 1 to 127816)		

AUTHORS	Waterfield,N.R. and french-Constant,R.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-AUG-2002) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK		
REMARK	Sequence update by submitter		
COMMENT	On Jan 3, 2003 this sequence version replaced gi:16416925.		
FEATURES	Location/Qualifiers		
source	1..127816		
	/organism="Photorhabdus luminescens"		
	/mol_type="genomic DNA"		
	/strain="W14"		
	/db_xref="taxon:29488"		
gene	<1..406		
	/gene="orf1"		
CDS	<1..406		
	/gene="orf1"		
	/codon_start=2		
	/transl_table=11		
	/product="Orf1"		
	/protein_id="AAO17167.1"		
	/db_xref="GI:27479640"		
	/translation="VLCASPAYIEASEKILIPENLASHNCLIIYSLSSSPRRMMFHNQN		
	DKVVDLKPGTYVNNGLAKOALSGHGVLLPELLVIDELQSGELVRLPEWEADT		
	QALYALQPHKERSIKARAFIDFLYNALDETC"		
gene	695..1432		
	/gene="orf2"		
CDS	695..1432		
	/gene="orf2"		
	/codon_start=1		
	/transl_table=11		
	/product="Orf2"		
	/protein_id="AAO17168.1"		
	/db_xref="GI:27479641"		
	/translation="MNSAISASENLVSLDGRQPTVGIEINKILFSVGRVSTAP		
	IPEAKPILEVSKTRALTGESEKILISLFLSHRGELLEOLRLAGROPEAHARGGFLSIS		
	ELGVAPYPKYDMKALISVARKTVLEKFKLHVNSSEDCMGIDVMTVVGAGWTWFF		
	RIVAPYIAKLSIGRVETGDPAWRLSTPGLMHAGFLDAKAGLLVAFAGHPKHFVMRYD		
	EFSVDGTEMLGNPMIDFSGDIPKLVK"		
gene	1769..2752		
	/gene="orf3"		
CDS	1769..2752		
	/gene="orf3"		
	/notes="Similar to putative Serratia heptosylIII		
	transferase WaaQ in GenBank Accession Number AAD28803"		
	/codon_start=1		
	/transl_table=11		
	/product="Orf3"		
	/protein_id="AAO17169.1"		
	/db_xref="GI:27479642"		
	/translation="MKIALLRRNGLGLICTOPLIKLYQVTFPIAIIHFLFESNNNEL		
	ADYLCEPITTHIIPKGNKYITTLGTALKWRKLFDAISAKPTMKLNINLFLWLLGAK		
	KRYAVTQSHQWHEKLYNPTCPQHIKGYHSLKILKTFDSEINKLSSELLPKISSOYL		
	LPIKQHSPTLILSVSNRQSSCIETHERIALIAQIRNHFPDVRPIIISTLRHDSHAE		
	KLLAMIGDQRIQVECSLSFLSLNSTDLIIIVDGGIGCHLAALBKLLVALYGVTKP		
	ENWAPIASENCQVTLTYPQNVNPIEDIIYQAVFKLLSPEKTLULFESSCR"		
gene	3949..4473		
	/gene="phfs"		
CDS	3949..4473		
	/gene="phfs"		
	/notes="Similar to Salmonella enterica serovar Typhi Stga		
	probable fibrillar subunit protein found in GenBank		
	Accession Number CAD03135"		
	/codon_start=1		
	/transl_table=11		
	/product="Phfs"		
	/protein_id="AAO17170.1"		
	/db_xref="GI:27479643"		
	/translation="MKNFILASLVAVLGISSFSALSVDGTIKFRGTIIEOTCTVKG		
	TSGKDIADVNDVNHKSLDKAGKFSDFKFTVNLTCPLKGFVKFDOTDKTSGN		
	YFKILSSSTAKNIAIALYKSGSSTPIKPGDSIKIPGVAGDTSFNLSKLVSTAATVTA		
	GSTFRDINTIISYP"		
gene	4531..5199		
	/gene="phfc"		

QY	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGly	200
Db	99238	GTCTGCTATCAATCTCAGCAACTACTCTCGTCAATGATAAAATGCTGACTGCACAGGT	99297
QY	201	GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Db	99298	GAAGACCAAGCCCTCTGGCAGCAAAACTGAGCAGTGATGCTATACCCCAAAATAAA	99357
QY	221	ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240
Db	99358	GCCGATGCCACCGGGCTTTATTTGACCCAGACCGATGCCAAGCAACATCCAGCGCTCG	99417
QY	241	AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db	99418	GCCTACGACCTAGCCGGCAGCTAAAGAGCTGTGTGGTTGACACTCAAAAGGTCAGGCCGAG	99477
QY	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluHis	280
Db	99478	CAAGTGATTATCAAAATCGCTGACCTACTCCGCCCGCGGACAAAAATTTACGCGAAGACAC	99537
QY	281	GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	99538	GGTAACGGGGTTACTGTAATACAGCTATGAACCAAGAACCCACCGGCTTATCGGTATT	99597
QY	301	ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Db	99598	GCCACCGCCGCTCGCTCAGACGCCAAAGTGTTCAGAGACTTACGCTATCAATATGACCCG	99657
QY	321	ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln	340
Db	99658	GTAGGCAATGTATCAATATCCGTAATGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG	99717
QY	341	LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Db	99718	AAAGTGTCTCCGGAGATAGCTATATCTACGACTCCCTGTATCAGCTTATCAGTGCACCC	99777
QY	361	GlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuPro	380
Db	99778	GGCGGGAAATGGCTAATATAGTTCAGCAAAATAAACCACTGCCCTCCCTCGCTACCT	99837
QY	381	SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn	400
Db	99838	TCTGACAAACAATACCTACACTAATATCTACGAGCTACAGCTATGATCATCAGTGGTAAT	99897
QY	401	LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr	420
Db	99898	CTGACGCAAAATTCGGCACGCTCGCCAGCTACCCAGAACCACTACACCGTGGCTATCACC	99957
QY	421	LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal	440
Db	99958	CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCGATCCAAATCAAGTG	100017
QY	441	AspThrLeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db	100018	GATACGTTGTTTGTATCGCGTGGTGCACAAACCAAGTTTATTATCCCGGACACACTTATC	100077
QY	461	TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArg	480
Db	100078	TGGACACACGAGAGAGTTAAAGCAGGTTAAATATGGCCCGGAAATGATGGTATCCGC	100137
QY	481	TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr	500
Db	100138	TACGACGACCAACGGCATGAGCAACTGAAATGAGTGAGTGAAACAGCCACCAAGTACTACG	100197
QY	501	GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla	520
Db	100198	CAGCAACAACGGGTAATCTATTTCGCGGACTGAGAGCTACGCAAAACCCAGAGCAACGCC	100257
QY	521	ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db	100258	ACACAACGGAAGAGTTTACAGTTTATCACCTCGTGAAGCCGGTCCGCGCACAGGTACGG	100317
QY	541	ValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSer	560
Db	100318	GTGTTGCACTGGGAGAGCGGTAAAGCAGCAAGATGTCTCAACAATAATCAACTACCTTACAG	100377
QY	561	TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer	580
Db	100378	TACGATATCTGATCGGCTCCAGCCAGCTTGAATGGACACCAACGACCAATATTATCAGC	100437
QY	581	GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu	600
Db	100438	GAGGAAGAGTATTATCCATTTGGCGGACAGCGCTGTGGGACAGCAACAGCCCAACAGAA	100497
QY	601	AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Db	100498	GCCAGCTATAAACCGATTCGCTATTTCCGCCAAGAACGAGATGCCACCGGTTGTATTAT	100557
QY	621	TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTyrTrpLeuSerAlaAspProAlaGly	640
Db	100558	TACGGTTATCGTTATTACCACCGTGGCGGCGCAGATGGTTAAGCCGGACCCCGGCAGGA	100617
QY	641	ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp	660
Db	100618	ACCATTGATGGGCTGAATCTATACCGAATGGTAAGAAATAATCTCTGTGAGTTTACAAGAT	100677
QY	661	GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGlu	680
Db	100678	GAATAATGGATTAGCGCAGAAAAAGGAAATATACCAAGAGGTAATTTCTTTTGATGAA	100737
QY	681	LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAsnGluLysGluSer	700
Db	100738	TTAAATTTCAATTTGGCAGCCCAAGTTTCAATGTTGTCTAATGGACGCAAGAAAGAGC	100797
QY	701	SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720
Db	100798	AGTTATACAAAAATAAATCATTTGAAAGTGGTTTCGTTGCGTGATTCGATCCGTCGGGT	100857
QY	721	TyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSer	740
Db	100858	TATTTCTAAGCCACCAAGAGTTACTTAAAGGTATAGAAAAAGTCAAAATCATATATAGC	100917
QY	741	ArgLeuGluGluAsnSerSerLeuLysSerLysThrAsnLeuSerLeuLysSer	760
Db	100918	CGACTTGAAGAAACAGCTCCCTTTTCAGAAAAATCAAAAACGAATCTTTCTTTAGGATCT	100977
QY	761	GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu	780
Db	100978	GAATATCCGTTATATGGCAAGAACCATACAGATACCATATCAGATATGCCGAAGAG	101037
QY	781	HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet	800
Db	101038	CATAAATATAGAAGTAAATCACCTGATTTTATTTCAGAAAAACCGATTTCTTTGGGTTAATG	101097
QY	801	AspLysSerGluLysAsnAspTyrSerGlyLysGluArgLysIleTyrAlaAlaMetGluVal	820
Db	101098	GATTAAGGTGAAAAAATGATTATTCGGTGAAGAAAAAATTTATCGGCACATGGAGTT	101157
QY	821	LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla	840
Db	101158	AAGTTTATCATGATTTAAAAAATAAACAATCAGATTACATCTCACTATGCTATGGCC	101217
QY	841	HisProTyrThrGlnLeuSerAsnGluArgAlaLeuLeuGlnGluThrGluProAla	860
Db	101218	CATCCCTATACGCAATGAGTAATGAAGAAAGAGCGCTGTTCAGAAAAACAGAACCCGCT	101277
QY	861	IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla	880
Db	101278	ATTGCAATAGATAGAGAAATATAATTTCAAAGGTGTGGCAAAATTCCTGACAAATGAAAGCA	101337
QY	881	IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle	900
Db	101338	ATTAAAAAATCATTTGAAGGACATAAATTTATAGATATCAACAGAGGCTATTATATT	101397
QY	901	ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgThrSer	915


```

/db_xref="UniProt/TREMBL:Q7N838"
/translation="MVAVRSALHTPAGEFAVNRWIASLNIAIQLQEKLAETWRYCHE
KAQHDPSELLWRGVEWVEILSTLSDSDSMEAALLFLPMDAKLJGDETVEAFGSA
ITNLVKGWEMDAIROLKATHDPSICSVQDVNRVRLMLAMVEDFRVCVIIKLAERIAHL
REVKEATEDVERLAAKESNIYAPLANRLGIGOLKWELEDYCFRYLHPDPEYKXIAKLL
HERIRDEQYIDYFVNTLRHMLKEGVTEIYGRPKHYSIMWRKQKSLADELPDV
RAVRIVERLQDCYALGALGVHTYRHLPLDEFDDYVANPKNQVQSHTVVLPGGKTL
EIQIRTRQWEDAEGLIAAHWKYEGAGSRVYEGRIAMLRKLIJAWBEEWADSGEM
LDEVRQSDVDRYVTPFGDVVDLPTGTPDLPFYHIIHSDVGHRCIGAKISGRIVPF
SYQLQMDQIETITQKPNPDRDLNPNLGYVTTSGRAKIHNFKQDRDNKIIAGR
QMLNLEHLIDSLKEAKELIIARYNVHTLDEVLGIGVGDIRINOLVNFPLQSLAKKT
TADADREALNLESKHPORSAXDDGRIVVEGVGNLMHHIARCCQPIPGDEIVGFI
TRRGSIHWDCEQLAELOANAPERVDRAVWGESYSYSGYSLIVRVVANDRSGLLRDI
TTILANEKNVLGVSSRSDVKQIATIDNMNIEIYNQVLGRILAKINQLPVDVIEAKRL
HGN"
/genes=".8485
/locus tag="plu0911"
7689..7694
/genes="mazG"
7706..8485
/locus tag="plu0911"
/genes="mazG"
/locus tag="plu0911"
/function="Unknown"
/codon_start=1
/transl_table=11
/product="MazG protein"
/protein_id="CAE13206.1"
/db_xref="GI:36784329"
/db_xref="InterPro:IPR004518"
/db_xref="InterPro:IPR011551"
/db_xref="UniProt/TREMBL:Q7N837"
/translations="MTGIKRLGIMQLRHPQOGCPWDKEQTEKTIAPTYLTERTYVI
DAIERDPSDLKEELGDLPOVVFYAEKGEQQLFDFDDICNAISDLKERRHPHISQ
QDISDVAISGHEKKAQRAQDLHSLVDLDDIPASLPALMKAYKIKRCAAVGFWD
TLGPDLVDVEIDEVWDEAHQAVDQOHLBEEIGDLLFAVNLRSRLHLYKPKSIALQK
ACKNFNRFEIEKLILKOGHTLEAATLEEMERWQVKKQ"
8707..10344
/genes="pyrG"
/locus tag="plu0912"
8707..10344
/genes="pyrG"
/locus tag="plu0912"
/codon_start=1
/transl_table=11
/product="CTP synthetase"
/protein_id="CAE13207.1"
/db_xref="GI:36784330"
/db_xref="GOA:Q7N836"
/db_xref="InterPro:IPR000991"
/db_xref="InterPro:IPR004468"
/db_xref="UniProt/TREMBL:Q7N836"
/translations="MKNIYIFVGGVSSLGKGAASLAAILBARGNLVNTIMKLDPY
INVDPGTMSIQHGVFTEDEGADTDLGHEFRFTKWTNRNFTTGRVYSEVLRK
ERGDYLGATQVPIPHITEIKDRIISGGEHDVILVEGVGTDESIPFLSEAIRQM
AVEVGRHTLYLHLTPVLYAAAGEVKTPTQHSVKELLSIGIOPDILICRDRVTPA
NERAKALFCNVPEKAVISLKVDVSIKIPGLKSLQGLDDYICKRFSLDPCPENLSEW
EQVIYEANPSGVTIGWVKYVELPDAYKSVIEALKHGLKRLNLTWNILKLDSDQVE

```

Alignment Scores:

Pred. No.:	4,72e-229	Length:	349519
Score:	4429.00	Matches:	847
Percent Similarity:	95.96%	Conservative:	31
Best Local Similarity:	92.57%	Mismatches:	37
Query Match:	93.44%	Indels:	0
DB:	1	Gaps:	0

US-10-647-956A-6 (1-915) x BX571862 (1-349519)

Qy	1	MetSerSerTyrAnSerAlaIleAapGlnYsThrProSerIleYsValLeuAapAen	20
Db	60923	ATGACGAGTTTATCGTTCTGAAATTTGACAAAAAACACCATTAATCAGTGTATTGGATAAC	60864

Qy	21	ArgLysLeuAanValArgThrLeuGluTyrLeuArgThrGlnAlaAapGluAanSerAap	40
Db	60863	AGCAGGTTAAATGCTACGTACTTTAGAAATATCTACGTACTCAAGCTGATGAAAAACAGTGAT	60804
Qy	41	GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValYsSerThrAapPro	60
Db	60803	GAATTGATCACACTCTATGAGTTCAATATTCAGGATTTTGAGGTAAGAAAGTACTGTATCCT	60744
Qy	61	ArgLysAanLysAanGlnSerGlyProAanPheIleArgValPheAanLeuAlaGlyGln	80
Db	60743	CGTAGAATAAATAATCAGACGCGCCGGAATTTTCATTCGGGTCTTTAATCTCGCGGTCTAG	60684
Qy	81	ValLeuArgGluGlnSerValAapAlaGlyArgThrIleThrLeuAanAapIleGluSer	100
Db	60683	GTTCTACGTGAAGAGGGGTGATGCGGTGCAACTATCATCTCAACGATGTTGAAGGT	60624
Qy	101	ArgProValIleIleAanAlaThrGlyValArgGlnAanHisArgTyrGluAapAan	120
Db	60623	CGCCCGGTATTAAACATCAATGCAACCGGTGTCGCGCAGACTTCACTACGAAAGATAAC	60564
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluYsThrThr	140
Db	60563	ATCCTACCCGGTCGCTTACTTGTCTATCACCGAACAGGTGCAGCGCAGAAAGAAAATGACC	60504
Qy	141	GluArgLeuIleTrpAlaGlyAanThrProGlnGluLysAapTyrAanLeuAlaGlyGln	160
Db	60503	GAGCGCTTATCTGGCGCGCAATACCGCGCAAGAAAAAGATACAACTTGTGCTGCTAG	60444
Qy	161	CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAanSerLeuSerLeuAlaGly	180
Db	60443	TGTGTCCGCCTACGATACCGCTGAGTCACTCAACTCAACAGCCTTTCTCTGGCTGGC	60384
Qy	181	ValValLeuSerGlnSerGlnGlnLeuLeuThrAapAanGlnAapAlaAapTyrThrGly	200
Db	60383	GTCGTGCTATCANAATCTCAACAATCTGCTGCTGATGATCAAAATGCCCACTGACAGGT	60324
Qy	201	GluAapGlnSerLeuTrpGlnGlnLysLeuSerSerAapValTyrIleThrGlnSerAan	220
Db	60323	GAAGTCAAAAGCCTCTGGCAGCAAAAATCGAGCAGTGTCTATACCAACCAAAATAGC	60264
Qy	221	ThrAapAlaThrGlyAlaLeuLeuThrGlnThrAapAlaYsGlyAanIleGlnArgLeu	240
Db	60263	ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAGGCAACATCCACGCTCTG	60204
Qy	241	AlaTyrAapValAlaGlyGlnLeuLysGlySerTyrLeuThrLeuLysGlyGlnAlaGlu	260
Db	60203	GCTATGATGTAGCCGGCAGCTTAAAGGCTGTTGGTTAACACTCAAGGTCAAGCCGAA	60144
Qy	261	GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis	280
Db	60143	CAAGTGATTTCAAAATCGCTGACCTACTCTGCGCGCGGCAAAAATTCGTGAAGAGCAC	60084
Qy	281	GlyAanGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db	60083	GGTAACGGGGTATCACCCGAATACAGTATGAACCAAGAAACCCACCGCTTATTTGTATC	60024
Qy	301	ThrThrArgArgProSerAapAlaLysValLeuGlnAapLeuArgTyrGlnTyrAapPro	320
Db	60023	ACTACCCCGCGCTCCGTCAGATCAAGGTGTTGCAAGCTTACGCTATCAATATGATCCG	59964
Qy	321	ValGlyAanValIleAanIleArgAanAapAlaGluAlaThrArgPheTrpArgAanGln	340
Db	59963	GTAGGCAATGTGATCAATATCCGTACGATCGGAAGCCACCCGCTTTTGGCGCAATCAG	59904
Qy	341	LysValAlaProGluAanSerTyrThrTyrAapSerLeuTyrGlnLeuIleSerAlaThr	360
Db	59903	AAAGTGGTCCCGAGAAATAGCTATATTACGACTCCCTGTACCAGCTTATCAGTGTACT	59844
Qy	361	GlyArgGluMetAlaAanIleGlyGlnGlnAanAanGlnLeuProSerProAlaLeuPro	380
Db	59843	GGCGCGTAATGGCCAAATAGGTGACAAAAATAATCAACTGCCCTCCCTCGCGCTACCT	59784


```
Qy 381 SerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 59783 TCCGACAAACAATACCTACCTAATCTACTCGCGCTACAGTTATGATCATCAGCGGTAA 59724
Qy 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr 420
Db 59723 CTGACGCAAAATTCGGCACAGTTTCATCGCTACCCCAAATAAATCACTACACCGCTATCACC 59664
Qy 421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal 440
Db 59663 ATCTCGAATCGCAGTAAACCGCGCGGTCTCAGTAGCTGACCAACAGATCCAAATCAAGTG 59604
Qy 441 AspThrLeuPheAepAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 59603 GATACGTTATTGATGCGGTGGTGCACAAACCAAGTTTATTCACCGGTGACACTGGTC 59544
Qy 461 TrpThrProArgGlyGluLeuLeysGlnValAenAenGlyProGlyAenGluTyrTrpArg 480
Db 59543 TGGACATCACGAGCAGAGTTAAACGAGTCAATTAACGGTTCCAGGAATGAATGTCACCGA 59484
Qy 481 TyrAspSerAenGlyMetArgGlnLeuLeysValSerGluGlnProThrGlnAenThrThr 500
Db 59483 TACGGCACCAACGGAATGAGCAACTGAAAGTGAGTGAACCAACCCAGCAATACTACG 59424
Qy 501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla 520
Db 59423 CAGCAGCAGCGGGTAATCTATCTCGCGGGGTGGAATCATCGCACACCCAGCAACGACACC 59364
Qy 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 59363 ACAACACAGAAAGATTACACGTGATCACACTAGTGAAGCGGTTCGGCACACGGTCGG 59304
Qy 541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer 560
Db 59303 GTGCTGCACCTGGAGAGCGGTAAACACCAAGAGTATCAACAACAATCACTACGTACAGC 59244
Qy 561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer 580
Db 59243 TACGATTAATCTGATCGGCTCCAGCGAGCTTGAATCTGGACAACCAAGGCGAGTTATTAGT 59184
Qy 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu 600
Db 59183 GAGCAAGAGTATTATCCATCTCCGGCGGCACACGCGATGGCGCAGCCATAGCCAAACAGAA 59124
Qy 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 59123 GCCAACTATAAACTATTTCGTATTTCAGGCAAAAGAACGGGATACCCCGGCTGTATTAT 59064
Qy 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 59063 TACGGTTACCGCTATTATCAACCGTGGCGGCGAGATGTTAAGCGCGGATCCCGCAGGA 59004
Qy 641 ThrIleAepGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp 660
Db 59003 ACCATTGATGGCTGAATCTATACCGAATGGTGAGAAATAATCCAGTAAGTTTCAGGAT 58944
Qy 661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAepGlu 680
Db 58943 GAAAAATGGATTAGCACCAAGAAAGGAAAAATATATACTAAAGAGGTGAATTTCTTTGATGAA 58884
Qy 681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTyrAenGluLysGluSer 700
Db 58883 TTAAATTTCAAATTTGGCAGCCAAAATAATTCATATGTTGTCAATGGACGAGAAAGAAAGT 58824
Qy 701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyApsSerAspProSerGly 720
Db 58823 AGTTATACAAAAATAAATCAATTTGAAAGTGGTTTCGCGTCGCTGATTCGATCCGCTCGGT 58764
Qy 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 58763 TATTTCGTAAGCCGCAAGAGATTACTAAAGGCGCATAGAAAAAGCCAAATATATATAGC 58704
Qy 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
```

```
Db 58703 CGGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAAATCAAAAAACAAATCTTTCTTTGGGATCT 58644
Qy 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAepThrIleSerGluTyrAlaGluGlu 780
Db 58643 GAAATATCCGGTTATATGGCAAAAAACGATAAAAGATACGATATACGAATATACAGAAAGG 58584
Qy 781 HisLysTyrArgSerAenHisProAepPheTyrSerGluThrAspPhePheAlaLeuMet 800
Db 58583 CATAGGTATAGAACCAATCATCCCGATTTTATGCGACACACAGATTTCTTTGCTTTAATG 58524
Qy 801 AspLysSerGluLysAenAepTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 58523 GATAAAGTGAAAAAATGATTATTCGCGTGAAGAAAAAATTTATCGCGCAATAGAGGTT 58464
Qy 821 LysValTyrHisAepLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 58463 AAGGTTTATCATGATTAAAAAAATAAACCAATCAGAATTAATCATGCAACTATGCACCTGGCT 58404
Qy 841 HisProTyrThrGlnLeuSerAenGluAlaGluAlaLeuLeuGlnGluThrGluProAla 860
Db 58403 CATCCCTATACGCAATTTAGTAAATGAAGAGAGAGCGCTGGTGCAAGAACAGAACCCGCT 58344
Qy 861 IleAlaIleAepArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 58343 ATTGCAATAATAGAGAAATATAATTTCAAAGCGGTTGGTAAATTCCTCGCAATGAAAGCA 58284
Qy 881 IleLysLysSerLeuLysGlyHisLysIleAenArgIleSerThrGluAlaIleAenIle 900
Db 58283 ATTAATAAATCATVTGAAGGCGCAGAAAGATCAATAAATAATCAACAGAGGCTATTAAATTT 58224
Qy 901 ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 58223 CGCTCGCGCTATCGCTAAGAAATTTAGGAATCGGAGAGCTTCA 58179
```

RESULT 4

```
LOCUS       CQ824622             2817 bp            DNA             linear      PAT 21-JUN-2004
DEFINITION   Sequence 15 from Patent WO2004044217.
ACCESSION   CQ824622
VERSION     CQ824622.1   GI:49021703
KEYWORDS    .
SOURCE      Photorhabdus luminescens
            Photorhabdus luminescens
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
```

REFERENCE

```
1.
AUTHORS     French-Constant,R.H. and Waterfield,N.R.
TITLE       Dna sequences from tcd genomic region of photorhabdus luminescens
JOURNAL     Patent: WO 200404217-A 15 27-MAY-2004;
            UNIVERSITY OF BATH (GB)
```

FEATURES

```
source      location/Qualifiers
            1..2817
            /organism="Photorhabdus luminescens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:29488"
CDS         1..2817
            /note="unnamed protein product"
            /codon_start=1
            /transl_table=11
            /protein_id="CAG38452.1"
            /db_xref="GI:49021704"
            /translation="MENIDPKLYHHTPTVSVDNRGLAERNISPHRTTAENTDTRIT
            RHYNAGGYNLQSIDPRLDAKQNNNAVQNFWRHNLNLTGNIERTESVDAGRITLND
            IEGRPVHTINAGVRQNHRYEDNTLPGLRLIAISQQQAEEKTERLIERLWAGTPOEKDH
            LKQCVRHYDTAGLTALYSALTGVALSQQLLTNDQADMTGEDQSLWQKLSLD
            VYITQSNLTATGALLTQDAKNIQRLAYDVALGQKSLWTLKGAQEQVTKSLTYGA
            AGQLEEHGNGIVTEYSVEPTEORLIGITRRPDAKVLQDLRYQDPPGVNVSIRN
            DASATFRNQKVPENSYTDSLYQLISATGEMANIGQSNQSPALPSDNNTYT
            NYHTYIDRGNLTKIHSSPAQQNYTTDITVSNRSRAVLSTLTADTQVDALPD
            AGHQYSLSGSVLTTPFGEELKQANNSAGNWRYSNRSRAVLSTLTADTQVDALPD
            RVYLPGLERITQNNATTEELHVTILGKAGRAQVRVLHWESGKPEDINNQLRYSY
            DNLIGSSQLQDSDGQIIISEEYYPFGGTALWAARNQTEASYKTIYRSGKRDVTGLY
```

YGVRYYPWAGRWLGADPAGTIDGLNLYVMVNNPVTDFVGLSPANRTEAIIKQ
 GSTGMEEAIVYKMAEPQFQRORATAAQTEQEAHESLNNPVSVDISPKNYTTDSQ
 INAIARENITPAVESLDATLSLQDRQMRVTVMTYVDNSTPSPHWPQEGNSIN
 GDVSDNAYLSTSAHRGFLNFVHKSETSEYVYKMAFLTNAGVNPAAANNYNAGSEQ
 VFKMDLNDRSKSLAEKLLKRVSGPQSQABILLPRETOFEVSMKHQGRDYYVLLQDI
 NQSAATHRNVRNVTYTGFXSSS"

ORIGIN

Alignment Scores:

Pred. No.: 1,85e-151 Length: 2817
 Score: 2956.00 Matches: 608
 Percent Similarity: 73.01% Conservative: 90
 Best Local Similarity: 63.60% Mismatches: 186
 Query Match: 62.36% Indels: 72
 DB: 6 Gaps: 14

US-10-647-956A-6 (1-915) x CQ824622 (1-2817)

QY 1 MetSerSerTyrAsnSerAlaIleAapGlnLysThrProSerIleLysValLeuAapAsn 20
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1 ATGGAAACATTGACCCAAACATTTATCACCATACCGCTACCGTCAAGTGTTCAGATAAC 60
 QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAapGluAenSerAsp 40
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 61 CTGGGACTAGTATCCGTATATATAGTTTTCACCGCACTACCGAAGAGCAATATCCGAT 120
 QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 121 ACCGTATTACCGCCATCAATATATGTCGCGGGATATTTGAACCAACCATTTGATCCT 180
 QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelleArgValPhe 75
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 181 CGCCTGTATACGCCCAACAGACTAACACACGCTGTACACCGCAATTTTATCTGGCGACAT 240
 QY 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 241 AATTGACCGCAATATCTCGCAACAGAGGCGTGCATCCCGTGGAGATATCCCTC 300
 QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 301 AACGATATTGAAGCGCCCGGTGTGACCATCAATGCAGCCGGTGTCCGGCAAAACCAT 360
 QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 361 CGCTACAGATAACACCTCGCCCGTGCCTGCTATCAGCGAACAAGCACAGGCA 420
 QY 136 GlyGluLysThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGluLysAspTyr 155
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 421 GAAGAGAAAACGACCGAGCGCCTTATCTGGCGCGCAATACGCGCAAGAAAAGACCAC 480
 QY 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 481 AACCTTGGCGGTGAGTGGTCCGCATTACGATACCGCAGGACTCACTCAACTCAACAGC 540
 QY 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 541 CTGGCCCTGACCGCGCGCTTCTATCAATCTCAACAACTGCTTACCGATAACAGGAT 600
 QY 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 601 GCCGACTGGA CAGGTGAAGACCAAGAGCCTCTGGCAACAAAACCTGAGTAGTGTCTAT 660
 QY 216 IleThrGlnSerAsnThrAspAlaThrGlyValAlaLeuLeuThrGlnThrAspAlaLysGly 235
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 661 ATACCCAAAGTAACACTGATGCCACCGGGGCTTTACTGACCCAGACCGATGCCAAAGGC 720
 QY 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 721 AACATTACCGCGCTGCGCTATGATGGCCGGGCGAGCTAAAGAGGAGTGTGTTAAACATC 780
 QY 256 LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 781 AAAGGTGAGCGGAACAGGTGATTATCAAAATCGCTAACCTTACTCCGCGCGCGGCAAAA 840

QY 276 LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
 Db 841 TTACGTGAAGAGCAGCGTACCGGATGTCCTGAATACAGCTACGAAACCGGAAACCCAA 900
 QY 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 901 CGGCTTATCGGCATTTACCACTCGCCGTCCATCAGACCCAGGTGTTCAGACCTACGC 960
 QY 316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 961 TATCAATATGACCCAGTAGCAATGTCTAGTATCCGTAATGATCGGAAAGCCACTCGC 1020
 QY 336 PheTrpArgAsnGlnLysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGln 355
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGTATACCTACGATTTCCCTGTATCAG 1080
 QY 356 LeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGlnAenAenGlnLeuPro 375
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1081 CTTATCAGCGCACCGGGCGGAGATGGCCAATATCGGTACGAAAGCAACCAACTTCCC 1140
 QY 376 SerProAlaLeuProSerAspAsnAenThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1141 TCTCCGGCGCTACCTTCGTATACCAATACCTACCACTACTACTCGCACTTATCTTAT 1200
 QY 396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1201 GACCGTGGCGGCAATTTGACGAAATTCAGCATAGTTCACGACCGCGCAAAATAACTAC 1260
 QY 416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1261 ACAGCGATATTAACGGTTCCTCAATCGACCAACCGCGCGGTACTCAGCACATTTGAC 1320
 QY 436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1321 GATCCAACTCAAGTCGATCGCTTATTTGATCGGGAGGCGCATCAACACGAGCTTGTATCC 1380
 QY 456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGly 475
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1381 GGCCAAAGTCTAACTTGGACACCGCGAGCGCAATTTGAAACCAAGCCCAATAAGCGGAG 1440
 QY 476 AsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro 495
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1441 AATGAGTGGTATCGCTACGATAGCAACGCGCATACCGCAGCTAAAGTGAATGAACAA 1500
 QY 496 ThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1501 ACTCAATATCCCGCAACAAAGGGTAACTTATCTACCGGGGCTGGAAATACGTACA 1560
 QY 516 ThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1561 ACCCAGAACACCGCCACACACAGAAAGATTACAGTTATCACACTCGGTAAAGCGCGC 1620
 QY 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAenAenAsn 555
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1621 CGCGCCAAAGTCCGAGTATTTGGAGAGCGGTAAACACAGAGATATTAATAACAAT 1680
 QY 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAapAenGln 575
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1681 CAGCTTCGTTACAGCTACGATTAATCTTATGGTCCAGCCAACTTCAATTAGATACGAC 1740
 QY 576 GlyGlnIleIleSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaLys 595
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1741 GACCAATTTACGTGAAGAAAGATATTAATCCATTTGGTGTGACGCGTGTGGGCGGCA 1800
 QY 596 AsnSerGlnThrGluAlaSerTyrTrpThrIleArgTyrSerGlyLysGluArgAspAla 615
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1801 AGCAATCAAAACCGAGCCAGCTATAAAACCAATTCGTTATTCGTAAAGAGCGGATGTT 1860
 QY 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1861 ACCGGGCTGTATTTATGAGCTACCGTTATTACCAACCGGTGGCGCGGAGATGGTTAGGT 1920

```
Qy 636 AlaaspProLaGlyThrIleAaspGlyLeuAsnLeuTyrArgMetValArgAsnAspPro 655
Db 1921 GCAGACCGGCGAGCAACCATTTGATGGACTGAATTTATTCGATGTTGAGAAATAACCCG 1980
Qy 656 ValSerLeuGlnAaspGluAengGlyLeuAlaPro----- 666
Db 1981 GTGACGCAATTTGATGTTGATGGGATTATCCCGGCCCAACAGAAACAGAGGCGATAAATA 2040
Qy 667 GluLysGlyLysTyrThrLysGluValAsnPhePheAaspGluLeuLysPheLysLeuAla 686
Db 2041 AAACAGGGTTCCTTTACGGGA-----ATGGAAGAAGCTGTTTATAAAAAAATG 2088
Qy 687 Alalys-----SerSerHisValVallYsTsrAsnGluLysGluSer 700
Db 2089 GCTAAACCTCAAACTTTCNAAGCGCAAGAGCTATCGTCGCCCAACAGAGCAAGAGGCC 2148
Qy 701 -----SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAaspSerAspPro 718
Db 2149 CATGAATCATTTGACCAACACCTTAGTGTAGATATT-----AGCCCAATT 2193
Qy 719 SerGlyTyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIle 738
Db 2194 AAAAATAACACACAGATAGCTCAAAATTAATCCCGGATAGGAAATCGTATTACG 2253
Qy 739 TyrSerArgLeuGluAsnSerSerLeuLysSerLysTyrAsnLeuSerLeu 758
Db 2254 CCACAGTGGNAAGTTTAGAGCCACATATCTTCCCTACNAGATAGACAAATGAGGGTA 2313
Qy 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTTATCGGGTGATGACCTATGTAGATAATTCACGCCGATCGCCTTGGCACTGCCACAG 2373
Qy 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAAATAGTATTAAATGTTGGTGATATCGTATCGGTACCGCTATTATCAACATCG 2433
Qy 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe--- 796
Db 2434 GCCCATCGTGTTTCTGAAATTTGTTTCAAAAAAGAACCACTGAAACTCGATAGTC 2493
Qy 797 ---PheAlaLeuMetAaspLysSerGluLysAsn-----AspTyr 808
Db 2494 AAGATGGCATTTTAAACGAATGCGGTGTCAATGTCCAGCAGCATCTATGTATAATAAT 2553
Qy 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAaspLeuLysAsn 828
Db 2554 GCTGCGGAGGACCAATGTTTAAATG-----GATTTAAACGAT 2592
Qy 829 LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAAGAAAAAGCCTTGCTGAAAAAATTAAACTAAGAGTCAGTGGACCAACATCGGACAA 2652
Qy 849 GluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAaspArgGluTyrAsn 868
Db 2653 CGCGAAATTAATCTACTACCTAGGMAAACACAGTTCGAAGTTGTT-----TCAATGAA 2703
Qy 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAAGGCAGAGATACCTATGATTATTGCAAGATATTAAACCAATCGCAGCCACTCAT 2763
Qy 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTACGTAACACTTACACCGGTAAATTTCAAAATCATCCAGT 2808

RESULT 5
LOCUS CQ854091 2817 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 57 from Patent WO2004067727.
ACCESSION CQ854091
VERSION CQ854091.1 GI:51510128
KEYWORDS
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
```

```
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
1
REFERENCE
AUTHORS Hey,T.D., Schleper,A.D., Bevan,S.A., Bintrim,S.B., Mitchell,J.C.,
Li,Z.S., Ni,W., Zhu,B., Merlo,D.J. and Apel-Birkhold,P.C.
TITLE Mixing and matching tc proteins for pest control
JOURNAL Patent: WO 2004067727-A 57 12-AUG-2004;
Dow Agrosciences LLC (US)
FEATURES
source
1..2817
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/strain="W14"
/db_xref="taxon:29488"
1..2817
exon
ORIGIN
Alignment Scores:
Pred. No.: 1.85e-151 Length: 2817
Score: 2956.00 Matches: 608
Percent Similarity: 73.01% Conservative: 90
Best Local Similarity: 63.60% Mismatches: 186
Query Match: 62.36% Indels: 72
DB: 6 Gaps: 14
US-10-647-956A-6 (1-915) x CQ854091 (1-2817)
Qy 1 MetSerSerTyrAsnSerAlaIleAaspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGGAAAAATGACCCCAAACTTTATCACCATACGCCTACCGCTAGTGTTCACGATAC 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAsnSerAsp 40
Db 61 CFTGGACTAGCTATCGGTAATATTAGTTTACCGCACTACCGCAGACGAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCGTATTATCCCGCCATCAATATAATGCGGGGATATTGAAACCAAAAGCATTCCT 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTGTATGACCCCAACAGACTAAACAACGCTGTCAACCGGAATTTTATCTGGCGCAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTGACCGCAATATCTCGCAACAGAGAGGTGATGCGGTCCGACGATTACCTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AACGATATTGAAGCGCCCGGTGTGACCATCAATGCAGCCGCTGTCCGCAAAACCAT 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTACGAAGATAACCCCTGCGCGCTCTCGCTATCAGCGAACCAAGACAGGCA 420
Qy 136 GlyGluLysThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGluLysAspTyr 155
Db 421 GAAGAGAAAAAGACCGAGCGCTTATCTGGCGCGCAATACGCGCGCAAGAAAAGACCAC 480
Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
Db 481 AACCTTGGCGGTGAGTCCGCTCCGCCATTACGATACCGCAGGACTCACTCAACTCAACAGC 540
Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp 195
Db 541 CTTGGCCCTGACCGCGCGCTTCTATCACAATCTCAACAACTGTCTACCGATAACCGAGAT 600
Qy 196 AlaAspTrpThrGlyGluAaspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
Db 601 GCGGACTGGACAGGTGAAGACCAAGAGCTCTGGCAACAAAACTGAGTAGTAGTGTCTAT 660
Qy 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
```

1
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

Hey,T.D., Schleper,A.D., Bevan,S.A., Bintrim,S.B., Mitchell,J.C.,
Li,Z.S., Ni,W., Zhu,B., Merlo,D.J. and Apel-Birkhold,P.C.
Mixing and matching tc proteins for pest control
Patent: WO 2004067727-A 57 12-AUG-2004;
Dow Agrosciences LLC (US)

1..2817
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/strain="W14"
/db_xref="taxon:29488"
1..2817

exon
ORIGIN
Alignment Scores:
Pred. No.: 1.85e-151 Length: 2817
Score: 2956.00 Matches: 608
Percent Similarity: 73.01% Conservative: 90
Best Local Similarity: 63.60% Mismatches: 186
Query Match: 62.36% Indels: 72
DB: 6 Gaps: 14

US-10-647-956A-6 (1-915) x CQ854091 (1-2817)

Qy 1 MetSerSerTyrAsnSerAlaIleAaspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGGAAAAATGACCCCAAACTTTATCACCATACGCCTACCGCTAGTGTTCACGATAC 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAsnSerAsp 40
Db 61 CFTGGACTAGCTATCGGTAATATTAGTTTACCGCACTACCGCAGACGAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCGTATTATCCCGCCATCAATATAATGCGGGGATATTGAAACCAAAAGCATTCCT 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGCTGTATGACCCCAACAGACTAAACAACGCTGTCAACCGGAATTTTATCTGGCGCAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTGACCGCAATATCTCGCAACAGAGAGGTGATGCGGTCCGACGATTACCTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 AACGATATTGAAGCGCCCGGTGTGACCATCAATGCAGCCGCTGTCCGCAAAACCAT 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTACGAAGATAACCCCTGCGCGCTCTCGCTATCAGCGAACCAAGACAGGCA 420
Qy 136 GlyGluLysThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGluLysAspTyr 155
Db 421 GAAGAGAAAAAGACCGAGCGCTTATCTGGCGCGCAATACGCGCGCAAGAAAAGACCAC 480
Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
Db 481 AACCTTGGCGGTGAGTCCGCTCCGCCATTACGATACCGCAGGACTCACTCAACTCAACAGC 540
Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp 195
Db 541 CTTGGCCCTGACCGCGCGCTTCTATCACAATCTCAACAACTGTCTACCGATAACCGAGAT 600
Qy 196 AlaAspTrpThrGlyGluAaspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
Db 601 GCGGACTGGACAGGTGAAGACCAAGAGCTCTGGCAACAAAACTGAGTAGTAGTGTCTAT 660
Qy 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235

Db 661 ATCAACCAAGTAACACTGATGATCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGC 720
Qy 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
Db 721 AACATTGAGCGGCTGGCTATGATGTGGCGGCGAGCTAAAGAGGAGTGGTTAACTC 780
Qy 256 LysGlyGlnAlaGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
Db 781 AAAGGTGAGCGGAAAGAGGTGATTATCAAAATCGCTAACTTCCCGCGCGGGCAAAA 840
Qy 276 LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlnThrGln 295
Db 841 TTACGTGAAGAGACCGGTACGGGATGTCTACCTGAATACAGCTACGACCGGAACCCAA 900
Qy 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
Db 901 CGGCTTATCGCATACCACTCGCTCGCTCATCAGACCGCAAGGTGTGCAAGACCTACGC 960
Qy 316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
Db 961 TATCAATATAGCCAGTAGGCAATGCTATTAGTATCGTAAATGATCGGAAGCCACTCGC 1020
Qy 336 PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATCCCTGTATCAG 1080
Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuPro 375
Db 1081 CTTATCAGCGCCACCGGGCGAGATGGCCAAATATCGGTGAGCAAAAGCAACCACTTCC 1140
Qy 376 SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
Db 1141 TCTCCGGCGTACTCTTGATAACAATACCTACCAACATATATCTCGCACTTATCTTAT 1200
Qy 396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
Db 1201 GACCGTGGCGCAATTTGAGAAATTCAGCATAGTTCACCGCGCGCAAAATAACTAC 1260
Qy 416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
Db 1261 ACGACGATATAACGGTTTCAATTCGACGACCGCGGTACTCAGCACATTTGACCGCA 1320
Qy 436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
Db 1321 GATCCAACTCAAGTCGATGCTTATTGTGTCGGGAGCGGCATCAAAACCACTGTTGTATCC 1380
Qy 456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly 475
Db 1381 GGCCTAGTCTAACTTGGACCGCGGAGCGGAATGAAACACCCCAACATAGCGCAGGA 1440
Qy 476 AsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro 495
Db 1441 AATGAGTGGTATCGCTACGATAGCAACGGCATACCGCAGCTAAAGTGAATGAACAACAA 1500
Qy 496 ThrGlnAsnThrThrGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
Db 1501 ACTCAGAATATCCGCAACCAACAAAGGGTAACTTATCTACCGGGCTGGAATACGTACA 1560
Qy 516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 1561 ACCGAGAACCAACCGCAACCAACAGAGAGTTCACAGTTATCATCTCGGTAAAGCGGCG 1620
Qy 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsn 555
Db 1621 CGCGCGCAAGTCCGAGTATTCATTTGGGAGAGCGGTAAACCAAGAGATATATTAACAA 1680
Qy 556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
Db 1681 CAGCTTCTGATACGATACGATAATCTTATTGGTCCAGCCCACTCAATATAGATAGCGAC 1740
Qy 576 GlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595
Db 1741 GGAACAAATATCATGTAGAAGAATAATATATCCATTTTGGTGTACAGCGCTGTGGCGGCA 1800

Qy 596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla 615
Db 1801 AGGAATCAAAACGAAAGCCAGCTATAAAACCAATTCGTATTCTTGGTAAAGAGCGGATGT 1860
Qy 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
Db 1861 ACGGGCTGTATATATATGGCTACCTGTTATACCAACCGTGGCGGCGAGATGGTTAGGT 1920
Qy 636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
Db 1921 GCAGACCGCGCAGGAACCAATTCATGACTGAATTTATATCGCATGCTGAGAAATAACCCG 1980
Qy 656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
Db 1981 GTGACGCAATTTGATGTTTCAGGGATTTATCAGCGGCAACAGAACAGAAAGCGATAATA 2040
Qy 667 GluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeuAla 686
Db 2041 AAACAGGGTTCCTTTACGGGA-----ATGGAAGAAGCTGTTTATTAATAAANAATG 2088
Qy 687 AlaLys-----SerSerHisValValLysTrpAsnGluLysGluSer 700
Db 2089 GCTAAACCTCAAACTTTCAACCGCAAGAGCTATCGCTGCCCAACAGACAGCAAGAAGCC 2148
Qy 701 -----SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspPro 718
Db 2149 CATGAATCATTACCAACCAACCTAGTGTAGATATT-----AGCCCAATT 2193
Qy 719 SerGlyTyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIle 738
Db 2194 AAAAATACTACCAACAGATAGCTCACAATAATTAATCGCGCATAGGGAANAATCGTATTACG 2253
Qy 739 TyrSerArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeu 758
Db 2254 CCAGCAGTGGAAAGTTTAGACCGCCACATTTCTTCCCTACAAGATAGACAAATGAGGGTA 2313
Qy 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTTATCGGGTGTACCTATGACCTATGTAGATATTCACGCCATTCGCTTGGCACTCGCCACAG 2373
Qy 770 -----IleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAAATAGTATTAAATGTTGGTGATATCGTTTCGGATAACGCTTATTTTCAACATCG 2433
Qy 780 GluHisLysTyrArgSerAsn-----HisProAspPheTyrSerGluThrAspPhe--- 796
Db 2434 GCCATCGTGGTTCGTGAATTTTGTTCACAAAAAAGAACCCAGTGAACCTCGATACGTC 2493
Qy 797 ----PheAlaLeuMetAspLysSerGluLysAsn-----AspTyr 808
Db 2494 AAGATGGCATTTTAAACGAATCGGGTGTCAATGTCCACAGCAGCATCTATGTATAATAAT 2553
Qy 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAsn 828
Db 2554 GCTGCGAGGACCAAGTATTAAATG-----GATTAAACAGAT 2592
Qy 829 LysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyrThrGlnLeuSerAsn 848
Db 2593 TCAGGAAAGGCTTGCTGAAAAAATAAATTAAGAGTCAGTGGACCAACATCGGGACAA 2652
Qy 849 GluGluArgAlaLeuLeuGlnGluThrGluProAlaIleAlaIleAspArgGluTyrAsn 868
Db 2653 CGGGAATATTTACTACCTAGGGAACACAGTTCGAAGTTGTT-----TCAATGAAA 2703
Qy 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAGGCGAGATACCTATGTATTATTCGAAGATATTAAACCAATCCCGACCCATCAT 2763
Qy 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaAla 904
Db 2764 AGA---AATGTAGTAAACACTTACCCGGTAAATTTCAATCATCCAGT 2808

gene	RGSMYGLTIROVFLD"	27601	CGAGGGTTAAATATACATACGCTGGGAATATCTCGGACTCAAGCTGATGAACCAATAGC	27660
RBS	/complement(5853..5658)			
gene	/locus_tag="plu4464"	40	AspGluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValIysSerThrAep	59
CDS	/complement(5824..6147)	27661	AACGAATTGATCAGTCGCTATCAATTAATACTACGCGGACTTCAAGTAAAGACACAGAC	27720
	/locus_tag="plu4466"	60	ProArgLysAsnIleAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGly	79
	/complement(5824..6147)	27721	CCACGTAGATATAAAACCAGAGTGGTTCAAACTTCTCCTGATCTTTAGTCTCGCTGGG	27780
	/function="Unknown"	80	GlnValLeuArgGluSerValAepAlaGlyAtrGThrIleThrLeuAenAepIleGlu	99
	/notes="unnamed protein product; Highly similar to unknown protein"	27781	AATACACTCGGTGAGAGAAAGTATCGATGCTGCGCGAACCATTACCTTGAACGATATCGAA	27840
	/codon_start=1	100	SerArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAep	119
	/transl_table=11	27841	GGACGCCAGTACTGACTATCAATGCAATCGCGGCTCGTCAGACCCATCACTATGAAGGT	27900
	/protein_id="CAE16838.1"	120	AenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr	139
	/db_xref="GI:36787725"	27901	AATACCTTCCCGCGCGCTTGTGCTGTCACCGAGTTAATACAAAGAACGAGAAACC	27960
	/db_xref="GOA:Q7M241"	140	ThrGluArgLeuIleThrAlaGlyAenThrProGlnGluLysAepTyrAenLeuAlaGly	159
	/db_xref="InterPro:IPR001387"	27961	ACGGAGCGCTTATTTGGCNAACATACAGATGCAGAGAAAACACAGAAATCTCGCGGG	28020
	/db_xref="UniProt/TREMBL:Q7M241"	160	GlnCysValArgHisTyrAepThrAlaGlyLeuThrGlnLeuAenSerLeuAenAla	179
	/translation="MAAKSKFKSPAFEAHSAAGLFSVDATPQETMRHFDKACLNV	28021	CAATGTATACGCCATTATGATCTCGCGGGCTGGTACAACTGGGAAAGTTTGTCTTAAACA	28080
	DLQPVETKALREKLVNSQVFASYLNTSVTVQWESGVYKRPGLALKLLTVVQRHG	180	GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAepAlaAepThr	199
	LKVLV"	28081	GGATCGGTTTATACAGATCTCGTCAATTAATAGCCGACGATCAGGAAGCTGATGGCGC	28140
	complement(join(6131..6490,6499..6504))	200	GlyGluAepGlnSerLeuThrGlnGlnLysLeuSerSerAepValTyrIleThrGlnSer	219
	/locus_tag="plu4467"	28141	GGTGTATGATGAATATAGCTGGCGTACAAAAGTGAATGGCAACATATTCAGACTCAACAT	28200
	/complement(6131..6490)	220	AenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArg	239
	/function="Unknown"	28201	AAAACCTGATGCCATTGGTCTCTGCTAACTCAATCGACGCCAAGGMAATATGCAACGG	28260
	/notes="unnamed protein product; Similar to unknown protein"	240	LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAla	259
	/codon_start=1	28261	CTGGCTATGATGTCGCGGCCAACCTGAAAGGTAGCTGGTTAACTAAAGGCCAAGCC	28320
	/transl_table=11	260	GluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuAtrGluGlu	279
	/protein_id="CAE16840.1"	28321	GAATAAGTTTATGTACAGTCTATTACCTGTCAGCAGCCGGAACAAATTCAGAGAAGAG	28380
	/db_xref="GI:36787727"	280	HisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGly	299
	/translation="MPIGESTLVISRLLSRLNRYHVIGAFLLTIPAFKGGQVYRIQR	28381	CACGGTAAATGGCGTTATTACGGAATATACCTATGAACACGAGACCCCAACGATTAAATTAAC	28440
		300	IleThrThrArgArgProSerAepAla---LysValLeuGlnAepLeuArgTyrGlnTyr	318
		28441	ATTACAACCGCGCGAATAGATAGATACAAAAACCACTACACAGATTACGCTTATGAATAT	28500
		319	AspProValGlyAenValIleAenIleArgAenAepAlaGluAlaThrArgPheTrpArg	338
		28501	GATCCCGTTGGCAATGTGATCAATATTCGTAATGATGCGAGAACCAACCCGATTCGCGCT	28560
		339	AenGlnLysValAlaProGluAenSerTyrThrTyrAepSerLeuTyrGlnLeuIleSer	358
		28561	AATCAGAAAATAGTACCGGNAATGCATATTCCTATGATTCTCTGTACCAACTCATCAA	28620
		359	AlaThrGlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuProSer-----	376
		28621	GCAACGGCGCGGAAATGGCTAACTTGGTCAGCAAGGAAGCAGCTCCCTCCTTTAATT	28680
		377	ProAlaLeuProSerAepAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAep	396
		28681	ACCCCTTCTCCTACCGATGACAACTACTTACTATATTCGTACTTATTCCTTACTACGAC	28740

Alignment Scores:

Pred. No.: 1.83e-131 Length: 349907
 Score: 2631.50 Matches: 529
 Percent Similarity: 69.89% Conservative: 100
 Best Local Similarity: 58.78% Mismatches: 152
 Query Match: 55.52% Indels: 119
 DB: 1 Gaps: 13

US-10-647-956A-6 (1-915) x BX571874 (1-349907)

Qy	1	MetSerSerTyrAenSerAlaIleAepGlnLysThrProSerIleLysValLeuAepAen	20
Db	27541	ATGATTCGTTACAAATTCGAAATTAACCGAAATACCCCATCTGTACCGTACGAGATAAT	27600
Qy	21	ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAepGlu---AenSer	39

Qy	397	HisSerGlyAsnLeuThrGlnIleAerHisSerProAlaThrGlnAsnAsnTyrThr	416
Ds	28741	GATAGCGGCACTGACACAATCCAGCAGTGTCTCGGCAAGTAACAATACTACACC	28800
Qy	417	ValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAsp	436
Ds	28801	ACAAATATCAACATTTCAAACCGTAATAAACCGCGGTGCTCTCAGTACCCCTCACCAAGAC	28860
Qy	437	ProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGly	456
Ds	28861	CCCAATCTCGTGTGATACATCTTTGATGACGGTGTATCAACACAGTCTGTTCTCAGGG	28920
Qy	457	GlnThrLeuIleTyrThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsn	476
Ds	28921	CAATCTTAACCTGGACACACCGGGGAGAACTACACAAAGTGAACCAAGT--GGTAAT	28977
Qy	477	-----GluTyrTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGlu	493
Ds	28978	ACCGCGGTGAGTGGTACCACTATGACAGTACGCGCATGCGGCTACTGAAATAAAGAA	29037
Qy	494	GlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeu	513
Ds	29038	CAGCAACATCCAATACACGAGCAGCAACGAGTCACTTATCTGCCAGGGTGGAAATTA	29097
Qy	514	ArgThrThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGlu	533
Ds	29098	CACACCACAAAGCGGCACCAATATCACCGAGACTTACAAGTTATTACTGTGAGGCNA	29157
Qy	534	AlaGlyArgAlaGlnValArgValLeuHisTyrGluSerGlyLysProGluAspValAsn	553
Ds	29158	GCAGGAAAGCACAAAGTACGGGTACTACACTGGGAAAGGCGCAACCCACCGCATAAAT	29217
Qy	554	AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp	573
Ds	29218	AACGATCAAGTCAGATATAGTACGATAATCTTACACACAGCAGCGAATTAGAACTGGAT	29277
Qy	574	AsnGlnGlyGlnIleIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTyr	593
Ds	29278	ATGCACGGAGAAATGATCAGTTGGGAGAGATTATACCCCTATGTGGCACCAGTATGG	29337
Qy	594	AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg	613
Ds	29338	GCAGCAAAATCAGATTGAAGCTGGTTACAAACCACTTCGTTATTACAGGTAAAGAACGT	29397
Qy	614	AspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTyrAlaGlyArgTyr	633
Ds	29398	GATGCACGGGACTGTACTATTACGGCTACCGCTATTATTCAACCGTGGCGCGGTAGATGG	29457
Qy	634	LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn	653
Ds	29458	TTAAGCGTGAACCGGCTGGAAACCGTAGATGGTCTGAATTTGTACCGTATGGTAAGAAAT	29517
Qy	654	AsnProValSerLeuGlnAspGluAsn-----	662
Ds	29518	AATCCAATGACCGGCATAGATGAAGATGGCGGTATGTTTAAACCGTAGCAACAGGTGCA	29577
Qy	663	-----GlyLeuAlaProGluLysGlyLysTyrThrLysGlu-----	674
Ds	29578	TTAGGCATTGGCGGTATGGCATACAGCTTTTACAAATATAAAAAATCAACAAGTTGAAAG	29637
Qy	675	-----ValAsnPhePheAspGluLeuLeuPheLysLeuAla	686
Ds	29638	CCTCAGATGCCATCTCCTGTCTCTGAATCCCTACGGTGATCAACAAGTCAGCAAAATACCC	29697
Qy	687	AlaLysSerSer-----	690
Ds	29698	CAAAAAGCGAGTGTCTTTAAAGCAAACTATGACCCGATGAAGCAGATGCCCATTAACATA	29757
Qy	691	-----HisValValLysTyrAsnGluLysGluSerSerTyr	702
Ds	29758	ACGGGGCGTAAAGAACCGCAGAACATCTCGCACAGGGTCAAGTCCCTGGCGCTCAAGCA	29817
Qy	703	ThrLysAsnLysSerLeuLysValValA-gValGlyAspSerAspProSerGlyTyrLeu	722
Ds	29818	ATAAAGAAGGGCAAGCTTAGTTCGGGTGCGGAGAAATTTCTGCGGTGGCAATGTC	29877
Qy	723	-----LeuSerHisGluGluLeuLeuLys-----	730
Ds	29878	GGTGAATTAACAAAAACCGCTTAACAAAAAGCCCGCGCACCGCAATTAATAATTTT	29937
Qy	731	-----GlyIleGluLys-----	737
Ds	29938	AGTCTACCTTGCACGGTATAAAAAAGGTATTTAAGCAGCGCGGCTAGTGTACCGTC	29997
Qy	738	IleTyrSerArgLeuGluGlu-----AsnSerSerLeuSerGlyLysSerLys	753
Ds	29998	AGCCAGAAAAATTGGAAGAGCTGCAAAAAGCAACTGATGATTTTAAAGAGGTGCAACA	30057
Qy	754	ThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGln-----	771
Ds	30058	GATACGCTAATTACCGGGCATCGTAGTGTGCGACAGTCGGAGCCACACTGGATACCGCC	30117
Qy	771	-----	771
Ds	30118	GCCGCGGTCTGCCACACCCGGTAGCCAAAGTGGCACTCAAAAGTCTGTCTATTGGCATGG	30177
Qy	772	-----AspThrIleSerGluTyrAlaGluGluHisLys	782
Ds	30178	AAAGTTACCGGCATTGTTACACCGCAGAGAATAAAGCGAGCTCGCAGAAAAACAATAAG	30237
RESULT 7			
BX571873 349107 bp DNA linear BCT 17-APR-2005			
LOCUS Photorhabdus luminescens subsp. laumondii TT01 complete genome; segment 15/17.			
ACCESSION BX571873 BX470251			
VERSION BX571873.1 GI:36787441			
KEYWORDS complete genome.			
SOURCE Photorhabdus luminescens subsp. laumondii TT01			
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.			
REFERENCE 1 Duchaud,B., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S., Bocs,S., Boursaux-Eude,C., Chandler,M., Dassa,E., Derose,R., Derzelle,S., Freyssinet,G., Gaudriault,S., Givaudan,A., Glaser,P., Medigue,C., Lenois,A., Powell,K., Siguier,P., Wingate,V., Zouine,M., Boenare,N., Danchin,A. and Kunst,F. Complete genome sequence of the entomopathogenic bacterium Photorhabdus luminescens Nat. Biotechnol. 11 (1) (2003) In press			
2 Duchaud,B., Frangeul,L., Rusniok,C. and Kunst,F. Direct Submission Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: lfrangeul@pasteur.fr, fkunst@pasteur.fr			
TITLE Location/Qualifiers			
JOURNAL 1. 349107			
REFERENCE /organism="Photorhabdus luminescens subsp. laumondii TT01"			
AUTHORS /mol_type="genomic DNA"			
TITLE /strain="TT01"			
JOURNAL /db_xref="taxon:243265"			
FEATURES complement(80..3225)			
source /genes="tccC1"			
gene /locus_tag="plu4167"			
CDS complement(80..3211)			
/genes="tccC1"			
/locus_tag="plu4167"			
/function="Unknown, probable insecticidal toxin"			
/notes="Highly similar to insecticidal toxin complex protein tccC of W14."			
/codon_start=1			
/transl_table=11			
/product="Insecticidal toxin complex protein TccC1"			

```

/protein_id="CAE16539.1"
/db_xref="GI:36787442"
/db_xref="GOA:Q7MZV7"
/db_xref="InterPro:IPR000408"
/db_xref="InterPro:IPR002345"
/db_xref="InterPro:IPR004530"
/db_xref="UniProt/TREMBL:Q7MZV7"
/translation="MSTPDTALYTPPTVSVLDNRGLSIRDIGFHRVWVGIDTRVTV
RHOYDARGVYLNHSDIPRLYDAQADNSVKNFVQWYDLAGHALRTEFSDAGRTVALND
IEGRVPMWNAATGVQRTYEGNTLPGRLLSVSEVFOETQVTERFTWAEVNTAEK
EYNSLCIRHYDTAGVYRLMSQSLAGAILTSOSHOLAEGQEAWSGDDQETVQWRLA
SEVYTTQSTTHAIGALLTQTDAGKNIOQLAYDIAGQLKGSWLTVGQREQVIVKSLW
SAAGHKTEHNGVITEYSYEPETQRLMGITTRAEBSSEARVLQDLRYEIDPVGN
VISIHNDAEATFWNQKVEPNRYVYDSLYQMSATGREMANIQOQNSQLPSPAMPY
PADNTEYNTYQRTYSDRGNGLVQIRHSPATQNSYVTEMTVSSNRVTLSLTATDP
TOVDGLFAGHGOKTLLIPQONLDMMRGELQRTVPSRENSDSSEWRYSSDGVRLKK
VSEQQTGNSOVQRTVYLPGLRLRTVGVADTKTQNLQVITVYGEAGAOVRVLHWSGK
PADIDNNQVRYSYDNLSSQIELSQGLSQEBEYYPYGGTAVAAKQTEASYKFI
RYSGERDATGLYYGYRYQPWGRKWSADPAGTVGDLNVYVMVNNPITLTDHGL
APSPNRNRTFWFASFLPKPDEGMSAMRRQKI GRAIAGGLATGGLAAATAGTAGA
ALPVLILGVAAGVAGICGALMGVNGSLLEKGGALLARLVQKSTLVQSAAGAAGASSA
AAYGARAQCVGASAGAVTGAVGWSINNADRGIGCAIGAGSAVGTIDTMLGTSSTLT
HEVAAGAAGAGMTTGTQGSFAGIHAGIGTYGSGWIGFGLDVASNPAGHLANYVG
YAAGLGAEMANRVIGGFLGRLGRAVSPYAAGLARQLVHFISARPEPFISSVLGQ
LAGGIGTGLHRVWGRDSWVSRLSAGSGIDHLAGMIQNQIRGRVLTITTTGIANAVLGG
TSAIGAARRVVISL"
complement(3220..3225)
/gene="tccB1"
/locus_tag="plu4167"
complement(3345..8051)
/gene="tccB1"
/locus_tag="plu4168"
/function="Unknown, probable insecticidal toxin"
/notes="Highly similar to insecticidal toxin complex
protein TccB of W14 Putative transmembrane protein."
/codon_start=1
/transl_table=11
/product="Insecticidal toxin complex protein TccB1"
/protein_id="CAE16540.1"
/db_xref="GI:36787443"
/db_xref="UniProt/TREMBL:Q7MZV6"
/translation="WLSTWKEKOLNESQDALVTGYMNFVASTLKGVGQPVTVDELVE
YLLIDPEVADDEVETSRVAQIASIQVMTLVNGSEPGRCQAMELSTANEWRDNDQYA
IWAAGAEVRNVAENYISPTTROEKSHYFSELETTLNQRLDPRQDQAVLGYLNEFEA
VSNLVLSGYINQDKPDQAIYFIQRTTKPYRYVWRQMLSKNQRDPAGNPVTPNCW
NDMQBITLPLSGDTVLEHTVRFVYNDRLYVAVVERDPVAKDQKNGIKTHYSIK
FGYKRYDDTWTAPNTTILMTQQADESSETSQSSLLIDSKTTLRKVNLIATLDFSIDP
TEETDSNPYGRMLGVFVRNFTGTPHONRPAVYGLYCDSAFNHHLRLPLSKDFLST
VRDETNDQNLQFAYVDKYYITKVISGKPTEDPENTGWGKVDLKLGTTCAYVYID
QDGLTLHTQTTNGDFVNRHIFGYNDIVYDSKSGYGTWSGNEGFLYDHGNYITFH
NAAINYPAGYGGSPVNGTWALEQRVNEGWAISPLLDAAHTITVQGSYIAWGETPA
SYTLIPDGTMLLDSKDINFALSNKLESFVTPSPDPTLTIRKFSKIADNRKFQE
INAEATDGNLFKHYSEOTFOLASGATPYTTLSEADFTSDPKNKLQVCLNVVWDH
YDRPSRGKSAWSKWNVYVELODSKAPDAI PRLISRYDSKRGVLOYLDPWTSSLP
AKTRLANTVFVTLIEKANGLVLDLYTLQADPLSEADLVTDGKSEPMDFGNSGLYF
WELFPHLPLVATRFANEQOQSPAKSLHYIFDPAMKPKHAPAYVNRVPLVEVHSD
LSRHLDGPDIDPOTQAYAHVYIYQKAVIAYVSNLIAQFQDMWYRQLTRDGLTQARVYN
LAAELLRPDPVLSLSTVPTQTLTAAQKQALRDQHEQLANSNTVLPALPNNHSH
LKLADNGYFNEBLMLSHMDTLDLARNLNRHNLTVDGKLSPLLYAAPADPVALLA
QRAQSGTLANGVSGAILTVPPYRFSAMLPRAYSAGVTLTSCFQNLILLSERSAQOE
ELAQOQLDMSYATLQOQALDGLAADRLALLASQATAQQRDHYHTLYLQNNISSAE
QUMVDITQSLSISSSTQVTSAGALKVIFNI FGLADGGSRYEGVETAEIAIGLMAAG
QATSVAERLATENYRRREEMQIYOQAQSEVDALQQLDALAREKAQTSIQQA
KAQQVIRTMLTLYTFTFQATYQLWSQLSALYQYADVVSCLSAQAQCKVELG
DYATFTOTGWNDRHYGLQVGTQLQLNLOMEALYVVRHRRLVNRTVSLQWSLLGD
DGFGLKTEGKVDPELSEKLPNDYEGHVLRQIKTVSVTLPTLIGPYQNVKATLQTS
SSTLTADINGVKRLNDPFGKGDATHITVNRASQOQVALSSGINDGVSFEARLDEER
YLSFEGTGAVSKWTLTTFPFSVDEHDDDKTLKADQEQMALLANNDVILVQVHYTACDG
ASFANQVKKTLF"
complement(8046..8051)

```

RBS

```

/gene="tccB1"
/locus_tag="plu4168"
complement(8134..11034)
/gene="tccA1"
/locus_tag="plu4169"
complement(8134..11034)
/gene="tccA1"
/locus_tag="plu4169"
complement(8134..11034)
/gene="tccA1"
/locus_tag="plu4169"
/function="Unknown, probable insecticidal toxin"
/notes="Highly similar to insecticidal toxin complex
protein Tcca of W14."
/codon_start=1
/transl_table=11
/product="Insecticidal toxin complex protein Tcca1"
/protein_id="CAE16541.1"
/db_xref="GI:36787444"
/db_xref="InterPro:IPR003518"
/db_xref="UniProt/TREMBL:Q7MZV5"
/translation="WNQASPLISRTBEIHNLPKGKLTDLGTSVDFVDMRPRFRFIRE
HRADLGRSAEKMYDLAVGYAHQVLFHFRHNSLSEAVQFSLRFPFSVSDPYANQFLDA
NTGMDKAPSSPSEANDAPVAYLTHIYQLADQEKSGASAIMNTLVERRPDIQALLIN
DKAINEVIPQLQVNEILSKAIQKKLSLTDLQVNAKLSSTTRYPNNLPHYHQIQOT
RQSVLGTTLQDITLPTQTLDPQNFWATAKGLSDATAGALTLOIMASOLSPEQOKIM
VETVQNTFYQNYGDSLLTANSFSDMTVLTDRTSILYPOVELMLCSTVGSGSTVVKSDN
VSSGQTTATPAYGARFTHAGKPKQAITLSRSGAEAFALTNNLTDKLDNRINRTVRL
QKMLNPYEDIDLTVTSAMDABETNTALSMNDNTLMLGVFPHYQAKYGTAKQFAGM
LRVTPFAITPATPFLDQVNSVGTFTDPFVIDNQDFVYTLTGGDGRVVKHISTALG
LNHRQFLLADNINARQOGNITOSTLNCNLVVVSFVRLANLAIQAOOQORDLPLETALL
LDAGTGIYVQQLAGKPIIMVPOKDSPLAADILSLQALSIAQOQOORDLPLETALL
LSSGSTTAQGTDDQNFIRQVQNLGTSFVSATILSRSGAPLVNDINGHAIDFALLS
AGNSPLIDQVGLVTDAGIESVITMVVKTQSLSDDEKKAITLTNTLYQAQQTQQGVA
VSLAQTLNVQSOLPALLRSGGTTYQWLSATWALKDTVKIAADIPAGYLSLLREV
RRSLTQOFTLSPANVQTLDDYPAYFGASAEVVTIDISLMMYTLSTRYSLLQVQKAG
GGTEDDLVAYLRVANAAATPLSQADAAOTLATLLGWETNELOAAWEVLGGIAKTPQLD
TLRLQQAQSGTGLGVTTQQQGVLSRSDSYTLQSTQGMVAGVSHVKGSH"
complement(11462..11943)
/locus_tag="plu4170"
complement(11462..11929)
/locus_tag="plu4170"
/function="Unknown"
/notes="unnamed protein product; Similar to pyocin S3
immunity protein and to Photorhabdus luminescens proteins"
/codon_start=1
/transl_table=11
/protein_id="CAE16542.1"
/db_xref="GI:36787445"
/db_xref="UniProt/TREMBL:Q7MZV4"
/translation="WAINTEALINSIGKTYQBIFFEGLIPYKTKPSGYPGSDISLDM
AKEGIFLFLRENKVLBITLTFINHKRPNFIIPNKLPSPLIPLMSRKLIIHORFKPE
KSLPPRKLTKEIGWTELYTLDFRIPITSMQVDYDLQERVLVTLFTPTSEIRW"
complement(11938..11943)
/locus_tag="plu4170"
complement(12038..12505)
/locus_tag="plu4171"
complement(12038..12505)
/locus_tag="plu4171"
/function="Unknown"
/notes="unnamed protein product; Similar to pyocin S3
immunity protein and to Photorhabdus luminescens proteins"
/codon_start=1
/transl_table=11
/protein_id="CAE16543.1"
/db_xref="GI:36787446"
/db_xref="UniProt/TREMBL:Q7MZV3"
/translation="MTVNVDALINSIGKSYQBIFFEGLIPYKTKPGYGCASFIALNM
AKEGHLAFKRDGKILFAVELFLQDKRPLYQFPNELSPPLKPLMTRMVWHEQFKPE
KALPPRKLTKEIGWTELYTLDFRIPITSMQVDYDLQERVSVAFSLTSEVLW"
complement(12597..13081)
/locus_tag="plu4172"
complement(12597..13064)
/locus_tag="plu4172"
/function="Unknown"
/notes="unnamed protein product; Similar to pyocin S3

```

gene

CDS

RBS

gene

CDS

RBS

gene

CDS

RBS

Qy	605	ThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArg	624
Db	26743	ACGATCCGGTATTCTGGTAAGAGCGGATGCCACCGAGCTGATTATTACGGCTATCGG	26802
Qy	625	TyrTyrGlnProTrrAlaGlyArgTrrPleuSerAlaAspProAlaGlyThrIleAspGly	644
Db	26803	TATTATCATCCCGTGGGTGGGAAGATGGCTAAGTGTGATCCAGCAAGACGATAGATGGG	26862
Qy	645	LeuAsnLeuTyrArgMetValArgAenAenProValSerLeuGlnAspGluAenGlyLeu	664
Db	26863	CTAAATTTATATCGGATGTCTCAGGATATATCCATTTCTCATCAGATATAACGATTA	26922
Qy	665	AlaProGluLysGlyLysTyrThrLysGluValAsn-----	676
Db	26923	CATCCAATAGTAATAACAATGAGCTAGAACGAATATCATCCATTTACTATCTGGATTTA	26982
Qy	677	-----PhePheAspGluLeuLysPheLys	684
Db	26983	GCTGGAGTTTATTATTAATGTCAACGATAAAGAACCAATTTTATCTACATTTAAAGAAAT	27042
Qy	685	LeuAlaAlaLysSerSerHisValVallYsTrrPAsnGluLysGluSerSerTyrThrLys	704
Db	27043	TTTGGCGCACTCT-----TGGGGAACAAGCTCACTGATTAACAACACAA	27087
Qy	705	AsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyrLeuLeuSer	724
Db	27088	ACAATACTTTCCGCCCTCAGCAGAAATATGAAAT-----TTAAAA	27126
Qy	725	HisGluGluLeuLeuLysGlyLysGluLysSerGlnIleIleTyrSerArgLeuGluGlu	744
Db	27127	CAC-----AAAAACAATGGAATATAAT-----	27150
Qy	745	AsnSerSerLeuLysSer-----LysThrAsnLeu	756
Db	27151	ACAAAAAGTTAATGAGACATCTCTGATGTGAATTCAAATATCGAAAAACAATAATTA	27210
Qy	757	SerLeuGlySerGluIleSerGly-----TyrMetAlaArgThrIleGlnAspThrIle	774
Db	27211	CRAAGATCAAGCGGCACATCGCGGATCGCATTTTAACCTGCACCGCATCCGATAAC---	27267
Qy	775	SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisProAspPheTyrSerGluThr	794
Db	27268	-----GAGAAAGAGATGGACATTTAATTAATAAGAT-----	27300
Qy	795	AspPheAlaLeuMetAspLysSerGluLysAsnAspTyrSerGlyGluArgLysIle	814
Db	27301	GAATTTGTTAACTTAAAGATAAA-----GAAAAATCC-----TTAGAAAAAGGAAATTA	27351
Qy	815	TyrAlaAlaMetGluVal-----LysValTyr	823
Db	27352	TTCCCTGGTGTGCACTCTCGCGGATAATCCAGACACTATAAAGTTCAGAAATGTTAGC	27411
Qy	824	HisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr	843
Db	27412	GAATTTATTCTCGGATGAATCCGCTACAAAAATAATGGAGTAGATTTACATCCATTT	27471
Qy	844	ThrGln-----LeuSerAsnGluGlu	850
Db	27472	ACATCATTAATTAATAAAAAACACATTTCTTAAAAAATGAAGAG	27513
RESULT	8		
LOCUS	CO824618	2883 bp	DNA
DEFINITION	Sequence 11 from Patent WO2004044217.		
ACCESSION	CO824618		
VERSION	CO824618.1		
KEYWORDS	GI:49021695		
SOURCE	Photorhabdus luminescens		
ORGANISM	Photorhabdus luminescens		
REFERENCE	1		
AUTHORS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.		
	French-Constant, R.H. and Waterfield, N.R.		

TITLE		Dna sequences from tcd genomic region of photorhabdus luminescens	
JOURNAL		Patent: WO 2004044217-A 11 27-MAY-2004; UNIVERSITY OF BATH (GB)	
FEATURES		Location/Qualifiers	
source		1..2883	
		/organism="Photorhabdus luminescens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:29488"	
CDS		1..2883	
		/note="unnamed protein product"	
		/codon_start=1	
		/transl_table=11	
		/protein_id="CAG38450.1"	
		/db_xref="GI:49021696"	
		/translation="MKNIDPKLYQKTPVSVYDNRGLIIRNIDFHRHTTANGDPDTRITRHYDIGHLNGSIDPRLYEAKQTNNTIKPNFLQWLDGNPLCTESIDAGRTVLNDIEGRPLLVTTATGVIOTQYETSLSLGRLLSVAEOTPEKTSRITERLIWAGTEAEKDHNLACQVRHYDTAGVTRLESLSLTGTVLSOSSOLLIDTOBANWTGDNETVQNNMLADIIYTYLSTFDATGALLTQDAKNIQRLAYDAGQLAGSLTLKGOTQVIVIKSLTYSAAQOKLREEHGNDVITYSEPEFQRIKTRRPSDTKVLQDRIEYDQVGNVLSIRNDABATFMHKNQMPENTYDSLYQLISATGREMANIGQSHQFPSPALPSQDNTYTNRYTRYDRGNLTKIQHSPPATQNNYTTNITSNRSRAVLSTLREDPAQVDALPADAGHONTLISQNLNWNTRGELQOVLTKRDKGANDDRWRYSGDGRWMLKINEQOASNNAQRTVYLPNLELRLTONSTATTEDLOVITVGEAGRAOVRVLHWSGKPEDIQDNQKYSTDNLIGSSQLSEGGQIISSEETYPYGGTALWAARQTEASYSKTIKRYSGKERDATGLYYGYRYQPMIGRWLSSDPAGTIDGLNLYRMVNRNPNVLDPDGLMPTIASERIAALKKNKYVTSAPANATVAINIRPPVAPKPSLPKASTSQPTTHPIGAANIKPTTSGSSIVAPLSVGNKSTSEISLPESAQSSSTSTNLQKSKSTLYRADNRSEFEEMQSPFGFKAWTPLDTKMARQFASIFIGQKDTSNLTKETVKNISTWGAQPKLKDLSNYIKTKDKSTVWVSTAINTEAGGSSGAPLHKIDMDLYEFALDQGLKPLPSGRTKNMVPSSLDDTPQIETSSIIALNHGPNVDABISFLTTIPLKNVPHKR"	
ORIGIN			
Alignment Scores:			
Pred. No.:		9.98e-129	
Score:		2337.50	
Percent Similarity:		74.12%	
Best Local Similarity:		62.94%	
Query Match:		53.53%	
DB:		6	
		Length: 2883	
		Matches: 518	
		Conservative: 92	
		Mismatches: 159	
		Indels: 55	
		Gaps: 12	
US-10-647-956A-6 (1-915) x CQ824618 (1-2883)			
Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	1	ATGAAAAACATTCATCCCAACCTTTATCAAAAAACCCCTACTGTCAGCGTTTACGATAAC	60
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	61	CGTGGTCTGATAATCCGTAACATCGATTTTCATCGTACTACCGCAATGGTGATCCCGAT	120
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	121	ACCGTATTACCGCCCTCAATACGATATTCACGACACCTAATAACAGCATCGATCCG	180
Qy	61	Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe	75
Db	181	CGCTATATGACCAAGCAACCAACCAATACGATCAACCAATTTCTTGGCAGTAT	240
Qy	76	AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu	95
Db	241	GATTTGACCGGTAATCCCTATGTACAGAGAGCATTTGATGCGAGTGCCTGTCCACCTTG	300
Qy	96	AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis	115
Db	301	AATGATATTGAAGCGCGTCCGCTACTTAACCGTGACTGCAACAGGGGTTATACAACTCGA	360
Qy	116	ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla	135
Db	361	CAATATGAAACTTCTTCCTCCGCGTCTGTTATCTGTTCCGCAACAAACACCCGAG	420
Qy	136	GlyGluLysThr-----ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGlu	152

Db 421 ---GAAAAAACAATCCCGTATACCGAAGCGCTGATTGGCTGGCAATACCGAAGCAGAG 477
 QY 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
 Db 478 AAAGACCATAACCTTGGCGCCAGTGGCTGCTCACTATGACACGGCGGGAGTTACCCGG 537
 QY 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
 Db 538 TTAGAGATTATCACTGACCGGTACTGTTTATCTCAATCCAGCCAACTATTGATCGAC 597
 QY 193 AsnGlnAspAlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLeuSerSer 212
 Db 598 ACTCAAGAGCCAACTGGACAGGTGATAACGAAACCGCTCTGGCAAAACATGCTGGCTGAT 657
 QY 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
 Db 658 GACATCTACAAACCCCTGAGCACCTTCGATGCCACCGGTGCTTTACTGACTCAGACCGAT 717
 QY 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTyr 252
 Db 718 GCAGAAAGGGAAACATTACAGACTGGCTTATGATGTGGCCGGGACACTTAAACGGGAGCTGG 777
 QY 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAla 272
 Db 778 CTAACACTCAAGCCACAGCGAACAAGTATTATCAATCCCTGACCTACTCCGGCGCC 837
 QY 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
 Db 838 GGACAAAAATTACGTAGGAAACACGGCAATGATGTTATCACCGCAATACAGTTATGAACCG 897
 QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
 Db 898 GAAACCCAAACGGCTGATCGGTATCAAAACCCCGCTCCGTCACACACTAAAGTGCTACAA 957
 QY 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
 Db 958 GACCTGGCTATGAATATACCCGGTAGGCAATGTCAATCAGCATCCGTAATAGCGCGAA 1017
 QY 333 AlaThrArgPheTyrArgAsnGlnLysValAlaProGluAsnSerTyrThrAspSer 352
 Db 1018 GCCACCCGCTTTTGGCAATACAGAAAGTAGTCCGGGAAACACTTATACCTACGATTCC 1077
 QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
 Db 1078 CTGTATCAGCTTATCAGCGCCACCGCGCGGAAATGGCGAATATAGGTCAACAAGTCAC 1137
 QY 373 GlnLeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSer 392
 Db 1138 CAATTTCCCTCACCCGCTCTACCTTCTGATAACAACACCTATACCAACTATACCCGTACT 1197
 QY 393 TyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGln 412
 Db 1198 TATACTTATACCGTGGCGCAATCTGACCAAAATCCAGCACAGTTTCCACCGCGACGCAA 1257
 QY 413 AsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThr 432
 Db 1258 AACAACTACACCAATATCACCGGTTCAATCGCAGCAACCCGCGAGTACTCAGCACA 1317
 QY 433 LeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSer 452
 Db 1318 TTGACCGAAGATCCGGCGCAAGTAGTGTCTTGTGATGCGCGGACATCAGAACACC 1377
 QY 453 LeuLeuProGlyGlnThrLeuIleTyrThrProArgGlyGluLeuLysGlnVal----- 470
 Db 1378 TTGATATCAGGACAAAAACCTGAATCTGCTGGTGAACCTGCAACAAGTAACACTG 1437
 QY 471 -----AsnAsnGlyProGlyAsn-----GluTyrTyrArgTyrAspSerAsnGly 485
 Db 1438 GTTAAACGGGACAGGGCCCAATGATCGGGAATGGTATCGTTATAGCGGTGACGGA 1497
 QY 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArgVal 505
 Db 1498 AGAAGGATGTTAAAAATCAATGAACAGCAGCGCCAGCAACCGCTCAACACACACAGGTG 1557

QY 506 IleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
 Db 1558 ACTTATTTCCGAACCTTAGAATCTTGGCTAAACAAACAGCAGCCGACACCGAAGAT 1617
 QY 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTyrGlu 545
 Db 1618 TTGCAAGTTATCACCGTAGCGGAAGCGGCGGCACAGTACGAGTATTACATTGGGAG 1677
 QY 546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
 Db 1678 AGCGGTAAACCCGGAAGATATCGACAATAATAGTTGCGTTATAGTTACGATAATCTATC 1737
 QY 566 GlySerSerGlnLeuLeuLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
 Db 1738 GGTTCAGTCAACTTGAATAGATAGCGAAGGACAAATATCAGTGAAGAGATATTAT 1797
 QY 586 ProPheGlyGlyThrAlaLeuTyrAlaLeuSerGlnThrGluAlaSerTyrLysThr 605
 Db 1798 CCCTATGGTGAACACAGCATTTATGGCGCGCCAGGAATCAGACAGACCGAGTTATAAACT 1857
 QY 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
 Db 1858 ATCCGTTATTACGGCAAGAGCGGATGCCCGGCTATATTACTACGGCTATCGGTAT 1917
 QY 626 TyrGlnProTyrAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
 Db 1918 TACCAACCGTGGATAGACGGTGTAGCTCCGATCCGCGCAGGAACATCGATGGGCTG 1977
 QY 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
 Db 1978 AATTTATATCGGATGTGAGGAATAATCCAGTTACCTTCCTTCATCTGATGATTAAATG 2037
 QY 666 Pro-----GluLysGlyLysTyrThr----- 672
 Db 2038 CCAACAATTTGCAGAACGCATAGCAGCACTAAAAAAAATAAAGTAACAGACTCAGCGCCT 2097
 QY 673 -----LysGluValAsnPheAspGluLeuLysPheLysLeuAlaLysSer 689
 Db 2098 TCCCAGCAAAATCCCAAAACAGTAGCGATAAACATCGCCCGCTGTAGCACCAAACT 2157
 QY 690 SerHisValValLysTyrAsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLys 709
 Db 2158 AGCTT-ACCGAAAGCATCAACGAGTAGCCAAACCAACACACACCTATCGAGCTGCAAA 2216
 QY 710 -----ValValArg-ValGlyAspSerAspProSerGlyTyrLe 722
 Db 2217 CATAAACCAACGACGCTCGGTCATCTATTGTGTCTCCATTGAGTCCAGTAGGAATAA 2276
 QY 722 uLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
 Db 2277 ATCTACTTCTGAATCTCTCTGCCA-----GAAAGCGCTCAA----- 2313
 QY 742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluIle 762
 Db 2314 -----AGCAGTTCTTCAAGCACTACCTCGACAAATCTACAGAAAAATCA---TT 2360
 QY 762 eSerGlyTyrMetAla-----ArgThrIleGlnAspThrIleSerGluTyrAlaGluGln 780
 Db 2361 TACTTTATATAGACAGATAACAGATCTCTTGAAGAAATGCAAAAGTAAATTCCTGAAGG 2420
 QY 780 uHisLys 782
 Db 2421 ATTTAAA 2427

RESULT 9
 LOCUS CO854080 2883 bp DNA linear PAT 23-AUG-2004
 DEFINITION Sequence 46 from Patent WO200406727.
 ACCESSION CO854080
 VERSION CO854080.1 GI:51510119
 KEYWORDS Photorhabdus luminescens

```
ORGANISM      Photorhabdus luminescens
REFERENCE      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AUTHORS        Enterobacteriaceae; Photorhabdus.
1
TITILE         Hey, T.D., Schleper, A.D., Bevan, S.A., Bintrim, S.B., Mitchell, J.C.,
JOURNAL        Li, Z.S., Ni, W., Zhu, B., Merlo, D.J. and Apel-Birkhold, P.C.
                Mixing and matching lc proteins for pest control
                Patent: WO 2004/067727-A 46 12-AUG-2004;
FEATURES       Dow Agrosciences LLC (US)
source         Location/Qualifiers
1..2883
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/db_xref="taxon:29488"
1..2883
/note="unnamed protein product"
/codon_start=1
/translation="GI:51510120"
/protein_id="CH19032.1"
/db_xref="GI:51510120"
/feature_id="1"
CDS
1..2883
/translation="MKNIDPKLYQKTPVSVVYDNRGLIIRNIDFHRITANGDPDTRIT
RHYQDIHGLNQSIDPRLYEAKQTNNTIKPNFLWQYDLNPLCTESIDAGRTVLND
IGRPLLTATVGTCTOVETSSLPGRLLSVAEOTPEBKTSTRIERLWAGTWAEK
DNLAQCVRHVDYTAGVTELESISLTGTVLSQSSOLLIDTOEANTGDNETWQNLW
DIYITLSTFDATGALLTQDAKNIQRLAYDVAGLNGSWLTKGTQVQVILKSLTY
SAAGQKLRBEHNDVITEYSYEPETQRLIGIKTRPSDVKVLQDLRYEYDPVGNVISI
RNDAAETFRHKNQVMPENTYTDLYQLISATGREMANIGQSHQFPALPSPNNT
YTNTRYTYDRGGLNLTQHSKPATONNTYNTI TVSNRSRAVLSTLTEDPAQVDAL
PAGGHONTLYSGONLWNTGELQOVLTKRDKGANDREWRYSGDGRMLKNEQ
QASNAQOTRVYFLENLELRLTQNSTATTEDLQVTVGEAGRAQVRVLWESGKREDI
DNNQRUTLYYGLSGLDSEGGIISBEIYPYGGTALWAARNQTEASYKTIIRYSG
KERDATGLYYGRIYQIRWGLSDPAGTIDGLNLYRMVRNPNVTLDDPDLMPYTI
ABRIALAKKQVDSPPANATNVAIRNPVAPKPSLPKASTSQPTTHPIGAAANI
KPTTSGSIVAPLVGNSKSTSEISLPESAQSSSSTSTNLQKSFSTLYRADNRSE
EMQSKPEFGKPLATDKWQAFASIFIGOKDTNLPKSTVKNLSTWCAKPKLDLS
NVIKYTKDSTWVSTAINTEAGGQSGAPLHKIDMDLYEPALDQKLNPLPEGRYKN
MVPSELLDTPQIETSIILNHNPGVNDABISFLTIPLKNVPHKR"
ORIGIN
Alignment Scores:
Pred. No.:      9,98e-129      Length:      2883
Score:          2537.50      Matches:     518
Percent Similarity: 74.12%      Conservative: 92
Best Local Similarity: 62.94%      Mismatches:  159
Query Match:    53.53%      Indels:      55
DB:             6            Gaps:        12
US-10-647-956A-6 (1-915) x CQ854080 (1-2883)
QY      1 MetSerSeryTAsnSerAlaIleAapGlnLysThrProSerIleLysValLeuAapAen 20
DB      1 ATGAAAAACATTGATCCCAAACTTTATCAAAAAACCCCTACTGTCCAGCGTTTACGATAAC 60
QY      21 ArgLysLeuAenValArgThrLeuGluThrLeuAthrGlnAlaAapGluAenSerAap 40
DB      61 CGTGGTCTGATATCCGTAACATCGATTTTTCATCGTACTACCGCAAAATGGTGTCCCGAT 120
QY      41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAapPro 60
DB      121 ACCCGTATTACCGCCCATCAATACGATATTTCACGGACACCTAAATCAAAAGCATCGATCCG 180
QY      61 Arg-----LysAenLysAenGlnSerGlyProAenPheIleArgValPhe 75
DB      181 CGCCTATATGAAGCAAGCAACCAACATACGATCAAAACCAATTTCTTTGGCAGTAT 240
QY      76 AenLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
DB      241 GATTTCACCGGTAATCCCTATGTACAGAGAGCATTCATGCGAGTCCGACCTGTCCACTTG 300
QY      96 AenAspIleGluSerProValLeuIleAenAlaThrGlyValArgGlnAenHis 115
DB      301 AATGATATTGAAGCGCGTCCGTACTTAACGGTGACTGCAACAGGGGTATATACAAATCGCA 360
```



```
Db 1438 GTTAAACGGGACAAAGGCGCAATGATGATCGGGAATGGTATCGTTATATAGCGGTGACGGA 1497
Qy 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgVal 505
Db 1498 AGAAGAGTGTAAATAATCAATGACAGCGAGCGGCGGCAACACGCTCAACACACGCGTGTG 1557
Qy 506 IleTyrLeuProGlyLeuGluLeuAArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
Db 1558 ACTATTTCGCGAACTTAGAACTTCGCTCAACAAACAAACAGCAGCGGCCACACCGAAGAT 1617
Qy 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
Db 1618 TTGCAAGTTATCACCGTAGCGGAAGCGGCGGCGGCAACAGTACGAGTATTACATTGGGAG 1677
Qy 546 SerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
Db 1678 AGCGGTAACCGGAAGATATCGACAATAATCAGTTGCGTTATAGTTACGATAATCTTATC 1737
Qy 566 GlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
Db 1738 GGTTCAGTCACTTGAAATTAGATAGCAAGGACAAATTAATCACTGTAAGAAGAAATATAT 1797
Qy 586 ProPheGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
Db 1798 CCCTATGTTGGAACAGCATTTATGGCGCGCCAGGAATCAGACAGAGCGCAGTTATAAACT 1857
Qy 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyr 625
Db 1858 ATCCGTTATTTCAGCAAGAGCGGATGCCACCGGGCTATATTACTACGGCTATCGGTAT 1917
Qy 626 TyrGlnProTrpAlaGlyArgTyrLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
Db 1918 TACCACCGTGGATAGACCGGTGTTAAGCTCCGATCCGACGAGAACATCGATGGCGCTG 1977
Qy 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
Db 1978 AATTATATCGGATGTTGAGGAATAATCCAGTTACCTCTCTGATCTCGATGATTAAATG 2037
Qy 666 Pro-----GluLysGlyLysTyrThr----- 672
Db 2038 CCAACAATTTCAGAACGCATAGCAGCACTAAACAAAAATAAAGTAACAGACTCAGCGCCT 2097
Qy 673 -----LysGluValAsnPheAspGluLeuLysPheLysLeuAlaAlaLysSer 689
Db 2098 TCGCCAGCAATGCCAACAACGTAGCGATAAATCCCGCGCGCTGTAGCACCAAAACCT 2157
Qy 690 SerHisValValLysTrpAsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLys 709
Db 2158 AGCTT-ACCGAAAGCATCAAGAGTAGCCCAACCAACACACACCCCTATCGGAGTGCAAA 2216
Qy 710 -----ValValArg-ValGlyAspSerAspProSerGlyTyrLe 722
Db 2217 CATAAACCAACGACGCTCGGCTCATCTATTGTTGCTCCATTTGATCCAGTAGGAATAAA 2276
Qy 722 uLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLe 742
Db 2277 ATCTACTTCTGAAATCTCTCTGCCA-----GAAAGCGCTCAA----- 2313
Qy 742 uGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluI1 762
Db 2314 -----AGCAGTTCTTCAAGCACTACCTCCAGCAAAATCTACAGAAAAATCA---TT 2360
Qy 762 eSerGlyTyrMetAla-----ArgThrIleGlnAspThrIleSerGluTyrAlaGlu1 780
Db 2361 TACTTTATAGACAGATACACATCCTTTTGAAGAAATGCAAGTAATTCCTCGAAGG 2420
Qy 780 uHisLys 782
Db 2421 ATTTAAA 2427
RESULT 10
CQ824620
```

```
LOCUS CQ824620
DEFINITION Sequence 13 from Patent WO200404217.
ACCESSION CQ824620
VERSION CQ824620.1
KEYWORDS GI:49021700
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS French-Constant,R.H. and Waterfield,N.R.
TITLE Dna sequences from tcd genomic region of photorhabdus luminescens
JOURNAL Patent: WO 200404217-A 13 27-MAY-2004;
UNIVERSITY OF BATH (GB)
FEATURES
source Location/Qualifiers
1..2850
/organism="Photorhabdus luminescens"
/mol_type="unassigned DNA"
/db_xref="taxon:29488"
1..2850
/notes="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAG38451.1"
/db_xref="GI:49021701"
translation="MKNIIDPKLYQHTPTVNVYDNRGLTIRNIDFHRSDVAGDTRIT
RHOYDPRGHSQSIDPRLYDAKQNTNPNFLWYNLTGDTLRTSDVAGRTVALND
IGRQVLIYVATGATQTRQYEANTLPGRLLSVSEQAPGQTPRTVEHFVWAGNTQAEK
DINLQYVRRHYDQATGVLQSLTENILSRQSLQADGQEAQDNDGTNDLTKLN
SEATYTTQSTFDATGALLTQDAGNMRLAYNVAGLQSLWLTQKQSEVIVKSLTY
SAAGKLRHEHNGVITEYSYEPETLRLITGTTTTRQSDSKVLQDLRYEHPVGNIIISV
RNDAAETFRWQKIVPENTYTVDSLYQLISATISATREMANIQOOSNLPSPILPTDE
NSVTNYSRVYDRCGLNVOIRHSSPAQONVTTDITVSNRNRVLSLSTPTDQVE
ALFDAGHQTLLPGQELSWNTRGELKQTPVPSRESASDREWRYRGNDGWRLLKVSQ
QTGNSQQQRTVLPDLLETQGTITTSDELHATVGAAGHAQVRLVHWETTPAGI
NNQLRSLYDNLIGSQELDNAGQIISQSEYYPFGGTALWAARNQIEASYKILRVSG
KERDATGLYGVYGVYVQWVWVSADPAGTIDGLNLYMRNPNSTLVDISGLATPK
YNIPEGDFVEIDQKRLPTLIRIKDFLHYPGVKLLKLEKPGLNVPSELFORG
PSNGVSTITFKKDLPISCISNTYETLDILYNKHETKPPPEYENATVGADLGVMSVE
FGNKSIGNASDEDLKEEHLPLGKSTMDKTDLPDLKQGLMAEKIKSGKAYPHEFGAA
IAVYGEDKKVAASLIITLUSEPRDSEYLQSTRKVSAMPTITVNEFRGHDPKSKYS
IGLVTAERKQPVISKRRANPEAPSSSRNKKLHVH"
ORIGIN
Alignment Scores:
Pred. No.: 2,39e-127 Length: 2850
Score: 2512.00 Matches: 497
Percent Similarity: 76.17% Conservative: 88
Best Local Similarity: 64.71% Mismatches: 143
Query Match: 53.00% Indels: 40
DB: 6 Gaps: 10
US-10-647-956A-6 (1-915) x CQ824620 (1-2850)
Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAAAAACATTCACCCCAAACTTTATCAATACGCCACCACCGTTAACGCTACGATAAC 60
Qy 21 ArgGlyLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 CGTGGCTGACCATTCGTAAACATCGACTTTTCACCGTGACGTCGCGGAGCGATACAGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACTCGTATTACCCGCCCAACCAATATGATACCCGAGGACACTTGAGCCCAAGCATTTGATCCA 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CGGCTGATGACGCCCAACCAACCAATAACTCGACAAACCCCACTTCCTCTGSCAATAC 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATCTCACCAGCACACTTTTGGCGGACAGAAAGTGTGATGCCGCCGCGGTACCGTAGCCCTC 300
```

```
QY 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
DB 301 AATGATATTGAAGCGCGTCAAGTGTGTTAATGTAACCGCAACCGCGCCATTTCAGACCCGA 360
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgValLeuAlaIleThrGluGlnValGlnAla 135
DB 361 CAATATGAAGCAATACCCCTGCGCGTGTCTATTATTCGTAAGTGAACAAGCC---CCC 417
QY 136 GlyGluLeuThr-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGlu 152
DB 418 GGAGAACAGACTCCCGCGTTACTGAGCATTTTATTGGGCTGTGTAATACACAGCGCGAG 477
QY 153 LysAspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGln 172
DB 478 AAAGATCATAACTTTCGCGCCAGTAGTGTGCGCACTTACGACACAGCAGGAGTGAGCGCA 537
QY 173 LeuAsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAsp 192
DB 538 CTGGAAGCCCTGTCATGTGACAGAAACATCTTATCTCAATCCCGTCAATTATTAGCCGAC 597
QY 193 AsnGlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSer 212
DB 598 GGTTCAGGAAGCAGACTGGACAGTAACGATGAACCCCTCTGGCAGACCAAACTCAATAGC 657
QY 213 AspValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAsp 232
DB 658 GAAACTTACACGACACAAAGCACCTTTGATGCTACCGGGCGCTTTGCTGACCCAAACCGAT 717
QY 233 AlaLysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrp 252
DB 718 GCAAAAGGCAACATGCAACGCTCGGCTTACACGTGGCAGGACAAATTACAAAGTAGCTGG 777
QY 253 LeuThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAla 272
DB 778 CTGACATTGAAAAACCAAGTGAGCAAGTCATTGTCAATCCCTGACCTATTTCGCGGCA 837
QY 273 GlyGlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluPro 292
DB 838 GGCCAGAAATTCGGTGAAGAACACGGTAATGGCGTTATCACTGAATACAGCTATGAACCG 897
QY 293 GluThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGln 312
DB 898 GAAACTCTACGATTGATCGGTACCACTACTCGCGCTCAATCAGATAGCAAGGTGTACAA 957
QY 313 AspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGlu 332
DB 958 GATCTAGCTATGAACATGATCTCTGTAGGGAATTTATTAGTGTCTGTAATGATGCAGAA 1017
QY 333 AlaThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSer 352
DB 1018 GCCACCGCTTCTGGCGCAATCAGAAAAATAGTCCCTGMAAATACCTACACCTACGATTCC 1077
QY 353 LeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsn 372
DB 1078 CTGTATCAGCTTATCATGTGCAACAGCAGCGTGAATGGCTAAACATCGCCAGCAAGCAAC 1137
QY 373 GlnLeuProSerPro-----AlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThr 390
DB 1138 CAATCTCTTCGCGCAATCATCCCTCTTCTTACTGTATGAAACACTATATCAACTATACT 1197
QY 391 ArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAla 410
DB 1198 CGCAGCTATAATTACGATCGCGCGCAATTTGTTTCAATCCGCGCACAGTTCCTCCCGCC 1257
QY 411 ThrGlnAsnAsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeu 430
DB 1258 GCCCAAAATAACTACACACAGATATACCGCTTTCGAATCGCAGTAACCGCGCAGTGCTG 1317
QY 431 SerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGln 450
DB 1318 AGTTCGCTAACCTTCAGACCCCAACACAGGTGGAGGCACCTGTTTGTATGCCGCGGACATCAA 1377
```

```
QY 451 ThrSerLeuLeuProGlyGlnThrLeuIleIleTrpThrProArgGlyGluLeuLysGlnVal 470
DB 1378 ACATAAATTTGTACCGGGCAAGAGCTGAGTTGGGAATACACAGAGGTGAACACTAAAACAGGTA 1437
QY 471 -----AsnAsnGlyProGlyAsnGluTyrArgTyrAspSerAsnGly 485
DB 1438 ACGCCAGTCAGTCGCGAGAGCCCGCATCGGGAATGTTATCGTTACGCGCACAGCGGC 1497
QY 486 MetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnGlnArgVal 505
DB 1498 ATCGCAGCGTTAAAGTCACTGAGCAACAGACTGGCAACAGCAGCAGCAGCAACAGTA 1557
QY 506 IleTyrLeuProGlyLeuLeuLeuArgThrThrGlnSerAsnAlaThrThrThrGluGlu 525
DB 1558 ACTTATCTTCCCGATCTGGAGCTACGTACAACAACAAATGGGACTACTACATCAGAAGC 1617
QY 526 LeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrpGlu 545
DB 1618 CTGCATGCTATTACCGTGGGAGCAGCGCCACGACACAGTGGGAGTTCTACACTGGGAA 1677
QY 546 SerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIle 565
DB 1678 ACTACGCCACACGCGGTATCAATAACAATCAGCTTCGCTATAGCTATGATAATTGATT 1737
QY 566 GlySerSerGlnLeuLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyrTyr 585
DB 1738 GGTTCAGTCAACTTGAACCTGGATAACGAGGACAAATTTATCAGTCAGGAAGATTTAT 1797
QY 586 ProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGluAlaSerTyrLysThr 605
DB 1798 CCATTTGGCGGCACACATTATGGGCGACGACGACGACGACGACGACGACGACGACGAC 1857
QY 606 IleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrTyrGlyTyrArgTyr 625
DB 1858 CTCCGTTACTCAGTAAAGAACGCGATGCTACCGGCTCTATTATTAGCGCTACCGCTAT 1917
QY 626 TyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeu 645
DB 1918 TATCACCGCTGGGTTCGTAGTGGTTAAGCGCGCATCCGCTCGAACAATTCGATGGACTG 1977
QY 646 AsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeuAla 665
DB 1978 AATCTATACCGATGTGAGAAATAATCCGTCAACACTGGTGTGATATTCTCGGCTTGCA 2037
QY 666 ProGluLysGlyLysTyrThrLysGluValAsnPheAspGluLeuLysPheLysLeu 685
DB 2038 CCTACG-----AATACAAATATTCGCGGATTTGACTTTGAT----- 2073
QY 686 AlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrThrLysAsn 705
DB 2074 -----GTAGAAATAGATGAGCAAAAAAGATCTAAATTTAAAACCA 2112
QY 706 LysSerLeuLysValValArgValGlyAspSer-----AspProSerGlyTyr 721
DB 2113 -----ACGTGTATAAGAAATCAAAAGATGAATTTTTCATTATGGTCTGTAGATAAG 2163
QY 722 LeuLeuSerHisGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArg 741
DB 2164 CTGTTA-----GAAGAAAAAACCAGCGGCTCAATGTACCAGGAGGCTATTGTAGATA 2217
QY 742 LeuGluGluAsnSerSerLeuSer 749
DB 2218 GGTCCATCCGAGAATGGAGTGCA 2241
RESULT 11
LOCUS AR166758 37948 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6281413.
ACCESSION AR166758
VERSION AR166758.1 GI:16242227
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM
```


Qy	611	LysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAla	630
Db	17025	AAAGAGCGGATCCACCGGACTATATTATACGGTTACCGATATTATCAGCCTCGGTA	17084
Qy	631	GlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGlyLeuLeuTyrArgMet	650
Db	17085	GGACGATGGTTAAGTCGGCATCCGAGGAGCAAGTAGATGGGTGAATTTATATCGGAT	17144
Qy	651	ValArgAsnProValSerLeuGlnAspGluAsnGlyLeuAlaPro	666
Db	17145	GTAAAGATTAATCCGGTTACTCTGCTGATCCTGATGATTAATGCCAATATGCAGAA	17204
Qy	667	-----GlyLysGlyLysTyr-----	674
Db	17205	CGCATAGCAGCACTGCAAAAATAAAGTAGCAGATTTCAGCGCTTCGCCAACAATGCC	17264
Qy	675	ValAsnPhePheAspGluLeuLysPheLysLeuAlaAlaLysSerSerHisValValLys	694
Db	17265	ACAAACGTAGCGATAAACATCCCGCCGCGGTAGCACCAAAACCTACC-----TTACCCAA	17321
Qy	695	TrpAsnGluLysGluSerSerTyrThr-----LysAsnLysSerLeuLysValVal	711
Db	17322	GCATCAACGAGTAGCCAAATCACTACATACCCCATCAATCTCGAAGCATAAACCAACG	17381
Qy	712	ArgValGlyAspSer-----AspProSerGlyTyrLeuLeuSerHisGlu	726
Db	17382	ACGTCGGGATCATCCATTACTGCTCCACTGAGTCCAGTAGGAATAAATCTACTCTCTGAA	17441
Qy	727	GluLeuLeuLysGlyIleGluLysSerGlnIleTyrSerArgLeuGluGluAsnSer	746
Db	17442	ATATCTCTTCCA-----GAAAGCACTCAA-----AGC	17468
Qy	747	SerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMet	766
Db	17469	AATCTTCAAGCGCTATTTCAACAATCTACAGAAAAGTCA---TTTACTTTATATAGA	17525
Qy	767	Ala-----ArgThrIleGlnAspThrIleSerGluTyrAlaGluGluHisLys	782
Db	17526	CGCGATAATAGATCCCTTTGAAGACATGCAGAGTAAATTCCTCGAAGGATTAA	17579
RESULT 12			
BD136648			
LOCUS		37948 bp	DNA linear PAT 18-SEP-2002
DEFINITION		Insecticidal toxin from Photobhabdus.	
ACCESSION		BD136648	
VERSION		BD136648.1	GI:23231593
KEYWORDS		JP 2002504336-A/6.	
SOURCE		Photobhabdus luminescens	
ORGANISM		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photobhabdus.	
REFERENCE		1 (bases 1 to 37948)	
AUTHORS		Kramer, V.C., Morgan, M.K., Anderson, A.R., Hart, H.P., Warren, G.W., Dunn, M.M. and Chen, J.S.	
TITLE		Insecticidal toxin from Photobhabdus	
JOURNAL		Patent: JP 2002504336-A 6 12-FEB-2002;	
COMMENT		NOVARTIS AG	
		OS Photobhabdus luminescens	
		PN JP 2002504336-A/6	
		PD 12-FEB-2002	
		PF 18-FEB-1998 US 2000532529	
		PR 20-FEB-1998 US 09/027080, 20-JAN-1999 US 60/116439	PI
		VANCE CARY KRAMER, MICHAEL KENT MORGAN, ARNE ROBERT ANDERSON, PI	
		HOPE PRIM HART,	
		PI GREGORY WAYNE WARREN, MARTHA MARY DUNN, JENG SHONG CHEN	PC
		.C12N15/09, A01H5/00, A01N63/02, C07K14/24, C12N1/15, C12N1/19	PC
		.C12N1/21, C12N5/10.	
		PC C12P21/02, C12N15/00, C12N5/00	
		CC orf5	
		CC hph2	
		CC orf2	
		PH Key	
		Location/Qualifiers	

FT	CDS	(15171).. (18035)	
FT	CDS	(23768).. (31336)	
FT	CDS	(31393).. (35388)	
FEATURES		Location/Qualifiers	
source		1..37948	
		/organism="Photobhabdus luminescens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:29488"	
ORIGIN			
Alignment Scores:		Length: 37948	
Score:		2501.50	
Percent Similarity:		74.33%	
Best Local Similarity:		61.74%	
Query Match:		56	
DB:		Gaps: 13	
US-10-647-956A-6 (1-915) x BD136648 (1-37948)			
Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	15171	ATGAAAAACATCGATCCTAAACTTTATCAAAAGACCCCTGTCTGCAACATCTACGATAAC	15230
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
Db	15231	CGAGGCTTAACGATCCGTAACATCGACTTTCCACCGACCCGCAACCGCGATACCGAT	15290
Qy	41	GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db	15291	ATCCGTTATTCTCGCCATCAATATGACTCCTTGGGCACCTTAAGCCAAAGACCGATCCG	15350
Qy	61	ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln	80
Db	15351	CGTCTATATGAAGCCAAACAAAATCTAATCTTCTCGGCAGTATGATTTGACCGGTAAT	15410
Qy	81	ValLeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer	100
Db	15411	ATTTTGTGTACAGAAAGCGTCGATGCTGTGGTCGCACTGTCACTTGAATGATTTGAAGGC	15470
Qy	101	ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsn	120
Db	15471	CGTCCCTACTGACGTAAGTGCACAGGTGTCTACAAACCCGACACATATGAACGTCT	15530
Qy	121	ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr---	139
Db	15531	TCCTTACCCGGTCTGCTGTGTCTGTACCGCAACAAATACCA-----GAAAAACATCC	15584
Qy	140	-----ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeu	157
Db	15585	CGTATCACCGACCGCTGATTTGGGCTGGCAATAGCGAAGCAGAGAAAAACCAATCTTT	15644
Qy	158	AlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSer	177
Db	15645	GCAGCGAGTGGCTGCGCACTATGACCGCGGAGTCAACCGGATACCGGATTAGAGAGTTGTCA	15704
Qy	178	LeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAsp	197
Db	15705	CTGACCGGTACTGTTTTTATCTCAATCCAGCCCACTATTAGCGACACTCAAGAAGTAGC	15764
Qy	198	TrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThr	217
Db	15765	TGGACAGGTGATAATAAAGCCGCTCGCAAAACATGCTGGCTGATGACATCTACACAACC	15824
Qy	218	GlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIle	237
Db	15825	CTGAGGCGCTTTGATGCCCGCGCTTACTCACTCAGACCCGATGCGAAAGGGAACATT	15884
Qy	238	GlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGly	257
Db	15885	CAGAGGCTAACCTATGATGTGGCGGGCAGCTAAACGGGAGCTGGTTAACTTAAAGAC	15944
Qy	258	GlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArg	277

QY 1 MetSerSerTyrAsnSerAlaIleAaspGlnLysThrProSerIleLysValIeuAaspAen 20
Db 1 ATGAGTCCGCTGAGACTACTCTTTATACCAACCCCAACAGTCAGCGTGTAGATAAT 60
QY 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAap 40
Db 61 CGCGGTCTGTCATTGCGTATATGTTTACCGTATTGTAATCGGGGGGATACCTGAC 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAapPro 60
Db 121 ACCCGGCTCACCGCTCACAGTATGATGCCGCTGGACACCTGAATACAGTATTGACCCA 180
QY 61 Arg-----LysAenLysAenGlnSerGlyProAenPheIleArgValPhe 75
Db 181 CGTTTGTATGATCAAGCAGCGCTGATAACTAGTAAGCCTAATTTTGTCTGGCAGCAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAaspAlaGlyArgThrIleThrLeu 95
Db 241 GATCTGGCGGTGATGCCCTGGCGGACAGAGGTGTCGATGCTGCTGCTGTTGCTGATTTG 300
QY 96 AsnAspIleGluSerArgProValLeuIleAenAlaThrGlyValArgGlnAenHis 115
Db 301 AATGATATTGAAGTCTGTCGTAATGACAATGAATGCGACCGTGTTCGTACAGCCCGT 360
QY 116 ArgTyrGluAaspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
Db 361 CGCTATGAAGGCAACACCTTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 134 GlnAlaGlyGluLysThrThrGluArgLeuIleThrAlaGlyAenThrProGlnGluLys 153
Db 421 CAAGAGAGTCTAAAGTGACAGAGCGCTTTATCTGGCTGGGAATACAACTCTGGAGAAA 480
QY 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAaspThrAlaGlyLeuThrGlnLeu 173
Db 481 GAGTATAACCTCTCCGCTGCTGTATAGCCACTACGACACACGCGGAGTGACCCGGTTG 540
QY 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAaspAen 193
Db 541 ATGAGTCAGTCACCTGGCGGCGCATCTGCTATCCCAATCTCACCAATTTGCTGGCGAAGG 600
QY 194 GlnAaspAlaAaspThrGlyGluAaspGlnSerLeuThrGlnGlnLysLeuSerSerAap 213
Db 601 CAGAGGCTAACTTGGAGCGGTGACAGCAAACTGCTCTGGCAGGAATGCTGGCAAGTGAG 660
QY 214 ValTyrIleThrGlnSerAenThrAaspAlaThrGlyAlaLeuLeuThrGlnThrAaspAla 233
Db 661 GTCTATACGACACAAAGTACCACTAATGCCATCGGSGCTTTACTACCCCAACCGATGCG 720
QY 234 LysGlyAenIleGlnArgLeuAlaTyrAaspValAlaGlyGlnLeuLysGlySerThrLeu 253
Db 721 AAAGGCAATATTACGCGTCTGGCTTATGACATTTGCCGCTCAGTTAAAGGGGAGTTGGTTG 780
QY 254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
Db 781 ACCTGAAAGGCCAGAGTGAACAGGTGATTGTAAGTCCCTGAGCTGGTCCAGCCGAGGT 840
QY 274 GlnLysLeuArgGluGluHisGlyAenGlyValIleValThrGluTyrSerTyrGluProGlu 293
Db 841 CATAAATTCGCTGAAGACACGCTACCGGCTGGTTACGAGGTACAGTTATGAGCCGGA 900
QY 294 ThrGlnArgLeuIleGlyIleThrThrArgArg-----ProSerAaspAlaLys 309
Db 901 ACTCAACGCTGTAGTATACCAACCCCGGCTGCCGAAGGGAGTCAATCAGGAGCCAGA 960
QY 310 ValLeuGlnAaspLeuArgTyrGlnTyrAaspProValGlyAenValIleAenIleArgAen 329
Db 961 GTATTGAGGATCTAGCTATAGTATGATCCGCTGGGGAATGTTATCATGATATCCATAAT 1020
QY 330 AspAlaGluAlaThrArgPheThrArgAenGlnLysValAlaProGluAenSerTyrThr 349
Db 1021 GATGCCAGACTACCGCTTTGGCGTATCAGAAAGTGAGCGGAGGAATCCCTATGTT 1080
QY 350 TyrAaspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGln 369

Db 1081 TATGATTCTGTATCAGCTTATGAGTGGACACGGCGTGAATGCTAATATATCGGTACG 1140
QY 370 GlnAenAenGlnLeuProSerProAlaLeu-----ProSerAaspAenAenThrTyrThr 387
Db 1141 CAAAGCAACCAACTTCCCTCACCGTTATACCTGTTCTTACTGACGACGACACTTATACC 1200
QY 388 AsnTyrThrArgSerTyrSerTyrAaspHisSerGlyAenLeuThrGlnIleArgHisSer 407
Db 1201 AATTACCTTCGTACCTATATCTTATGACCGTGGCGGTAATTTGGTTCAAAATCCACACAGT 1260
QY 408 SerProAlaThrGlnAenAenTyrThrValAlaIleThrLeuSerAenArgSerAenArg 427
Db 1261 TCACCCGCACTCAAAATAGTTACACCACAGATATCACCGTTTCAGCCGCACTAACCGG 1320
QY 428 GlyValLeuSerThrLeuThrThrAaspProAenGlnValAaspThrLeuPheAaspAlaGly 447
Db 1321 GCGGTATTGAGTACATTAAACGACAGATCAACCCGAGTGGATCGCTATTGATTCGGC 1380
QY 448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIleThrProArgGlyGluLeu 467
Db 1381 GGTCAATCAGAAGATGTTAATACCGGGGCAAAATCTGGATTGGAAATTCGGGGTGAATTG 1440
QY 468 LysGlnVal-----AenAenGlyProGlyAenGluTyrTyrArgTyrAasp 482
Db 1441 CAACGAGTCACACCGGTGAGCCGTGAAATAGCAGTGACAGTGAATGGTATCCTATAGC 1500
QY 483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThrGlnGln 502
Db 1501 AGTGATGCGATCGCGTCTAAAGAGTGAACACGACGACGCGGCAACAGTACTCAAGTA 1560
QY 503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAlaThrThr 522
Db 1561 CAACGGGTGACTTATCTCGCGGATTAGAGCTACGGAACAACCTGGGGTTGCAGATAAACA 1620
QY 523 ThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
Db 1621 ACCGAAGATTGCGAGTGATTACGTAGGTGAAGCGGGTCCGCGCAGAGTAAGGTATTG 1680
QY 543 HisTrpGluSerGlyLysProGluAaspValAenAenAenGlnLeuArgTyrSerTyrAasp 562
Db 1681 CACTGGGAAGTGGTAAGCCGACAGATATTGACAACAATCAGTGGCTACAGTACGAT 1740
QY 563 AsnLeuIleGlySerSerGlnLeuGluLeuAaspAenGlnGlyGlnIleIleSerGluGlu 582
Db 1741 AATCTGCTGGCTCCACGACGCTTGAATCGATAGCGAAGGGCAGATTCTCAGTCAGGAA 1800
QY 583 GluTyrTyrProPheGlyGlyThrAlaLeuTyrAlaAenSerGlnThrGluAlaSer 602
Db 1801 GAGTATTATCCGTATGCGGTACGCGGTATGGCGCGGAGAAATCAGACAGAACGCGC 1860
QY 603 TyrLysThrIleArgTyrSerGlyLysGluAaspAlaThrGlyLeuTyrTyrTyrGly 622
Db 1861 TACNAATTATTCGTACTCCGTAAGAGCGGATGCCACTGGATTGATTATTATACCGC 1920
QY 623 TyrArgTyrTyrGlnProTrpAlaGlyArgTyrLeuSerAlaAaspProAlaGlyThrIle 642
Db 1921 TACCGTTATTATCAACCTTGGGTGGGTGATGGTGGTGTGATCTGATCCGCGGGAACCGTG 1980
QY 643 AspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAaspGluAen 662
Db 1981 GATGGGCTGAATTTGTACCGAATGGTGAGGAATAACCCCATCATGATTCACCATGAC 2040
QY 663 GlyLeuAlaProGluLysGlyLys 670
Db 2041 GGATTAGCACCGTCTCCAAATAGA 2064

RESULT 14

LOCUS AR285426 3132 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 60 from patent US 5528484.
ACCESSION AR285426
VERSION AR285426.1 GI:29722605


```
KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 3132)
AUTHORS        Ensign, J.C., Bowen, D.J., Petell, J., Fatig, R., Schoonover, S.,
                fferich-Constant, R.H., Rocheleau, T.A., Blackburn, M.B., Hey, T.D.,
                Merlo, D.J., Orr, G.L., Roberts, J.L., Strickland, J.A., Guo, L.,
                Cliche, T.A. and Sukhapinda, K.
TITLE          Insecticidal protein toxins from Photorhabdus
JOURNAL        Patent: US 6528484-A 60 04-MAR-2003;
                Wisconsin Alumni Research Foundation; Madison, WI
FEATURES       Location/Qualifiers
                1..3132
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:      7,37e-125      Length:      3132
Score:          2467.00        Matches:     470
Percent Similarity: 81.25%      Conservative: 89
Best Local Similarity: 68.31%    Mismatches: 111
Query Match:     52.05%         Indels:      18
DB:              6              Gaps:         5

US-10-647-956A-6 (1-915) x AR285426 (1-3132)
Qy 1 MetSerSerTyrAnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 1 ATGAGTCGGTCTGAGACTACTCTTTATATCTCAAAACCCACACAGTCAGCGTGTAGATAAT 60
Qy 21 ArgLysLeuAnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAnSerAsp 40
Db 61 CGCGGTCTGTCATCGTATCGTATGTTGGTTTCCACCGTATGTAATCGGGGGGACTATGAC 120
Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 ACCCGGTCAACCGTCACCGATGATGATGCCGTGGACACCTGAAGTACTAGTATGACCCA 180
Qy 61 Arg-----LysAsnLysAsnGlnSerGlyProAnPheIleArgValPhe 75
Db 181 CGCTTGATGATCAAGCAGCGGTGATAACTACGTAAAGCCCTAATTTTGTCTGCAGCAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 GATCTGCGCGTCAATCGCTCGGACAGAGAGTGTGATGCTGCTGCTACTGTTGCAATTG 300
Qy 96 AsnAspIleGluSerArgProValLeuIleLeuAsnAlaThrGlyValArgGlnAnHis 115
Db 301 ATGATATTGAGTGTGCTCGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 116 ArgTyrGluAspAnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
Db 361 CGCTATGAAGCAACACCTTCGCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 134 GlnAlaGlyGluLysThrThrGluArgLeuIleThrPalaGlyAnThrProGlnGluLys 153
Db 421 CAAGAGAGTGTCTAAAGTGACAGAGCGCTTTATCTGGGCTGGGAAATACAACTCGAGAAA 480
Qy 154 AspTyrAnSerLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
Db 481 GAGTATTAACCTCTCCGGTCTGTGTATACGCCATGATGATGATGATGATGATGATGATGAT 540
Qy 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
Db 541 ATGATCAGTCAGTCGGCGGCGCCATGATCCCAATCTCCACCAATTCCTGCGCGAAGGG 600
Qy 194 GlnAspAlaAspTTPThrGlyGluAspGlnSerLeuThrGlnGlnLysLeuSerSerAsp 213
Db 601 CAGGAGGCTAACTCGAGCGGTGACACAGAAACTGTCTGGCAGGGAATGCTGGCAAGTGAG 660
Qy 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAla 233
661 GTCTATACGACACAAAGTACCCTAATGCTCGGGCTTTACTGACCCCAACCGATGCG 720
234 LysGlyAnSerIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTTPLeu 253
721 AAAGGCAATATTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
781 ACGGTCAAGGCCAGAGTGNACAGGTGATTGTTAAGTCCCTGAGCTGGTTCAGCCGAGGT 840
274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
841 CATAAATTGCGTGAAGACGCGTAAACGCGTGGTTCAGGAGTACAGTTATGAGCCGGA 900
294 ThrGlnArgLeuIleGlyIleThrArgArg-----ProSerAspAlaLys 309
901 ACTCAACGCTGTAGGTATCACACCCCGCGTGCAGAGGGAGTCAATCAGGAGCCAGA 960
310 ValLeuGlnAspLeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsn 329
961 GTATTGAGGATCTACGCTATAGTATGATCCGCTGGGGAATGTTATCAGTATCCATAAT 1020
330 AspAlaGluAlaThrArgPheThrArgAsnGlnLysValAlaProGluAnSerTyrThr 349
1021 GATGCCGAGCTACCGCTTTTGGCGTAAATCAGAAAGTGAGCGCGGAGAAATCGTATGTT 1080
350 TyrAspSerLeuTyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
1081 TATGATTTCTGTATCAGCTTATGAGTGGACAGCGGCGTGAATGGCTAATATCGGTGAG 1140
370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAnSerThrTyrThr 387
1141 CAAAGCAACCACTTCCTCACCCTGTTATACCTGTTCTACTGACGACACACCTATATACC 1200
388 AsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSer 407
1201 AATTACCTCGTACCTATATCTATACCGGCGGTAATTTGGTTCAAATCCGACACAGT 1260
408 SerProAlaThrGlnAnSerThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
1261 TCACCGCGGACTCAAAATAGTTACACCAACAGATATCACCGGCGGTAATTTGGTTCAAATCCGACACAGT 1320
428 GlyValLeuSerThrLeuThrThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
1321 GCGGTATTGATGATTAACACAGATCCAAACCGGAGTGGATGGCTATTGATTCGCGC 1380
448 GlyHisGlnThrSerLeuLeuProGlyGlnThrIleThrProArgGlyGluLeu 467
1381 GGTCAATCAGAAAGATGTTAATACCGGGGCAAAATCTGGATTGGAATATTCGGGGTGAATTG 1440
468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTyrTyrArgTyrAsp 482
1441 CAACGAGTCAACCGGTGACCGCTGAGTAAATAGCAGTACAGTGAATGGTATCGCTATAGC 1500
483 SerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAnThrThrGlnGln 502
1501 AGTATGGCATGCGCTGCTTAAAGTGAAGTGAACAGCAGACGGGCAACAGTACTCAAGTA 1560
503 GlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
1561 CAACGGGTGATCTATCTCGCGGATTAGAGTACGGGCAACTGGGGTTCAGATAAAACA 1620
523 ThrGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeu 542
1621 ACCGAAATTTGCGAGTGAATACGGTAGGTGAAGCGGGTCCGCGACAGGTAAGGGTATTG 1680
543 HisTyrGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSerTyrAsp 562
1681 CACTGGGAAAGTGGTAGCGCAGCAGATATTGACAAACATCAGGTGGCTCAGCTACGAT 1740
563 AsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGlu 582
```

```
Db      1741 AATCTGCTGGCTCCAGCCAGCTTGAACCTGATGAGCGAAGGCGAGATCTTCACTCAGGAA 1800
Qy      583 GLUTyTyProPheGlyGlyThrAlaLeuTIPAlaAlaAsnSerGlnThrGluAlaSer 602
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1801 GAGTATTATCCGTATGGCGTATGCGCGATATGCGCGGAGAAATCAGACAGAGCCAGC 1860
Qy      603 TyTyleThrIleArgTySerGlyGlyGluArgAspAlaThrGlyLeuTyTyTyGly 622
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1861 TACAAATTTATTCGTTACTCCGTAAGAGCGGATGCCACTGCATGATTTATTATTACGCG 1920
Qy      623 TyTArgTyTyGlnProTTPAlaGlyArgTTPLeuSerAlaAspProAlaGlyThrIle 642
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1921 TACCGTTATTATCAACCTTGGGTGGGTGCATGTTGAGTGCTCATCCGCGGGAACCGT 1980
Qy      643 AspGlyLeuAsnLeuTyTrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn 662
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1981 GATGGCGTGATTTGTACCGAATGTTGAGGAATAACCCCATCACATTGACTGACCATGAC 2040
Qy      663 GlyLeuAlaProGluTyGlyGly 670
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2041 GGATTAGCACCGTCTCCAAATAGA 2064

RESULT 15
AF047028
LOCUS
DEFINITION
  AF047028 11518 bp DNA linear BCT 30-JUN-1998
  Photorhabdus luminescens insecticidal toxin complex proteins Tccb
  (tccb), Tccb (tccb), Tccb (tccb), and TccZ (tccz) genes, complete
  cds.
ACCESSION
  AF047028
VERSION
  AF047028.1 GI:3265041
KEYWORDS
  Photorhabdus luminescens
SOURCE
  Photorhabdus luminescens
ORGANISM
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 11518)
    Bowen,D., Rocheleau,T.A., Blackburn,M., Andreev,O., Golubeva,E.,
    Bhartia,R. and ffrench-Constant,R.H.
    Insecticidal toxins from the bacterium Photorhabdus luminescens
    Science 280 (5372), 2129-2132 (1998)
    9641921
REFERENCE
  2 (bases 1 to 11518)
    Bowen,D.J., Rocheleau,T.A., Blackburn,M., Andreev,O. and
    ffrench-Constant,R.H.
    Direct Submission
    Submitted (08-FEB-1998) Entomology, University of
    Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706, USA
FEATURES
  source
    1. 11518
      /organism="Photorhabdus luminescens"
      /mol_type="genomic DNA"
      /strain="W-14"
      /db_xref="taxon:29488"
    1. 2898
      /gene="tccb"
    1. 2898
      /gene="tccb"
      /codon_start=1
      /transl_table=11
      /product="insecticidal toxin complex protein Tccb"
      /protein_id="AAC38628.1"
      /db_xref="GI:3265042"
      /translation="MQLASPLISRTTEEIHNLPKLTLDLGYTSVDFVVRPRFRITRE
      HRADLGRSAEKMYDLAVGYAHOVLHPRRNSLEAVQPLRSFSGPDYANQFLDA
      NTGWKAPSGSPEANDPAVALYTHIYQLALEQKNGATITMTLAERPDLDGLALLN
      DKAINVEIPQLQWITLSKAIQKLSLTDLEAVNARLSITRYPNNLPYHQIQT
      AQVLTGTTLDQITLPOTLDLPQNFATAGKLSDTTASALTRIQIMASQFSPQKII
      TETVGDQFYQLNGDSLTISFSDMTIMTDRSLTVPOVELMCSVTGSGTVVKGDN
      VSGSDTATPFAVCARFIHAGKEALTLSRSGAEHFALVNNTLDDKLDRIKTVRL
      QKWLNPYEDIDLVTSDMAETNGTALSNDNTLRLGVFKHQYQAKYSQAPAGH
      LRVVAPFAITPATPFDQVNSFTDTPFDVNDQFVYTLTGTDGARGVAKHSLTAG
      LNRQFLADLNATARQGNVOTSLNCLNFWSAFYRLANLARTLGINPESFCALVDLR
      LDAGTGLVMQLAGKPTITVPQKDSPLAADILSLQALSIAQWQQQHIDLEFSALLL
```

gene
CDS

gene
CDS

gene
CDS

```
LSDNPISTSQGTDQNLNFRQWQNLGSTFVGATLLSRSGAPLVDNTHAIDWFAALLS
AGNSLIDKVLSTLDAGISQVATVNTVNTQSLSDKKCAITLTNTLNQVQKTOQGVV
VSLAQTLNVSGSLPALLRWSGQTTYQWLSATWALKADWATAADPADYLRQURREV
RRSLTQOFTPLPAMVQTLDDYPVFGASAEVTVDISLWMLYTLSCYSLAKTLQMGAG
GGEDVLAVLRTANATPLSQSDAAQTLLATLLGWENELQAASWLVSGLAKTLTQPLDA
LRLQAQNVQTLGVTQOQGGYLLSRSDSYTLNQSTGQALVAGVSHVKSNN"
2992..7689
/gene="tccb"
2992..7689
/gene="tccb"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tccb"
/protein_id="AAC38629.1"
/db_xref="GI:3265043"
/translation="MLSTWMEKOLNESQRDALVTGMNFVAPTLKGVSGQPVTVEDIYE
YLLIDPEVADEVETSRVAQAIASIQOYMTLVNGSEPGQAMEPSTANWRDNDNOYA
IWAAGAENRYAENYISPIITROEKSHYSELETTLNQNRLLDPRQVADAVLYLNEFEA
VSNLYVLSGYINQDKFDQAIYIFIGRTTKPYRYWRQMDLSKNRQDPAGNPVTPCW
NDWQETPLSGDTVLEHTVRPFVYNDRLYVAVVERDPAVKDADGKNGIKGTHAYNIK
FGYKRYDDTWTAPNTTTLTQAGSESSQTSLLIDESSTLRQVNLATLTDSDIDP
TEETSDSNPYRLMLGVFVQFEGDGNRKNKPVVYLYLDCSFAFRHRHRLPLSKNLF
STVREDTQNSLQFAVYDKVITKVVTGATEDPENTGWSKVDLKGCTTCAYVVI
DODGLTLHIQTNGDGINRHTFGYNDLYDSKSGYGTWSGNEGFLYHGDYVTP
HNAILNYPSGGYGGSVNPTWALBORINEGWAIPLLDTLHTVTYVKGSIYIWEGETP
TGNLYIPDGTVLLDMFDKINFAIGLNKLESVFTSPDMPTLTITKNFSKIADNRKYQ
EINAETADGNLFRYSTQFTGLTSGATSTYTTLSEADFDSDPDKNYQLQVCLNVMD
HYDRPSGKKGASWKNVNVVQLQDSKAPDAIPRLVSRYSKRLGVQLDFTWFSLSL
PAKRLNTTFVTLIEKANLGLDLDYTLQADPSLEADLVTDGSKPMDFNGSLY
FWELFHLPLVATRFANEQFSPQAKSLHYIFDPAMKKNPNAWVNRPLVEGNS
DUSRLHDDSIDPDTQAYHPVYQKAVFIAYSNLIAQGDMMYTRQTRGLTQARVYI
NLAELLGPRDVSLSSTWPTQTLTAAQKAVLRDFBHLANSNTDLPALCPGRNV
YKQADQGLTFNGLVNLMLSHWTLDLARLYNRLNLTVDGKPLSLPYAAPDPAVALL
AORASGTLTNGVSGAMLTVPYPRFSMLPRAYSAVGLTSLFGONLSLLSERACQ
ESLAQQLDSSYAITLQOQALDGLAADLALLASQAQAQORHHDHYTLVYNNISSA
EGLVMDTQSAOSSLSSSTGVQTASGALKVIFNIFGLADGGSRYEGVTEAIALGLNAA
GQATSVSAERLATTENRRRREWQIQOQAEVNDALQQLDADLAVERKAQATSLQQ
AKAQVQITRMTLYTLTREFQTATLYQWLSGSLYQAYDAVVALCLSAQACWVEL
GYATTFIQGTWNHRYGLQVGETLQNLHQMEEAYLVHRHRRNLNIVTSLKSLG
DQFGKLTGEGKVDPLSEKLPDNDYPGHLQIKTVSVTLPLVGPVQNVKATLTQT
SSSLIADINGKBLNDPTGKEGDATHIVTLRASQOVALSGSIDAGSFELRLDE
RYLSFEGTGAVKWTLNFPERSVDEHIDDKTLKADENQAALLANMDVDLVQVHTACDG
GASFANQVKKTLIS"
7820..10951
/gene="tccb"
7820..10951
/gene="tccb"
/codon_start=1
/transl_table=11
/product="insecticidal toxin complex protein Tccb"
/protein_id="AAC38630.1"
/db_xref="GI:3265044"
/translation="MSPSETTLTYQTPTVSVLDNRLSIRDIGFHRIVIGGDTDTRTV
RHQYDARGHLNYSIDPLRDLQAQDNVKNFNFQWHDHLAGHALRTESVDAGRVALND
IEGRSVMTNATGVQTRRYEGNTLPGRLLSVSEQVFNQESAKVSRFVWAGNTSEK
EYNLSGLCIRHYDTAGVTRMLSGALMSQSHQLLAEQAEQANWSGDEBTVMQWMLA
SEVYTTQSTTNAIGALLTQDAGNIQRLAYDIAGQLKGSWLTVMQSEQVIVKSLSW
SAAGHKLREEHGNGVVTYYSRPELTORLIGITTRRAGSQSGARGLKYKYPVGN
VLSIHNDAAETFRNQKVEPNRYVYDSLYQLMSATGREMANIGQSNQPLPSVLPV
PIDDSTYTNLYRTTYDQGNLVQIRHSPFQTNSTYTTDTSVSRNRVLSLTITDP
TRVDALFDSGHQKMLIPQGNLDNIRBELQRTVPSRNSDSSEWRYRVRHWSGK
VSEQDTGNSQVQRTVYLPGLERTTGADKTTEDIQVTVGAGAQVRVLRHWSGK
PTDIDNNQVYSVDNLLGSQLELSEGOILSOEBYYPYVGGTAIWAARNQTEASYKFI
RYSGERDATGLYYGYRYVQPMVGRWLSADPAGTVGDLNLYRMVRNPTLTLDHDLG
AISPNNRNTFPAFLFRKPEGNSASHRRGOKIGRATAGGIAGGLAATTAAGA
AIPVLGVAAGVAGALMGVNVNLSLEGLKARLVQKSLTVQSAAGAAAGASA
AYGAQAQGVAGSAGAVTGAAGVAGVNNADRGIGGAGVAGTIDTLMGLTASTLT
HVEGAAGAAGAGMITGTQGSTAGIGAGITGYGWSIGFGLDVAGNPAGLVAVG
YAAGLIGTGLHRYMVGRESWISRLSAGSAGSIDHVAGMIGNQIRGRVLTITTTGIANADYG
LVGGTGTGLHRYMVGRESWISRLSAGSAGSIDHVAGMIGNQIRGRVLTITTTGIANADYG
TSAVGAARRVFSL"
complement(11117..11518)
/gene="tccz"
```

CDS	complement (11117..11518) /gene="tccz" /codon_start=1 /transl_table=11 /product="insecticidal toxin complex protein TccZ" /protein_id="AAC38631.1" /translation="MKNLFVIMLLSVITGSGKSTNRQTAEBGLKFAPSSGGNFI LTHACTKDIDYLPDEGGNDQETIAIKNDKOCFAHFADALINKINIGTQMAISFKGTILHA TATIQTLPLNPSPRMGVKDEQAISIMNALKN"
ORIGIN	
Alignment Scores:	
Pred. No.:	3,24e-124 Length: 11518
Score:	2467.00 Matches: 470
Percent Similarity:	81.25% Conservative: 89
Best Local Similarity:	68.31% Mismatches: 111
Query Match:	Indels: 18
DB:	Gaps: 5
US-10-647-956A-6 (1-915) x AF047028 (1-11518)	
Qy	1 MetSerSerTyRAnSserAlalleAspGlnLyThrProSerIleLeysValLeuAsn 20
Db	7820 ATGAGTCCTGCTGAGACTACTCTTTATACTCAAAACCCCAACAGTCGCTTGATGAAT 7879
Qy	21 ArgLyLeuAsnValArgThrLeuGluTyLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db	7880 CGCGGCTGTGCATTTCGTGATATGGTTTTACCAGTATTTGTAATCGGGGGGATCTGAC 7939
Qy	41 GluLeuIleThrPheTyrgluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db	7940 ACCCGGTCACCGTCACAGATGATGCCGCTGGACACCTGAACTACAGATATTGACCCA 7999
Qy	61 Arg-----LysAsnLyAsnGlnSerGlyProAsnPheIleArgValPhe 75
Db	8000 CGCTTGATGATGCAAGCAGGCTGATACTCAGTAAAGCCCTAATTTTGTCTGCGCAGCAT 8059
Qy	76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db	8060 GATCTGCGCGTCATGCCCTGCGACAGAGATGTCGATGCTGTCGACTGTTGTCATTG 8119
Qy	96 AsnAspileGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
Db	8120 AATGATATTGAAGTCGTTCCGTAATGACAATGAATGCACCGGTGTTTCGTCAGACCCGT 8179
Qy	116 ArgTyGluAspAsnThrLeuProGlyArgLeuLeuAlalleThrGluGlnVal----- 133
Db	8180 CGCTATGAAGGCAACACCTTGCCCGCTCGCTGTTATCTGTGAGCGACAAAGTTTTCAAC 8239
Qy	134 GlnAlaGlyGluLyserThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLys 153
Db	8240 CAAGAGAGTGCTAAAGTGACAGAGCCGCTTATCTGGCTGGGAATACAACTCGGAGAAA 8299
Qy	154 AspTyAsnLeuAlaGlyGlnCytsValArgHstYrAspThrAlaGlyLeuThrGlnLeu 173
Db	8300 GAGTAPAACCTCTCCGCTGTGTATACGCCACTACGACACAGCGGGAGTCACCGGTTG 8359
Qy	174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuThrAspAsn 193
Db	8360 ATGACGTCAGTCACCTGGCGGCGCATGCTATCCCAATCTCACCAATTTGTCGCGGAGGG 8419
Qy	194 GlnAspAlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAsp 213
Db	8420 CAGAGGCTTAACCTGGAGCGGTGACGACGAACATGTCCTGGCAGGAATGCTGCAAGTAG 8479
Qy	214 ValTyrlleThrGlnSerAsnThrAspAlaThrGlyValLeuLeuThrGlnThrAspAla 233
Db	8480 GTCTATACGACACAAAGTACCACCTAATGCCATCGCGGCTTTACTGACCCCAAACCGATCG 8539
Qy	234 LysGlyAsnIleGlnArgLeuAlatyAspValAlaGlyGlnLeuLysGlySerTrpLeu 253
Db	8540 AAAGGCAATATTCAGCGCTCTGGCTATGACATTCATTCATTCAGTTCGCGTCAGTAAAAAGGAGTGTGTTG 8599
Qy	254 ThrLeuLysGlyGlnAlaGluGlnValIlelleLysSerLeuThrTySerAlaAlaGly 273
Db	8600 ACCGTTAAAGCCAGAGTGAACAGGTGATTGTTAAAGTCCCTGAGTGGTCTGAGCCGAGGT 8659
Qy	274 GlnLyLeuArgGluGluHisGlyAsnGlylleValThrGluTySerTyGluProGlu 293
Db	8660 CATAAATTTTCGCTGAAGACACGCGTAACCGGCTGTTACCGAGTACAGTTATGAGCCGAA 8719
Qy	294 ThrGlnArgLeuIleGlylleThrArgArg-----ProSerAspAlaLys 309
Db	8720 ACTCAACGCTGTATAGGTATCACCCCGCGCTGCCAAGGAGTCAATCAGGAGCCAGA 8779
Qy	310 ValLeuGlnAspLeuArgTyGlnTyAspProValGlyAsnValIleAsnIleArgAsn 329
Db	8780 GTATTGCAAGTATACGCTAATGATATGATCCGCTGGGAATGTTATCAGTATCCATAAT 8839
Qy	330 AspAlaGluAlaThrArgPheTrpArgAsnGlnLysValalaProGluAsnSerTyThr 349
Db	8840 GATGCCGAAGCTACCCGCTTTTGGCTAANTCAGAAAGTGGAGCGGAGAAATCGCTATGTT 8899
Qy	350 TyrAspSerLeuTyGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGln 369
Db	8900 TAGTATTTCTGTATCAGCTTATGAGTGCACAGCGGTGNAATGGCTATATATCGGTGAC 8959
Qy	370 GlnAsnAsnGlnLeuProSerProAlaLeu-----ProSerAspAsnAsnThrTyThr 387
Db	8960 CAAAGCAACCAACTCCCTCCTACCTTATACCTGCTACTACGACACAGCACTATATACC 9019
Qy	388 AsnTyThrArgSerTySerTyAspHisSerGlyAsnLeuthrGlnIleArgHisSer 407
Db	9020 AATTACCTTCGTACCTATATATGACCGTGGCGGTAAATTTGGTTCAAAATCCGACACAGT 9079
Qy	408 SerProAlaThrGlnAsnAsnTyThrValAlaIleThrLeuSerAsnArgSerAsnArg 427
Db	9080 TCACCCGCGACTCAAAATAGTTACACACAGATATACCGTTTCACGCCCGCAGTAAACCG 9139
Qy	428 GlyValLeuSerThrLeuThrAspProAsnGlnValAspThrLeuPheAspAlaGly 447
Db	9140 GCGGTATTGAGTACATTAAACGACAGATCCAAACCGAGTGGATGCGCTATTTGATTCGGC 9199
Qy	448 GlyHisGlnThrSerLeuLeuProGlyGlnThrLeulleTrpThrProArgGlyGluLeu 467
Db	9200 GGTATCATGAAGATGTTAATACCGGGCAAAATCTGGAATTTTCGGGGTGAATG 9259
Qy	468 LysGlnVal-----AsnAsnGlyProGlyAsnGluTpTyArgTyArg 482
Db	9260 CAACGAGTACACACCGTGAGCGGTGAAATAGCAGTACAGTGAATGGTATCGCTATAGC 9319
Qy	483 SerAsnGlyWetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGln 502
Db	9320 AGTGATGATCGCGCTCTTAAGTGAGTGAACAGCAGACGCGCAACAGTACTCAAGTA 9379
Qy	503 GlnArgValIleTyLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThr 522
Db	9380 CAAACGGTGACTTATCTCGCGGATTTAGAGCTACGGCAACTCGGGGTTCAGATAAAACA 9439
Qy	523 ThrGluGluLeuHisValIleThrLeuClvGlualaGlyArgAlaGlnValAtqValLeu 542
Db	9440 ACCGAAGATTTCAGGTGATTACGGTAGTGAAGCGGTGCGGCACAGGTAAAGGATTG 9499
Qy	543 HisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTySerTyArg 562
Db	9500 CACTGGGAAGTGGTAAAGCCGACAGATATTGCAACAATCAGTGGCGCTACAGTACGAT 9559
Qy	563 AsnLeuIleGlySerSerGlnLeuLeuAspAsnGlnGlyGlnIlelleSerGluGlu 582
Db	9560 AATCTGCTGGCTCCAGCCAGCTTGAATGAGTATAGCGAAGCGGAGATTTCTCAGTCAGGAA 9619
Qy	583 GluTyTyTrpPheGlyGlyThrAlaLeuTrpAlaAsnSerGlnThrGluAlaSer 602
Db	9620 GAGTATTATCCGTATGCGCGGTATCGCGGATATGGCGCGGAGAAATCAGACGAAGCCAGC 9679

Qy	503	TyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGly	622
Db	9680	TACAAATTTATTCGTTTACTCCGGTAAAGAGCGGATGCCACTGGATTGTATTATACGGC	9739
Qy	623	TyrArgTyrTyrGlnProTtAlaGlyArgTTrpLeuSerAlaAspProAlaGlyThrIle	642
Db	9740	TACCGTTATTATCAACCTTGGTGGGTCGATGGTTGAGTGCTGATCCGGCGGGAACCGTG	9799
Qy	643	AspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsn	662
Db	9800	GATGGCTGAATTTGTACCGAATGGTGAGGAATAACCCATCACAATTGACTGACCATGAC	9859
Qy	663	GlyLeuAlaProGluLysGlyLys	670
Db	9860	GGATTAGCACCGTCTCCAAATAGA	9883

Search completed: December 14, 2005, 20:15:11
Job time : 11061 secs

Page Blank (uspb)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search; using frame_plus_p2n_model

Run on: December 14, 2005, 06:00:58 ; Search time 1144 Seconds

(without alignments)
5330.589 Million cell updates/sec

Title: US-10-647-956A-6

Perfect score: 4740

Sequence: 1 MSYNSAIDQKTPSIKVLND.....EAINIRSAIAENLGMRTS 915

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/cpn2_1/USPTO.spool.p/US10647956/runat_12122005_091817_29565/app_query.fasta_1.1095
-DB=N_Geneseq -QWTF=fasabp -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647956 @CGN 1.1.1096 @runat_12122005_091817_29565 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBFOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSEXT=7

Database : N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4740	100.0	2745	6	ABES52585 P. lumine
2	4686	98.9	2748	12	ADN61381 Photorhab
3	4429	93.4	2748	10	ACF69438 Photorhab
4	4429	93.4	110000	10	ACF67367_23 Continuation (24 o

5	4429	93.4	110000	10	ACF67367_24	Continuation (25 o	
6	4429	93.4	110000	10	ACF65386_4	Continuation (5 of	
C	7	2960	62.4	2817	12	ADN61384 Photorhab	
8	2956	62.4	2817	12	ADP18627	Photorhab	
9	2956	62.4	2817	13	ADR21537	Photorhab	
10	2845.5	60.0	2817	10	ACF69434	Photorhab	
C	11	2845.5	60.0	110000	10	ACF65386_5	Continuation (6 of
12	2627.5	55.4	2811	10	ACF70848	Photorhab	
13	2627.5	55.4	110000	10	ACF67367_39	Continuation (40 o	
C	14	2627.5	55.4	110000	10	ACF65388_08	Continuation (9 of
15	2578.5	54.4	2898	10	ACF71155	Photorhab	
C	16	2578.5	54.4	110000	10	ACF67367_42	Continuation (43 o
17	2578.5	54.4	110000	10	ACF65388_05	Continuation (6 of	
18	2537.5	53.5	2883	12	ADN61382	Photorhab	
19	2537.5	53.5	2883	12	ADP18623	Photorhab	
20	2537.5	53.5	2883	13	ADR21526	Photorhab	
21	2523.5	53.2	2913	10	ACF69431	Photorhab	
22	2512	53.0	2850	12	ADN61383	Photorhab	
23	2512	53.0	2850	12	ADP18625	Photorhab	
24	2507.5	52.9	2880	10	ACF69421	Photorhab	
25	2501.5	52.8	37948	2	AAZ06831	Photorhab	
26	2467	52.0	3132	2	AAT68850	Photorhab	
27	2467	52.0	3132	2	AAV29927	tccC gene	
28	2467	52.0	3132	12	ADN61380	Photorhab	
29	2467	52.0	3132	13	ADR21505	Photorhab	
30	2466	52.0	3132	10	ACF71170	Photorhab	
31	2466	52.0	110000	10	ACF67367_43	Continuation (44 o	
C	32	2466	52.0	110000	10	ACF65388_04	Continuation (5 of
C	33	2303	48.6	110000	10	ACF65388_05	Continuation (6 of
34	2217.5	46.8	37544	3	AA550029	Coamid ch	
35	2187.5	46.1	2889	13	ADR21530	Xenorhabd	
36	2187.5	46.1	2889	14	ABE47813	Native Xp	
37	2187.5	46.1	2947	13	ADR21533	Xenorhabd	
38	2187.5	46.1	2947	14	ABE47818	XbaI to X	
39	2187.5	46.1	7508	13	ADR21534	Xenorhabd	
40	2187.5	46.1	7508	14	ABE47819	XbaI to X	
41	2168	45.7	3048	13	ADR20366	Recombina	
42	2168	45.7	3048	13	ADR21495	Xenorhabd	
43	2168	45.7	3051	12	ADN61357	Xenorhabd	
C	44	2168	45.7	39005	13	ADR20357	Recombina
C	45	2168	45.7	39005	13	ADR21486	Xenorhabd

ALIGNMENTS

RESULT 1
ABES52585
ID ABES52585 standard; DNA; 2745 BP.
XX
AC ABES52585;
XX
DT 30-DEC-2002 (first entry)
XX
DE P. luminescens (W-14) tccC2 gene.
XX
KW Gene; db; toxin A; toxin B; TcdA; protoxin; TcdB; TccC2; transgenic;
KW monocot cell; dicot cell; oral toxin; insect; pest; TcBA.
XX
OS Photorhabdus luminescens.
XX
FH Key Location/Qualifiers
CDS 1..2745
FT /*tag= a
FT /product= "TccC2"
FT /partial
FT /note= "No stop codon shown"

US2002078478-A1.

20-JUN-2002.

26-MAR-2001; 2001US-00817514.

XX


```
PR 24-MAR-2000; 2000US-0191806P.
XX
XX (PFRE/) PFRENCH-CONSTANT R H.
PA (BOWE/) BOWEN D.
PA (ROCH/) ROCHELEAU T A.
XX (WATE/) WATERFIELD N R.
XX
PI Ffrench-Constant RH, Bowen D, Rocheleau TA, Waterfield NR;
XX
XX WPI; 2002-655379/70.
DR P-PSDB; ABG32653.
XX
XX Novel nucleic acid sequences which encode genes, tcdB and tccC2 from
PT Photorhabdus luminescens W-14, useful in heterologous expression of
PT orally active insect toxins.
XX
XX Claim 3; Page 24-27; 40pp; English.
XX
XX The invention discloses an isolated nucleic acid that encodes TcdB or
CC TccC2 from Photorhabdus luminescens W-14. Also disclosed is a transgenic
CC monocot or dicot cell and a transgenic plant (including the seeds) both
CC with genomes comprising tcdB and tccC2 nucleic acids. The nucleic acids
CC are useful for producing Toxin A or B of P. luminescens W-14 in a
CC heterologous host and for encoding TcdB or TccC2 for producing an orally
CC active insect toxin in a host, where the host also expresses TcdA or TcdA
CC from P. luminescens W-14. Heterologous expression of Toxin A does not
CC afford the level of oral toxicity to insects as that of the native toxin,
CC but the coexpression increases this toxicity. The transgenic plants
CC expressing effective amounts of the toxins protect themselves from insect
CC pests. When the insects feeds on the transgenic plant it also ingests the
CC toxins and this deters the insect from further biting into the plant and
CC may even harm or kill the insect. The sequence presented is the P.
CC luminescens (W-14) tccC2 gene
XX
SQ Sequence 2745 BP; 905 A; 623 C; 606 G; 611 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2745
Score: 4740.00 Matches: 915
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-647-956A-6 (1-915) x ABS52585 (1-2745)
Qy 1 MetSerSerTyrAsnSerAlaileAaspGlnlysthrProSerileLysValleuAspAsn 20
Db 1 ATGAGCAGTTACAATTCGCAATTCGACCAAGACCCCTCGATTAAAGTTATTAGATAAC 60
Qy 21 ArgLysLeuAsnValArgThrIeuGluTyrIeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 61 AGGAAATTTAAATGTACGTACTTTTGAATATCTACGCACCTCAAGCTGACGAAACAGTGAT 120
Qy 41 GluLeuileThrPheTyrGluPheAsnleProGlyPheGlnValLysSerThrAspPro 60
Db 121 GAATTAATTCGTCTATGAGTTCAATATTCGGGATTTTCAGGTAAAAGCACCAGATCCT 180
Qy 61 ArgLysAsnLysAsnGlnSerGlyProAsnPheilleArgValPheAsnLeuAlaGlyGln 80
Db 181 CGTAAATAAANAACACGAGCGGCCCAATTTTCATTCGTGCTTTTAAATCTTCCCGGTCAA 240
Qy 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer 100
Db 241 GTTTTACGTGAAGAAAGTGTGTGATCGCGGTGCGGACTATTACCCCTCAATGATATTGAAGT 300
Qy 101 ArgProValLeuilelleAsnAlaThrGlyValArgGlnGlnAsnHisArgTyrGluAspAsn 120
Db 301 CGCCCGGTGTGATCATCAATGCAACCCGTTGTCGCCCAAAACCACTCGTTTATGAAGATAAC 360
Qy 121 ThrLeuProGlyArgLeuLeuAlaileThrGluGlnValGlnAlaGlyGluLysThrThr 140
Db 361 ACCCTTCCCGTGTGCTCTGCTATCACCGAACAAGTACAGGCGAGAGAGAAACCGACC 420

141 GluArgLeuileTrpAlaGlyAenThrProGlnGluLysAspTyrAsnLeuAlaGlyGln 160
421 GAACGCTCTATTCTGGCCCGCAATACCGCGCAAGAAAAGATTACAACTCTCGCGGTGTCAG 480
Qy 161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly 180
481 TGTGTCCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTTCTCTGTGGTGGC 540
Qy 181 ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTrpThrGly 200
541 GTCGTGCTATCACAATCTCAACAACATGCTTACCGATAACGAGATCCGACTCGACAGGT 600
Qy 201 GluAsnGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn 220
601 GAAGACGAGAGCCTCTGGCAACAAAACCTGAGTAGTGATGCTATATACCCCAAGTAAC 660
Qy 221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu 240
661 ACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGCAACATTCAGCGGTG 720
Qy 241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpIeuThrLeuLysGlyGlnAlaGlu 260
721 GCCTATGATGTGGCCGGCAGCTAAAAGGAGTGTGTTAACTCAACTCAAGGTTCAGGCGAA 780
Qy 261 GlnValIleileLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluHis 280
781 CAGTGATATCAAAATCGCTTAACCTACTCGCCCGCGGCAAAATATTCGTGAAGAGCAC 840
Qy 281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuileGlyIle 300
841 GGTAAACGGGATTGCTACTGAATACAGTACGAACCGGAAACCAACCGCTTATCGGCATT 900
Qy 301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnIleThrAspPro 320
901 ACCACTCGCGTCCATCAGACGCAAGGTGTTTCAAGAGCCTACGCTATCAATATGACCCA 960
Qy 321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln 340
961 GTAGGCAATGTCAATTAATATTCCTGTAATGATCGCGAAGCACTCGCTTTTGGCGCAATCAG 1020
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuileSerAlaThr 360
1021 AAAGTAGCCCGCAGAAATAGCTATACCTACGATTCTCTGTATCAGCTTATCAGCGCCACC 1080
Qy 361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuPro 380
1081 GGGCGGAAATGGCCAATATCGGTTCAGCAAAAACAACCAACTTCCCTCCCTCGCGCTACCT 1140
Qy 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
1141 TCTGACAAACAATACCTACATACTATCTACGAGCTACAGCTATGATACAGTGTGTAAT 1200
Qy 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
1201 CTGACGCAATTCGGCACAGCTCGCCAGCTACCCAGAACAACTACACCGTGGCTATCACCC 1260
Qy 421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrIeuThrThrAspProAsnGlnVal 440
1261 CTCTCAAAACCGCAGCAATCGGGGTGTTCTCAGTACGCTAACCCACCGATCCAAATCAAGTG 1320
Qy 441 AspThrIeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuile 460
1321 GATACGTGTGTTGATCGCGGTGTACCAAAACCACTTTATACCCGAGACACACTTATC 1380
Qy 461 TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluIleTrpTyrArg 480
1381 TGGACACACGAGAGAGTAAAGCAGGTAAATTAATGGCCCGGAAATGAGTGTGTCGCGC 1440
Qy 481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr 500
1441 TAGCAGACCAACGCGATGACAACTGAAAGTAGTGAGCAACAGCCACCCCAAGATCTACG 1500
```

501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerSerAla 520
Db CAGCAACAACGGGTAAATCTATTTCGCGGACTGGAGCTACGACACACCCAGACGACGCC 1560
521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db ACAAACAACGAGAGATTACAGTTATCACTCGGTGAAGCCGGTCGCCACAGGTACGG 1620
541 ValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSer 560
Db GTGTTGCACCTGGGAGAGCGTAAAGCAGAAAGATGTCAACAATACTCACTGTTACAGC 1680
561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer 580
Db TACGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACACCAAGACAAATTTATCAGC 1740
581 GluGluGluTyrTrpProPheGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu 600
Db GAGAAAGAGTATTATCCATTTCGCGGACAGCCCTGTGGCGCAACAGCCAAACAGAA 1800
601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db GCCAGCTATAAACGATTGCTATTTCGGCAAGAACGAGATGCCACCGGTTGTATTAT 1860
621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db TACGGTTATCGTTATTACCAACCGTGGCGGCGAGATGGTTAAGCGCGACCGCGCAGGA 1920
641 ThrIleAspGlyLeuLeuLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Db ACCATTGATGGGCTGGAATCTATACCGAATGGTGAAGAAATAATCCTGTGAGTTTACAAGAT 1980
661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPhePheAspGlu 680
Db GAAATGGATTACGCCAGCAAGAAAGGAAATATACCAAGAGGTAATTTCTTTGATGAA 2040
681 LeuIlePheLysLeuAlaLysSerSerHisValValLysTrpAsnGluLysGluSer 700
Db TTAATAATTCAAATTCGAGCCAAAGTTTACATGTTGTCAATGTTGTAACGAGAAAGAGAGC 2100
701 SerTyrThrLysLeuLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db AGTTATACAAAAATAAATCATTTGAAGTGTTCGTGCGTGATTCGCGATTCGCGGT 2160
721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db TATTTGCTAAGCCACGAGAGTTACTATAAAGGTATAGAAAAAGTCAATCATATATAGC 2220
741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db CGACTTGAAGAAAACAGCTCCCTTCAGAAAAATCAAAAAACGAATCTTTCTTTAGGATCT 2280
761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db GAAATATCCGGTTATATGGCAAGAACCATACAGATACGATATCAGAATATGCCGAAGAG 2340
781 HisLysTyrArgSerSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db CATAAATATAGAAGTAAATACCTGATTTTTATTTCAGAAACCACTTCCTTTGGCGTTAAG 2400
801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db GATAAAGTCAAAAAATGATTATTCGGTGTAAAGAAAAATTTATCGCGCAATGGAGGTT 2460
821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db AAGGTTTATCATGATTATAAAAATAAACAATTCAGAAATTCATGCTCACTATGCAATGGCC 2520
841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db CATCCCTATACGAATTTAGTATGAAGAAAGAGCGCTGTTCGAAGAAACAGAACCCGCT 2580
861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880

2581 ATTGCAATAGATAGAGAAATATAATTTCAAGGTGTGGCAAAATTCCTGCAATGAAGCA 2640
QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db ATTTAAAAAATCATTCGAAAGGACATAAAAATTAATAGGATATCAACAGAGGCTATTAAATT 2700
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db CGCTCTGCGGTATCGCTGAGAAATTTAGGAATTCGCGAGAACTTCA 2745
RESULT 2
ADN61381
ID ADN61381 standard; DNA; 2748 BP.
XX
AC ADN61381;
XX
XX 01-JUL-2004 (first entry)
DT
XX
DE Photorhabdus strain W14 tccC2 toxin complex DNA.
XX
KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
KW ds; tccC2.
XX
OS Photorhabdus sp.
XX
PN W02004002223-A2.
PD 08-JAN-2004.
XX
XX 27-JUN-2003; 2003WO-US020082.
XX
PR 28-JUN-2002; 2002US-0392633P.
PR 21-JAN-2003; 2003US-0441647P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
PA
XX
PI Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
XX
XX WPI; 2004-082821/08.
XX
XX Screening a culture of Paenibacillus isolate for Cry protein or toxin
PT complex protein, useful for controlling lepidopterans, comprises
PT obtaining DNA or protein from the culture and assaying the presence of
PT the gene or protein.
XX
XX Example 12; SEQ ID NO 45; 220pp; English.
XX
XX The invention relates to a novel method for screening a culture of a
CC Paenibacillus isolate for a gene encoding a protein selected from a Cry
CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
CC The method comprises obtaining DNA from the culture and assaying the DNA
CC for the presence of the gene or obtaining a protein produced by the
CC culture and assaying the presence of a protein that indicates the
CC presence of the gene in the isolate. The method of the invention has
CC insecticide applications and may be useful for screening Paenibacillus
CC sp. for toxin complex (TC)-like genes and proteins which may themselves
CC be used to enhance or potentiate the activity of a stand-alone
CC Xenorhabdus toxin protein. The method may also be useful for screening
CC Paenibacillus sp. and others for insecticidal thiaminase genes and
CC proteins for controlling insects, particularly lepidopterans. The current
CC sequence is that of the Photorhabdus strain W14 tccC2 toxin complex DNA
CC of the invention.
XX
SQ Sequence 2748 BP; 907 A; 621 C; 608 G; 612 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 2748
Score: 4686.00 Matches: 902
Percent Similarity: 99.23% Conservative: 6
Best Local Similarity: 98.58% Mismatches: 7
Query Match: 98.86% Indels: 0
DB: 12 Gaps: 0

US-10-647-956A-6 (1-915) x ADN61381 (1-2748)		
Qy	1 MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db		
Db	1 ATGAGCAGTTACAAATCTCGCAATTTGACCAAAAGACCCCTCGATTAAAGGTATTAGATAAC	60
Qy	21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp	40
Db		
Db	61 AGGAAATTAATGATGATCTTTAGAAATATCTACGCACTCAAGCTGACGAAACAGTGAT	120
Qy	41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
Db		
Db	121 GAATTAATACGTTCTATAGTTCAATATATCCGGGATTTTCAGGTAAAAAGCACCGATCCT	180
Qy	61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln	80
Db		
Db	181 CGTAAATAAACCAGAGCGGCCCAATTTCAATTCGTGCTTTTAATCTTTGCCGGTCAA	240
Qy	81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAenAspIleGluSer	100
Db		
Db	241 GTTTTACGTGAAGAAAGTTGATGCCGTCGGACTATTACCCCTCAATGATATTGAAAGT	300
Qy	101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHisArgTyrGluAspAsn	120
Db		
Db	301 CGCCCGGTGTTGATCATCAATGCAACCGGTGTCGCCCAAAACCATCGTTATGAAGATAAC	360
Qy	121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
Db		
Db	361 ACCCTCCCGTCTGCTCGCTATCACCAACAGTACAGGAGGAGAGAAACGACC	420
Qy	141 GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAenLeuAlaGlyGln	160
Db		
Db	421 GAACGTCTTATCTGGCGCGCAATACCGCGCAAGAAAGATTACAACCTCGCCGGTCAAG	480
Qy	161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly	180
Db		
Db	481 TGTGTCGCCATTACGATACCGCGGACTTACTCAACTCAATAGCCTTCTCTGGCTGGC	540
Qy	181 ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAenAlaAspTrpThrGly	200
Db		
Db	541 GTCGTGCTATCACAACTCTCAGCAACTACTCTCGATGATATAAAATGCTGACTGACACGGT	600
Qy	201 GluAspGlnSerLeuTrpGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
Db		
Db	601 GAAGACCAACCCCTCTGCGACAAAACTGACGAGTGAATGCTATACCCCAAAATAAA	660
Qy	221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240
Db		
Db	661 GCCGATGCCACCGGGCTTTATTGACCCAGACCGATGCCAAAGGCAACATCCACGCTCG	720
Qy	241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
Db		
Db	721 GCCTACGACGTAGCGGCGCAGTAAAGGCTGTTGGTTGACACTCAAAAGGTCAGGCCGAG	780
Qy	261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluLysHis	280
Db		
Db	781 CAAAGTATTATCAATTCGCTACCTTACCTCCCGCGGACAAAAATTACGGAAAGAGAC	840
Qy	281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
Db		
Db	841 GGTAACGGGGTTATCACTGAATACAGCTATGAACGACTTACGCTATCAATATGACCCG	900
Qy	301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
Db		
Db	901 GCCACCGCGCTCGCTCAGACGCCAAAGTTGCAAGACTTACGCTATCAATATGACCCG	960
Qy	321 ValGlyAenValIleAenIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln	340
Db		
Db	961 GTAGCAATGATCAATATCCGTAATGATCGGAAGCCACCGCTTTTGGCGCAATCAG	1020
Qy	341 LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
Db		

Db	1021 AAAGTGGTCCCGAGAAATAGCTATATACCTACGACTCCCTGTATCAGCTTATCAGTGGCACC	1080
Qy	361 GlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuProSerProAlaLeuPro	380
Db		
Db	1081 GGGCGGGAATGGCTAATATAGTACGAAATAACCAACTGCCCTCCCTCGCTACCT	1140
Qy	381 SerAspAenAenThrTyrThrAenTyrThrArgSerTyrSerTyrAspHisSerGlyAen	400
Db		
Db	1141 TCTGCAACAATACCTACACTAACTATCTCGCAGCTACAGCTATGATCACAGTGGTAAT	1200
Qy	401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr	420
Db		
Db	1201 CTGACGCAATTCGGCACAGCTCGCCAGCTACCCAGAACCACTACACCGTGGCTATCACC	1260
Qy	421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal	440
Db		
Db	1261 CTCTCAACCGCAGCAATCGGGGTGTTCTCAGTACCTAACCCAGCTTCAAAATCAAGTG	1320
Qy	441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
Db		
Db	1321 GATACGTTGTTGATCGCGTGGTCACCAAAACCAAGTTTATTACCCGAGACACACTTATC	1380
Qy	461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTrpTyrArg	480
Db		
Db	1381 TGGACACACGAGAGAGTTAAAGCAGGTTAATAATGGCCCGGAAATGAGTGGTACCGC	1440
Qy	481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr	500
Db		
Db	1441 TAGCAGCAACCGCATGAGAACCTGAAGTGAGTGAACAGCAACCCAGCAATACTACG	1500
Qy	501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla	520
Db		
Db	1501 CAGCAACACGGGTAATCTATTTCGCGGACTGGAGCTACGCACAACCCAGACGACGCC	1560
Qy	521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg	540
Db		
Db	1561 ACAACAACGGAAGAGTTACACGTTATCACACTCGTGAAGCCGTCGCGCACAGTACGG	1620
Qy	541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenGlnLeuArgTyrSer	560
Db		
Db	1621 GTGTTGCACCTGGGAGAGCGGTAAAGCAGAGATGTCAACAATAATCAACTACGTTACAGC	1680
Qy	561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleLeSer	580
Db		
Db	1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAATCGACAACCAAGACAAATTTATCAGC	1740
Qy	581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu	600
Db		
Db	1741 GAGGAAGAGTATTATTCATTTGGCGGGACAGCGCTGTGGGACGCAAAACAGCAACAGAA	1800
Qy	601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr	620
Db		
Db	1801 GCAGCTTATAAACAATTCGCTATTCCGGCAAGAACGAGATGCCACCGGGTTGTATTAT	1860
Qy	621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly	640
Db		
Db	1861 TACGTTATCGTTATTACCAACCGTCGGCGGGCAGATGGTTAAGCGCGACCCCGCAGGA	1920
Qy	641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAenP	660
Db		
Db	1921 ACCATTGATGGGCTGAATCTATACCGAATGGTAAGAAATAATCTGTGAGTTTTACAAGAT	1980
Qy	661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenPheAspGlu	680
Db		
Db	1981 GAAAAATGGATTAGCGCCAGAAAAAGGAAATATACCAAGAGGTAATAATTTCTTTTGATGA	2040
Qy	681 LeuLysPheLysLeuAlaAlaLysSerSerHisValValLysTrpAenGluLysGluSer	700
Db		
Db	2041 TTAATAATTCAAATGGCAGCCAAAAGTTTCACATGTTGTCAAATGGAACGAGAAAGAGAC	2100
Qy	701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly	720
Db		
Db	2101 AGTTATACAAAAATAAATCAATTGAAAGTGGTTTCGTGTCGGTGAATTCGATCCGTCGGGT	2160

Db 481 TGTCTCGCCACTACGATACCGCTGGACTCACTCAACTCAACAGCCCTTCTCTCGCTGGC 540
Qy 181 ValValLeuSerGlnSerGlnGlnLeuThrAspAsnGlnAspAlaAspTrpThrGly 200
Db 541 GTCGTGCTATCACAACTCTCAACAACCTGCTCTGCATGATCAAAATGCGGACTGACAGGT 600
Qy 201 GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn 220
Db 601 GAAAGTCAAAGCCTCTGGCAGCAAAACTGAGCGAGTGATGTCATACCAACCAAAATAGC 660
Qy 221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu 240
Db 661 ACTGATGCCACCGGGCTTACTTATCCAGACCGATGCAAGGCTG 720
Qy 241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu 260
Db 721 GCCTATGATGAGCGGGCAGCTAAAGGCTGTTGGTTAACTCAAAAGGTCAAAGCCGAA 780
Qy 261 GlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280
Db 781 CAAGTGATTCAAACTCGCTACCTACTCTCGCGCGGACAAAATTTACGTGAAGAGCAC 840
Qy 281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
Db 841 GGTAACGGGGTTATCACCGAATACAGCTATGAACCCAGAAACCCACGGCTTATTGGTATC 900
Qy 301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro 320
Db 901 ACTACCGCGCTCCGTCAGATACCAAGGTGTGCAAGACTTACGCTATCAATATGATCCG 960
Qy 321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln 340
Db 961 GTAGGCAATGTATCAATATCCGTAACTGCGGAGGCCACCGCTTTGGCGCAATCAG 1020
Qy 341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Db 1021 AAAGTGGTCCCGAGATAGCTATATCTACGACTCCCTGTACCAGCTTATCAGTGTACT 1080
Qy 361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSerProAlaLeuPro 380
Db 1081 GGGCGTGAATGGCCAAATATAGGTACGCAAAATATCAACTGCCCTCCCTCGCGCTACCT 1140
Qy 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 1141 TCCGACAAACATACCTACACTAATATCTACTCGCGCTACAGTTATGATCAGACGGGTAA 1200
Qy 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
Db 1201 CTGACGCAAAATTCGGCACAGTTCTATCGGCTACCCCAAAATACTACACCACCGCTATCAC 1260
Qy 421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal 440
Db 1261 ATCTCGAATTCGAGTAACCGGGCGTCTCTAGTAGCTGACAAACAGATCCAAATCAAGTG 1320
Qy 441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 1321 GATACGTTATTGATCGCGGTGGTCACCAACCCAGTTTATTACCGGTCAGACACTGGTC 1380
Qy 461 TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTrpTyrArg 480
Db 1381 TGGACATCACGAGGAGAGTTAAAGCAGGTCAATACCGTTCCAGGAAATGAATGTACCGA 1440
Qy 481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr 500
Db 1441 TACGCGCAACCGGAATGAGCAACTGAAGAGTGAGTGAACGCCCAACCCAGAACTACG 1500
Qy 501 GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla 520
Db 1501 CAGCAGCAGCGGGTAAATCTATCTCGCGGGGCTGGAACTTACGCACAAACCCAGACGACC 1560
Qy 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540

Db 1561 ACAACAACAGAAAGAGTTACACGTGATCACTAGGTGAAGCGGGTCCGCGCACAGGTGCGG 1620
Qy 541 ValLeuHisTrpGluSerGlyLysProGluArgValAsnAsnAsnGlnLeuArgTyrSer 560
Db 1621 GTCTGCACTGGAGAGCGGTAAACCAAGGGTATCAACAACATCAGTACGTACGTACAGC 1680
Qy 561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleLeuSer 580
Db 1681 TACGATAATCTGATCGCTCCAGCCAGCTTGAATCGCATCGCAACCAAGGGCAGATTATTAGT 1740
Qy 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu 600
Db 1741 GAGCAAGAGATTATTATCCATTTCGGCGGCACAGCGATGTGGCAGCCCAATAGCCAAACAGAA 1800
Qy 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 1801 GCCAACTATAAACTATTTCGTATTTCAGCAAGAAGAGGATACCAACCGGGCTGTATTAT 1860
Qy 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 1861 TACGGTTACCGCTATTATCAACCGTGGCGGCAGATGGTTAAGCGCGGATCCGCGCAGGA 1920
Qy 641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Db 1921 ACCATTGATGGGTGAATCTATACCGAATGGTGAAGAAATAATCCAGTAAGTTTGCAGGAT 1980
Qy 661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAsnPheAspGlu 680
Db 1981 GAAATATGGATTAGCACAGAAAGGAAATAATATCTAAAGAGGTGAATTTCTTGTATGAA 2040
Qy 681 LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAsnGluLysGluSer 700
Db 2041 TTAATATTCAAATTCGACGCCAAAATTCACATGTTGTCAATGGAACGAGAAAGAAAGT 2100
Qy 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2101 AGTTATACAAAAATAAATCATTTGAAGTGGTTTCGGGTCCGTGATTTCCGATCCGTCGGGT 2160
Qy 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2161 TATTGTCTAAGCCACCAAGAGTTACTTAAAGGCTAGAAAAAGCCCAATATATATAGC 2220
Qy 741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db 2221 CGGCTCGAAGAAACAGATCCCTTTTCAGAAAAATCAAAACAAATCTTTCTTTGGGATCT 2280
Qy 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 2281 GAAATATCCGTTTATATGGCAAAACGATAAAAGATACGATATCAGAAATATACAGAAAGG 2340
Qy 781 HisLysTyrArgSerSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 2341 CATAGGTATAGAGCAATCATCCGATTTTATGCGAGCAACAGATTCTTTTGCTTTAATG 2400
Qy 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 2401 GATAAAGTCAAAAAATGATTATTCGGGTGAAAGAAAAATTTATCGCGCAATAGAGGTT 2460
Qy 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 2461 AAGTTTTATCATGTTTAAAAATAAACCAATCAGAAATACATGTCAACTATGCACGTGGCT 2520
Qy 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuGlnGlnThrGluProAla 860
Db 2521 CATCCCTATACGCAATGAGTAATGAGAGAGAGCGCTGGTGTGCAAGAAACAGAACCCGCT 2580
Qy 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 2581 ATTGCAATAATAGAGATATAATTTCAAAGGGCTTGGTAAATTCCTGGCAATGAAAGCA 2640
Qy 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 2641 ATTAATAAATCATTTGAAGGGCAGAAAGATCAATAAAATATCAACAGAGGCTATTATATT 2700

Qy 901 ArgSerAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 2701 CGCTCTCGGCTATCGCTAAGAAATTTAGGAATCGGAGAGCTTCA 2745

RESULT 4

Continuation (24 of 57) of ACF67367 from base 2300001 (Photorhabdus luminescens nucleotide)

WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

Fragment Name	Begin	End
ACF67367_00	1	110000
ACF67367_01	100001	210000
ACF67367_02	200001	310000
ACF67367_03	300001	410000
ACF67367_04	400001	510000
ACF67367_05	500001	610000
ACF67367_06	600001	710000
ACF67367_07	700001	810000
ACF67367_08	800001	910000
ACF67367_09	900001	1010000
ACF67367_10	1000001	1110000
ACF67367_11	1100001	1210000
ACF67367_12	1200001	1310000
ACF67367_13	1300001	1410000
ACF67367_14	1400001	1510000
ACF67367_15	1500001	1610000
ACF67367_16	1600001	1710000
ACF67367_17	1700001	1810000
ACF67367_18	1800001	1910000
ACF67367_19	1900001	2010000
ACF67367_20	2000001	2110000
ACF67367_21	2100001	2210000
ACF67367_22	2200001	2310000
ACF67367_23	2300001	2410000
ACF67367_24	2400001	2510000
ACF67367_25	2500001	2610000
ACF67367_26	2600001	2710000
ACF67367_27	2700001	2810000
ACF67367_28	2800001	2910000
ACF67367_29	2900001	3010000
ACF67367_30	3000001	3110000
ACF67367_31	3100001	3210000
ACF67367_32	3200001	3310000
ACF67367_33	3300001	3410000
ACF67367_34	3400001	3510000
ACF67367_35	3500001	3610000
ACF67367_36	3600001	3710000
ACF67367_37	3700001	3810000
ACF67367_38	3800001	3910000
ACF67367_39	3900001	4010000
ACF67367_40	4000001	4110000
ACF67367_41	4100001	4210000
ACF67367_42	4200001	4310000
ACF67367_43	4300001	4410000
ACF67367_44	4400001	4510000
ACF67367_45	4500001	4610000
ACF67367_46	4600001	4710000
ACF67367_47	4700001	4810000
ACF67367_48	4800001	4910000
ACF67367_49	4900001	5010000
ACF67367_50	5000001	5110000
ACF67367_51	5100001	5210000
ACF67367_52	5200001	5310000
ACF67367_53	5300001	5410000
ACF67367_54	5400001	5510000
ACF67367_55	5500001	5610000
ACF67367_56	5600001	564894

Alignment Scores:

Pred. No.:	1-03e-315	Length:	110000
Score:	4429.00	Matches:	847
Percent Similarity:	95.96%	Conservative:	31
Best Local Similarity:	92.57%	Mismatches:	37

Query Match:	93.44%	Indels:	0
DB:	10	Gaps:	0
US-10-647-956A-6 (1-915) x ACF67367_23 (1-110000)			
Qy 1 MetSerSerTyrAsnSerAlaIleAepGlnLysThrProSerIleLysValLeuAspAen 20			
Db 100781 ATGAGCAGTTATCGTCTCGAAATTGCAAAAAACACCAATTAATCATGCTGTTTGGATTAAC 100840			
Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAep 40			
Db 100841 AGGAGGTTAAATGTAGCTACTTTAGAAATATCTACGTACTCAAGCTGATGAACACAGTGAT 100900			
Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAepPro 60			
Db 100901 GAATTGATCACACTCTATGAGTTCAATATTCAAGGATTTGAGGTAATAAAGTACTGATCCT 100960			
Qy 61 ArgLysAenLysAenGlnSerGlyProAenPheIleArgValPheAenLeuAlaGlyGln 80			
Db 100961 CGTAAGAAATAAAATCAGAGCGCCGGAATTCATTCCGGTCTTTTAATCTCCGGGGTCAG 101020			
Qy 81 ValLeuArgGluGluSerValAepAlaGlyArgThrIleThrLeuAenAepIleGluSer 100			
Db 101021 GTTCTACGTGAAGAGGGGTTGATGCCGTCGAACCTATCATCTCAACGATGTTGAAGT 101080			
Qy 101 ArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHisArgTyrGluAepAen 120			
Db 101081 CGCCCGGTATTAAACCATCAATGCAACCGGTGTCCGCAAGACTATCACTACGAAGATAAC 101140			
Qy 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr 140			
Db 101141 ATCTTACCCGGTCGCTTACTTGTATCACCGAACAGGTGAGGACGAAGAGAAAATGACC 101200			
Qy 141 GluArgLeuIleTyrAlaGlyAenThrProGlnGluLysAepTyrAenLeuAlaGlyGln 160			
Db 101201 GAGCGCTTATCTGGCGCGCAATAGCCGCGCAAGAAAAGAGTACACCTTGCTGTCAG 101260			
Qy 161 CysValArgHisTyrAepThrAlaGlyLeuThrGlnLeuAenSerLeuSerLeuAlaGly 180			
Db 101261 TGTGTCCGCACATACGATACCGCTGAGCTCACTCAACTCAACAGCCCTTCTCTGGCTGGC 101320			
Qy 181 ValValLeuSerGlnSerGlnGlnLeuThrAspAenGlnAepAlaAepTyrThrGly 200			
Db 101321 GTCGTGCTATCAATCTCAACAACTGCTCGATGATCAAAATGCCAGCTGAGCAGGT 101380			
Qy 201 GluAepGlnSerLeuTyrGlnGlnLysLeuSerSerAepValTyrIleThrGlnSerAen 220			
Db 101381 GAAGATCAAAGCCTCTGGCAGCAAAAACCTGAGCAGTGATGTCTATACCAACCAATAGC 101440			
Qy 221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAenIleGlnArgLeu 240			
Db 101441 ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAGGCAACATCCAGCGCTG 101500			
Qy 241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTyrLeuThrLeuLysGlyGlnAlaGlu 260			
Db 101501 GCCTATGATGTAGCCGGGAGCTTAAAGGCTGTGGTTAACTCAACCTCAAGGCTCAAGCGAA 101560			
Qy 261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGluHis 280			
Db 101561 CAAGTGATTATCAATCCGCTGACCTACTCTGCCCGCGGCAAAAATTAATCGTGAAGAGCAC 101620			
Qy 281 GlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300			
Db 101621 GGTAAACGGGGTTATCACCCGAATACAGCTATGAACCAAGAAACCAACCGCTTATTGGTATC 101680			
Qy 301 ThrThrArgArgProSerAspAlaLysValLeuGlnAepLeuArgTyrGlnTyrAepPro 320			
Db 101681 ACTACCCGCGCTCCGTGAGATACCAAGGTGTTGCAAGACTTACGCTATCAATATGATCCG 101740			
Qy 321 ValGlyAenValIleAenIleAenAepAlaGluAlaThrArgPheTyrArgAenGln 340			
Db 101741 GTAGGCAATGTGATCAATATCCGTAACGATCGGGAAGCCACCCGCTTTTGGCGCAATCAG 101800			


```
Qy 341 LysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGlnLeuLeuSerAlaThr 360
Db 101801 AAGTGGTCCGGAGAAATAGCTATACCTACGCTCCCTGTACCAAGCTTATCAGTGTCTACT 101860
Qy 361 GlyArgGluMetAlaAenIleGlyGlnGlnAenGlnLeuProSerProAlaLeuPro 380
Db 101861 GGGCGTGAATGGCCAATATAGGTACGCAAAATAATCAACTGCCCTCCCTCGCTACCT 101920
Qy 381 SerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 101921 TCCGACCAACAATACCTACACTAACCTATATCTCCCGCTACAGTTATGATCAAGCGGTAAT 101980
Qy 401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyrThrValAlaIleThr 420
Db 101981 CTGACGCNAATTCGGCACAGTTTCATCGGCTACCCCAAAATAACTACACCACCGCTATCACC 102040
Qy 421 LeuSerAenArgSerAenArgGlyValLeuSerThrLeuThrThrAspProAenGlnVal 440
Db 102041 ATCTCGAATCGAGTAACCGCGCGCTTCTCAGTACGCTGACCAACAGATCCAAATCAAGTG 102100
Qy 441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 102101 GATACGTATTATGATCGCGTGGTCACCAAAACCAAGTTTATTAACCGGTCAGACACTGGTC 102160
Qy 461 TrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGlyAenGluTyrTyrArg 480
Db 102161 TGGACATCACGAGAGAGTTAAAGCAGGTCAATTAACGGTTCAGGAATGAATGGTACCGA 102220
Qy 481 TyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAenThrThr 500
Db 102221 TACGGCAGCAACGGAAATGAGACAACTGAAAGTGAGTGAACAGCCAAACCCAGAACTACG 102280
Qy 501 GlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAenAla 520
Db 102281 CAGCAGCAGCGGGTAACTATCTCGCGGGGTGGAACCTACGCACAAACCCAGACGACC 102340
Qy 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 102341 ACAACAACAGAAAGTTACAGTGATCACCTAGTGAAGCGGTGCGGCACAGCTGCGG 102400
Qy 541 ValLeuHisTrpGluSerGlyLysProGluAspValAenAenAenGlnLeuArgTyrSer 560
Db 102401 GTGCTGCACTGGAGAGCGGTAAACCAAGAGTATCAACAACATCAGTACGTTACAGC 102460
Qy 561 TyrAspAenLeuIleGlySerSerGlnLeuGluLeuAspAenGlnGlyGlnIleIleSer 580
Db 102461 TACGATATCTGATCGGCTCCAGCGAGCTTGAACCTGGCAACCAAGGCGAGATTATTAGT 102520
Qy 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAenSerGlnThrGlu 600
Db 102521 GAGGAAGAGTATTATCCATTGGGGGCACACGCGATGTGGGAGCCCAATAGCCAAACAGAA 102580
Qy 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 102581 GCCAACTATAAACTATTTCGCTATTACGCAAAAGAACGGGATACCCCGGCTGTATTAT 102640
Qy 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 102641 TACGGTTACCGCTATTATCAACCGTGGCGGCGAGATGGTTAAGCGCGGATCCGCGCAGGA 102700
Qy 641 ThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAenProValSerLeuGlnAsp 660
Db 102701 ACCATTGATGGCTGGAATCTATPACCGAATGGTGAGAAATAATCAAGTAAAGTTTCAGGAT 102760
Qy 661 GluAenGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAenAenPheAspGlu 680
Db 102761 GAAATGGAATAGCACCAAGAGAGGAAAAATATACTAAAGAGGTGAATTTCTCTTGATGAA 102820
Qy 681 LeuLysPheLysLeuAlaLysSerSerHisValValLysTrpAenGluLysGluSer 700
Db 102821 TTAATAATTCAAATTTGGCAGCCCAAAATTCACATGTTGTCAAATGGCAACGAGAAAGAGT 102880
Qy 701 SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
```

```
Db 102881 AGTTATACAAAAATAAATCAATTTGAAGTGGTTCCGCTCGGTGATTCCGATCCGTCGGGT 102940
Qy 721 TyrLeuLeuSerHisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 102941 TATTTGCTAAGCCACCAAGAGTTACTAAAGGCGATAGAAAAAGCCAAATTTATATATAGC 103000
Qy 741 ArgLeuGluGluAenSerSerLeuSerGluLysSerLysThrAenLeuSerLeuGlySer 760
Db 103001 CGGCTCGAAGAAACAGATCCCTTTTCAGAAAAAATCAAAAAAATCTTTCTTTGGGATCT 103060
Qy 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 103061 GAAATATCCGTTATATGCAAAACGATAAAAGATACGATATCAGATATACAGAAGGG 103120
Qy 781 HisLysTyrArgSerAenHisProAspPheTyrSerGluThrAspPhePheAlaLeuMet 800
Db 103121 CATAGGTATAGAAGCAATCATCCGATTTTATGTCAGCAACAGATTTCTTTGCTTTAATG 103180
Qy 801 AspLysSerGluLysAenAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 103181 GATAAAGTGAAAAAATGATTATTCGCGTGAAGAAAGAAATTTATGCGGCAATAGAGTT 103240
Qy 821 LysValTyrHisAspLeuLysAenLysGlnSerGluLeuHisValAenTyrAlaLeuAla 840
Db 103241 AAGGTTATCATGATTTAAAAATAAACAATCAGAATTACATGTAACATATGCACGTGCT 103300
Qy 841 HisProTyrThrGlnLeuSerAenGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 103301 CATCCCTATACGCAATTTGATTAATGAAGAGAGAGCGCTGCTGCAAGAAACAGAACCCGCT 103360
Qy 861 IleAlaIleAspArgGluTyrAenPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 103361 ATTGCAATTAATAGAGAAATAATAATTTCAAAGGCGTGGTAAATTCCTGGCAATGAAGCA 103420
Qy 881 IleLysLysSerLeuLysGlyHisLysIleAenAspArgIleSerThrGluAlaIleAenIle 900
Db 103421 ATTAAAAATCATTTGAAGGCGCAGAGATCAATAAAATATCAACAGAGGCTATTAAATAT 103480
Qy 901 ArgSerAlaAlaIleAlaGluAenLeuGlyMetArgArgThrSer 915
Db 103481 CGCTCTCGGCTATCGCTAAGAAATTTAGGAATTCGGAGAGACTTCA 103525
```

RESULT 5

ACF67367_24

Continuation (25 of 57) of ACF67367 from base 2400001 (Photorhabdus luminescens nucleotide sequence split into 57 fragments) LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000

WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000
WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000
WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Alignment Scores:
Pred. No.: 1,03e-315 Length: 110000
Score: 4429.00 Matches: 847
Percent Similarity: 95.96% Conservative: 31
Best Local Similarity: 92.57% Mismatches: 37
Query Match: 93.44% Indels: 0
DB: 10 Gaps: 0

US-10-647-956A-6 (1-915) x ACF67367_24 (1-110000)

QY	1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
DB	781 ATGAGCAGTATCGTCTGAAATGACAAAAACACCAATTAATCAGTGTATTGGATAAC	840
QY	21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp	40
DB	841 AGGAGGTTAAATGTACGTACTCTTGAATATCTACGTACTCAAGCTGATGAATAACAGTGAT	900
QY	41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro	60
DB	901 GAATTGATCACACTCTATGATGTTCAATATTCAAGGATTTGAGGTAAAGATCTGATCCT	960
QY	61 ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln	80
DB	961 CGTAAGATATAAATCAGACGCCGCCGAATTTCAATTCGCGTCTTTAATCTCGCGGGTCAG	1020
QY	81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer	100
DB	1021 GTTCTACGTGAAGAAGGGTTGATCGCGTTCGAACATATCATCTCAACGATGTTGAAGGT	1080
QY	101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisargTyrGluAspAsn	120
DB	1081 CGCCCGGTATTAACCATCAATGCAACCGGTTCGCCCAAGCACTATCACTACGAAGATAAC	1140
QY	121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThrThr	140
DB	1141 ATCCTACCCCGTTCGTTTACTTGTCTATCACCAGAACAGGTGAGGAGAGAAAAATGACC	1200
QY	141 GluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln	160

DB	1201 GAGCGCCTTATCTGGCCCGGCAATACGCCGCAAGAAAAAGAGTACAACCTTGTGTGTAG	1260
QY	161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly	180
DB	1261 TGTGTCCGCCACTACGATACCGCTGACTCACTCAACTCAACAGCCTTTCTCTGGCTGGC	1320
QY	181 ValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspThrThrGly	200
DB	1321 GTCGTCTATCAATCTCAACAACTGCTCGTCGATGATCAAAATGCCGACTGACAGGT	1380
QY	201 GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn	220
DB	1381 GAAGATCAAAAGCCTCTGGCAGCAAAACAGAGCAGTGTCTATACCACCAAAATAGC	1440
QY	221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu	240
DB	1441 ACTGATGCCACCGGGCTTTTACTTATCCAGACCGATGCCAAAGCAACATCCAGCGTCTG	1500
QY	241 AlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAlaGlu	260
DB	1501 GCCTATGATGTAGCCGGCAGCTAAAGGCTGTGTGGTTAACACTCAAGAGTCAAGCGAA	1560
QY	261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluHis	280
DB	1561 CAAGTGATTATCAATCGCTGACCTACTCTGCCCGCGCAAAATTTACGTGAAGAGCAC	1620
QY	281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle	300
DB	1621 GGTACGGGGTTATCACCGAATACAGCTATGAACCAAGAAACCCAAACGGCTTATGGTATC	1680
QY	301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro	320
DB	1681 ACTACCGCGCTCCGTGAGTATCAACAGGTGTGCAAGACTTACGTATCAATATGATCCG	1740
QY	321 valGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArgAsnGln	340
DB	1741 GTAGGCAATGTGATCAATATCCGTAAACGATCGCGAAGCAACCCGCTTTTCGGCGAATCAG	1800
QY	341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr	360
DB	1801 AAAGTGGTCCCGAGAGTAAGTATATCTACGACTCCCTGTACCGCTTATCAGTGTCTACT	1860
QY	361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuPro	380
DB	1861 GGCGGTGAATGGCCAATATAGTCAAGATAAATAAATAAATAAATAAATAAATAAATAAATAA	1920
QY	381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn	400
DB	1921 TCCGACAAACAATACCTACACTAATCTATCTCGCGCTACAGTTTATGATCAACAGCGGTAAT	1980
QY	401 LeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr	420
DB	1981 CTGACCAAAATTCGGCAGCATGTTCTCGGTATCCCAAAATAAATAAATAAATAAATAAATAA	2040
QY	421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal	440
DB	2041 ATCTCGAATCGCAGTAACCGCGCTTCTCAGTACGCTGACAAACAGATCCAAATCAAGTG	2100
QY	441 AspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle	460
DB	2101 GATACGTTTATTTGATCCCGTGTGTACCAAAACAGTTTATTTACCCCGTTCAGACACTGGTC	2160
QY	461 TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArg	480
DB	2161 TGGACATCAGGAGAGGTTAAAGCAGGTCAATTAACGGTTCAGGAAATGAATGGTACCGA	2220
QY	481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr	500
DB	2221 TACCGCAGCAACCGAATGAGACAACTGAAAGTCAAGTGAACAGCAACCCAGAAATACTACG	2280
QY	501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAla	520
DB	2281 CAGCAGCAGCGGTAAATCTATCTCTCGCGGGCTGGAATACGCAACAACCCCAAGACGACC	2340

```
QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 2341 ACAACAACAGAGAGTTACACGTGATCACACTAGTGAGCGGTCGCGACAGGTGCGG 2400
QY 541 ValLeuHisTrpGluSerGlyLysProGluAspValAlaAsnAsnGlnLeuArgTyrSer 560
Db 2401 GTGCTGCACTGGGAGCGGTAAACACAGAGAGTATCAACAACATCAGCTACGTTACAGC 2460
QY 561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer 580
Db 2461 TACGATAATCTGATCGCTCCAGCGACGCTTCAACTGGACAAACCAAGGCGAGATTATTAGT 2520
QY 581 GluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAlaAsnSerGlnThrGlu 600
Db 2521 GAGAAAGAGTATTATTCATTCGGGGGACAGCGATGTGGGAGCGCAATATGCCAAACAGAA 2580
QY 601 AlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyr 620
Db 2581 GCCAACTATAAACTATTCTGCTATTACGGCAAGAAACGGGATACCAACCGGGCTGTATTAT 2640
QY 621 TyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGly 640
Db 2641 TACGGTTTACCGCTATTATCAACCGTGGCGGGCAGATGGTTAAGCGCGGATCCGGCAGGA 2700
QY 641 ThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAsp 660
Db 2701 ACCATTGATGGCTGGAATCTATACCGAATGTGAGAATAATCCAGTAAGTTTGCAGAT 2760
QY 661 GluAsnGlyLeuAlaProGluLysGlyLysTyrThrLysGluValAlaAsnPheAspGlu 680
Db 2761 GAAAAATGATTAGCACCAAGAGAGGAAATAATATACTAAAGAGGTGAATTTCCITGATGAA 2820
QY 681 LeuLysPheLysLeuAlaLysSerSerHisValLysTrpAsnGluLysGluSer 700
Db 2821 TTAAAAATTCAAATTTGGCAGCCAAATAATTCATGTTCTGTCAAATGGAACGAGAAAGAAGT 2880
QY 701 SerTyrThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGly 720
Db 2881 AGTTATACAAAAATAAATCATTGAAAGTGGTTCGGCTCGGTGATCCCGATCCGCTCGGGT 2940
QY 721 TyrLeuLeuSerHisGluGluLeuLysGlyIleGluLysSerGlnIleIleTyrSer 740
Db 2941 TATTTGTAAAGCCACGAGAGTTACTTAAAGGCATAGAAAAAGCCAAATATATATATAGC 3000
QY 741 ArgLeuGluGluAsnSerSerLeuSerGluLysSerLysThrAsnLeuSerLeuGlySer 760
Db 3001 CGGCTCGAAGAAAAACAGATCCCTTTTCAGAAAAATCAAAAAACAATCTTCTTTGGGATCT 3060
QY 761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780
Db 3061 GAAATATCCGGTTATATGGCCAAACCAATAAAGATACGATATCAGATATATACAGAGGG 3120
QY 781 HisLysTyrArgSerAsnHisProAspPheTyrSerGluThrAspPheAlaLeuMet 800
Db 3121 CATAGGTATAGAACCAATCATCCGATTTTATGCAGCAACAGATTTCTTGTCTTTAATG 3180
QY 801 AspLysSerGluLysAsnAspTyrSerGlyGluArgLysIleTyrAlaAlaMetGluVal 820
Db 3181 GATAAAAAAGTCAAAAAATGATTATTCGGTCAAAAAAATTTATGCGGCAATAGAGGTT 3240
QY 821 LysValTyrHisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAla 840
Db 3241 AAGTTTTATCATGATTTAAAAAATAAACAATCAGAAATACAGATTTACATGTCAACTATGCACTGGCT 3300
QY 841 HisProTyrThrGlnLeuSerAsnGluGluArgAlaLeuLeuGlnGluThrGluProAla 860
Db 3301 CATCCCTATACGCAATTTGAGTAAATGAAGAGAGCGCTGGTGCAGAAACAGAACCCGCT 3360
QY 861 IleAlaIleAspArgGluTyrAsnPheLysGlyValGlyLysPheLeuThrMetLysAla 880
Db 3361 ATTGCAATAAATAGAGAATAATAATTTCAAAGGCGTTGGTAAATTTCTGGCAATGAAAGCA 3420
```

```
QY 881 IleLysLysSerLeuLysGlyHisLysIleAsnArgIleSerThrGluAlaIleAsnIle 900
Db 3421 ATTAANAATCATTTGAAGGCGCAGAGATCAATAAATATCAACAGAGGCTATTAAATATT 3480
QY 901 ArgSerAlaAlaIleAlaGluAsnLeuGlyMetArgArgThrSer 915
Db 3481 CGCTCTCGCGCTATCTGCTAAGAATTTAGGAATTCGGAGAGCTTCA 3525
RESULT 6
ACF65386_4/c
Continuation (5 of 7) of ACF65386 from base 400001 (Photorhabdus luminescens nucleotide
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386
WP Fragment Name Begin End
WP ACF65386_0 1 110000
WP ACF65386_1 100001 210000
WP ACF65386_2 200001 310000
WP ACF65386_3 300001 410000
WP ACF65386_4 400001 510000
WP ACF65386_5 500001 610000
WP ACF65386_6 600001 700779
Alignment Scores:
Pred. No.: 1.03e-315 Length: 110000
Score: 4429.00 Matches: 847
Percent Similarity: 95.96% Conservative: 31
Best Local Similarity: 92.57% Mismatches: 37
Query Match: 93.44% Indels: 0
DB: 10 Gaps: 0
US-10-647-956A-6 (1-915) x ACF65386_4 (1-110000)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 97845 ATGAGCAGTTATCGTTCTGAAATTTGACAAAAAACCATTATATCAGTGTATTTGGATTAAC 97786
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 97785 AGCAGGTTAAATGTACGTACTCTTTAGAAATATCTACGTACTCAAGCTGATGAAAAACAGTGAT 97726
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 97725 GAATTGATCACTCTATGAGTTCAATATTTCAAGGATTTTGAGGTAAAAAGTACTGTATCCT 97666
QY 61 ArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGlyGln 80
Db 97665 CGTAAGAATAAAAAATCAGACGCGCCGAAATTTCAATTCGCGCTTTTAATCTTCGCGGTCAG 97606
QY 81 ValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGluSer 100
Db 97605 GTTCTACGTGAAGAAGGGGTTGATCGCGTTCGAACATATCATCTCAACGATGTTGAAGGT 97546
QY 101 ArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAspAsn 120
Db 97545 CGCCCGGTATTAACCATCAATGCAACCGGTGTCGCCCAACTATCACTACGAAGATAAC 97486
QY 121 ThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 140
Db 97485 ATCTACCCCGTTCGTTTACTTTGCTATCACCAACAGGTGACGACAGAGAAATAATGACC 97426
QY 141 GluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGlyGln 160
Db 97425 GAGCGCTTATCTGGGCGGCAATACGCCCAAGAAAAAGATACAACTTCTGTGTGTCAG 97366
QY 161 CysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAlaGly 180
Db 97365 TGTGTCCGCCACTACGATACCGCTGGACTCACTCACTCAACAGCCCTTCTCTGGCTGGC 97306
QY 181 ValValLeuSerGlnSerGlnLeuLeuLeuThrAspAsnGlnAspAlaAspTyrThrGly 200
Db 97305 GTGTGCTATCACAACTCAACACTGCTGCTGATGATCAAAATGCCGACTGGACAGGT 97246
QY 201 GluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSerAsn 220
Db 97246
```

```
Db 97245 GAAGATCAAAAGCCCTCTGGCAGCAAAAACCTGAGCAGTGATGCTATACCAACCCCAAAATAGC 97186
QY 221 ThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArgLeu 240
Db 97185 ACTGATGCCACCGGGCTTTACTTATCCAGACCGATGCCAAGCGCAACATCCAGCGTCTG 97126
QY 241 AlaTyrAspValAlaGlyGlnLeuLysGlySerThrLeuThrLeuLysGlyGlnAlaGlu 260
Db 97125 GCCTATGATGTAGCCGGCAGCTAAAGGCTGTGTGGTTAACTCAAAAGTCAAGCCGAA 97066
QY 261 GlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluHis 280
Db 97065 CAAGTGATTAATCAATCGCTGACCTACTCTGCCCGCGCAAAAATACGTGAAGACAC 97006
QY 281 GlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGlyIle 300
Db 97005 GGTAAACGGGGTTATCACCGGNATACAGCTATGAACCAAGAACCCAAACGGCTTATGGTATC 96946
QY 301 ThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArgTyrGlnTyrAspPro 320
Db 96945 ACTACCGCGCTCCGTCAAGTATCAAGGTGTGCAAGACTTACGCTATCAATATGATCCG 96886
QY 321 ValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheThrArgAsnGln 340
Db 96885 GTAGGCAATGTGATCAATATCCGTAAACGATGCGGAAGCCACCCGCTTTTGGCGCAATCAG 96826
QY 341 LysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSerAlaThr 360
Db 96825 AAGTGGTCCCGAGAAATAGCTATCTTACGACTCCCTGTACAGCTTATCAGTGGTACT 96766
QY 361 GlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuProSerProAlaLeuPro 380
Db 96765 GGGCGTGAAATGGCCAATATAGTTCAGCAAAAATAATCAACTGCGCTCCCTCGCGCTACCT 96706
QY 381 SerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAspHisSerGlyAsn 400
Db 96705 TCCGCAACAAATACCTACATACTACTACTCGCGCTACAGTTATGATCAACGCGTAAT 96646
QY 401 LeuThrGlnIleArgHisSerProAlaThrGlnAsnAsnTyrThrValAlaIleThr 420
Db 96645 CTGACGCAAAATCGGCACAGTTTCATCGGCTACCACCAAAATAACTACACCACCGCTATCACC 96586
QY 421 LeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAspProAsnGlnVal 440
Db 96585 ATCTCGAATCGCAGTAACCGCGCTCTCAGTACGCTGACCAACAGATCCAAATCAAGTG 96526
QY 441 AspThrLeuPheAspAlaGlyHisGlnThrSerLeuLeuProGlyGlnThrLeuIle 460
Db 96525 GATACGTTATTGATCCCGTGTGTACCAAAACAGTTTATTACCCCGTTCAGACACTGGTC 96466
QY 461 TrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsnGluTyrTyrArg 480
Db 96465 TGGACATCAGCAGAGAGTTTAAAGCAGGTCAATTAACGGTTACGAAATGAATGGTACCGA 96406
QY 481 TyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThr 500
Db 96405 TACGGCAGCAACGGAATGAGCAACATGAAAGTGAGTGAAACAGCAACCCAGAACTACTACG 96346
QY 501 GlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThrGlnSerAsnAla 520
Db 96345 CAGCAGCAGCGGGTAAATCTATCTCGCGGGCTGGAATACGCAACACCCAGCAACAGCACC 96286
QY 521 ThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArg 540
Db 96285 ACAACAACAAGAGATTACACGTGATCACATAGGTGAACGGGTCCGCAACAGGTGCGG 96226
QY 541 ValLeuHisTrpGluSerGlyLysProGluAspValAsnAsnAsnGlnLeuArgTyrSer 560
Db 96225 GTGCTGCACCTGGAGAGCGGTAAACCAAGAGGTATCAACAACATCAGCTACGTTACAGC 96166
QY 561 TyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSer 580
Db 96165 TAGGATAATCTGATCGGCTCCAGCCAGCTTGAACCTGGACAACCAAGGGCAGATTATTAGT 96106
```

RESULT 7

ADN61384

ID ADN61384 standard; DNA; 2817 BP.

XX

AC ADN61384;
 XX 01-JUL-2004 (first entry)
 DE Photorhabdus strain W14 tccC5 toxin complex DNA.
 XX Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
 KW db; tccC5.
 XX Photorhabdus sp.
 OS WC2004002223-A2.
 XX 08-JAN-2004.
 XX 27-JUN-2003; 2003WO-US020082.
 XX 28-JUN-2002; 2002US-0392633P.
 PR 21-JAN-2003; 2003US-0441647P.
 XX (DOWC) DOW AGROSCIENCES LLC.
 PA Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
 XX WPI; 2004-082821/08.
 XX Screening a culture of *Paenibacillus* isolate for Cry protein or toxin
 PT complex protein, useful for controlling lepidoptera, comprises
 PT obtaining DNA or protein from the culture and assaying the presence of
 PT the gene or protein.
 XX Example 12; SEQ ID NO 48; 220pp; English.
 XX The invention relates to a novel method for screening a culture of a
 CC *Paenibacillus* isolate for a gene encoding a protein selected from a Cry
 CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
 CC The method comprises obtaining DNA from the culture and assaying the DNA
 CC for the presence of the gene or obtaining a protein produced by the
 CC culture and assaying the presence of a protein that indicates the
 CC presence of the gene in the isolate. The method of the invention has
 CC insecticide applications and may be useful for screening *Paenibacillus*
 CC sp. for toxin complex (TC)-like genes and proteins which may themselves
 CC be used to enhance or potentiate the activity of a stand-alone
 CC *Xenorhabdus* toxin protein. The method may also be useful for screening
 CC *Paenibacillus* sp. and others for insecticidal thiaminase genes and
 CC proteins for controlling insects, particularly lepidopterans. The current
 CC sequence is that of the *Photorhabdus* strain W14 tccC5 toxin complex DNA
 CC of the invention.
 XX Sequence 2817 BP; 902 A; 700 C; 614 G; 601 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.98e-209 Length: 2817
 Score: 2960.00 Matches: 607
 Percent Similarity: 73.01% Conservative: 91
 Best Local Similarity: 63.49% Mismatches: 186
 Query Match: 62.45% Indels: 72
 DB: 12 Gaps: 13

US-10-647-956A-6 (1-915) x ADN61384 (1-2817)

Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
 Db 1 ATGGAAACATGACCCCAAACTTTATCACCATACGCTACCGTCAGTGTTCACGATAAC 60
 Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
 Db 61 CGTGACTAGTATCCGTAATATTAGTTTTCACCGCACTACCGCAGAGCAATACCGAT 120
 Qy 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
 Db 121 ACCGGTATTACCGCCCAATATATAATGCCGCGGATATTTGAACCAAGCATTTGATCCT 180

61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
 181 CGCTGTATGACGCCCAACAGACTAACACGCTGTATCAACCGAATTTTATTCGCGACAT 240
 Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
 241 AATTTGACCGCAATATCTGCGAACACAGAGCGTGTGATCGCGTCCGACGATTACCTC 300
 Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
 301 AACGATATTGAAGCGCGCGGTGTGACCATCAATGACGCCGTGTCCGCAAAACCAT 360
 Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
 361 CGCTACGAAGATAACACCTGCGCGTGTGCTGCTATCAGCGAACAAAGGACAGGCA 420
 Qy 136 GlyGluLysThrThrGluArgLeuIleTyrAlaGlyAsnThrProGlnGluLysAspTyr 155
 421 GAAGAGAAAACGACCGAGCGCTTATCTGGCGCGCAATACGCGCGCAAGAAAAGACAC 480
 Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
 481 AACCTTGGCGGTGAGTCCGCTACGATACCGCAGGACTCACTCAACTCAACAGC 540
 Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
 541 CTTGCCCTGACCGCGCGCTTCTATCACAATCTCAACACTGCTTACCGATAACAGGAT 600
 Qy 196 AlaAspTyrThrGlyGluAspGlnSerLeuTyrGlnGlnLysLeuSerSerAspValTyr 215
 601 GCCGACTGGACAGGTGAAGACACGAGCGCTCTGGCAACAAAACTGAGTAGTGTCTAT 660
 Qy 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
 661 ATCACCACCAAGTAACACTGATGCCACCGGGCTTTTACTGACCAGACCGATGCCAAGGC 720
 Qy 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTyrLeuThrLeu 255
 721 AACATTACGGGTGGCTTATGATGTGGCGGCGAGCTAAAGGGAGTTGTTTAACACTC 780
 Qy 256 LysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
 781 AAAGGTGACGCGAACACAGGTGATTATCAATCGTAACCTACTCCGCGCGCGGCAAAA 840
 Qy 276 LeuArgGluLysHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
 841 TTACGTGAAGACGACGCTACGGGATTTGTCACATACAGCTACGAAACCGGAACCCAA 900
 Qy 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
 901 CGCTTATCGCATTTACCACTCCGCTCCATCAGACGCCAAGGTGTTGAAGACCTACGC 960
 Qy 316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
 961 TATCAATATGACCCAGTAGGCAATGATATGATATCGTAATGATGCGAAGCACCCTCGC 1020
 Qy 336 PheTyrArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
 1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGAAATAGCTATACCTACGATTCCTGTATCAG 1080
 Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuPro 375
 1081 CTTATCAGCGCCACCGCGCGAGATGGCCAAATATCGTCCAGCAACCAACCACTTCCC 1140
 Qy 376 SerProAlaLeuProSerAspAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
 1141 TCTCGCGCGTACCTCTGATAACAATACCTACACCACTATATCTACGACCTTACTTAT 1200
 Qy 396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAspTyr 415
 1201 GACCGTGGCGCAATTTGACGAAATTTTACGATAGTTTACACCGCGCGCAAAATACTAC 1260
 Qy 416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435


```

PS Claim 2; SEQ ID NO 15; 118pp; English.
XX
CC The present invention describes DNA sequences from the tcd genomic region
CC of Photobacterium luminescens W-14. Also described: (1) a transgenic
CC monocot or dicot cell having a genome comprising a nucleic acid sequence
CC that encodes SEQ ID NO:4, 6, 8, 10, 12, 14, or 16; (2) a transgenic plant
CC with a genome comprising a nucleic acid sequence that encodes SEQ ID
CC NO:4, 6, 8, 10, 12, 14, or 16; (3) a seed of the transgenic plant; (4) a
CC progeny of seed; (5) a method of producing Toxin A of Photobacterium
CC luminescens W-14 in a heterologous host; and (6) a method of producing an
CC orally active insect toxin. The nucleotide sequences are useful for
CC heterologous expression of orally active insect toxin. They can also be
CC used for generating transgenic plants with enhanced resistance to
CC insects. The present sequence encodes Photobacterium luminescens W-14
CC tccCS, which is used in the exemplification of the present invention.
XX
SQ Sequence 2817 BP; 901 A; 701 C; 615 G; 600 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9,84e-209      Length:      2817
Score:          2956.00      Matches:      608
Percent Similarity: 73.01%      Conservatives: 90
Best Local Similarity: 63.60%      Mismatches: 186
Query Match:      62.36%      Indels:      72
DB:              12          Gaps:        14

US-10-647-956A-6 (1-915) x ADP18627 (1-2817)
Qy 1 MetSerSerTyrAenSerAlaIleAaspGlnLysThrProSerIleLysValLeuAaspAsn 20
Db 1 ATGGAAACATTGACCCCAAACTTTATCACCATTACCGCTACCGTCAGTGTTCAGATAAC 60
Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAaspGluAenSerAasp 40
Db 61 CGTGGAGTAGCTATCCGTAATATTAGTTTTCACGCGACTACCGCGAAGCAAAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAasnIleProGlyPheGlnValLysSerThrAaspPro 60
Db 121 ACCCGTATTACCCGCCATCAATATATGCCGGCGGATTTGTAACCAAGCATTTGATCCT 180
Qy 61 Arg-----LysAenLysAasnGlnSerGlyProAenPheIleArgValPhe 75
Db 181 CGCTGTATGACGCCAACACAGACTAACACAGCTGTACACCGAATTTTATCTGCGCAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAaspAlaGlyArgThrIleThrLeu 95
Db 241 AATTTGACCGGCAATATCTCGGAACAGAGAGCGTCTGATCGCGTACCGGATTTACCCCTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleAenAlaThrGlyValArgGlnAasnHis 115
Db 301 AACGATATTGAGCCCGCCGGTGTGTGACCATCAATGACGCGGTGTTCGGCAAAACCAT 360
Qy 116 ArgTyrGluAaspAenThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CGCTACGAAGATAACACCTCGCCCGTCCGCTGCTATCAGCGAACAAGGACAGCA 420
Qy 136 GlyGluLysThrThrGluArgLeuIleThrAlaGlyAenThrProGlnGluLysAaspTyr 155
Db 421 GAAGAGAAAAACGACGAGCGCTTATCTGGCGCGGCAATACGCGCGCAAGAAAAAGACCAC 480
Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAaspThrAlaGlyLeuThrGlnLeuAasnSer 175
Db 481 AACCTTGGCGGTGAGTGGTCCGCCATTACGATACCGGAGGACTCACTCAACTCAACAGC 540
Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAaspAasnInasp 195
Db 541 CTTGCCCTGACCGCGCGCTTCTATCAACATCTCAACAACTGCTTACCGATAACCCAGAT 600
Qy 196 AlaAaspTrpThrGlyGluAaspGlnSerLeuTrpGlnGlnLysLeuSerSerAaspValTyr 215
Db 601 GCCGACTGGA CAGGTGAAGAC CAGAGCCTCTGGCAACAAAAA CACTGAGTAGTGTCTAT 660
Qy 216 IleThrGlnSerAenThrAaspAlaThrGlyAlaLeuLeuThrGlnThrAaspAlaLysGly 235

```

```

661 ATCAACCAAGTAACACTGATGCCCGGGCTTTACTGACCCAGACCGATGCAAGGC 720
236 AsnIleGlnArgLeuAlaTyrAaspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
721 AACATTTGAGCGGTGGCTTATGATGTGGCGGGCAGCTAAAGGGAGTTGGTTAACTC 780
256 LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
781 AAAGGTGAGCGGACAGGTGATTAATCAATCGCTAACTACTCCCGCGCGGGCAAAA 840
276 LeuArgGluGluHisGlyAasnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
841 TTACGTGAGAGACGACGTAAGCGGATTTGTCACCTGATACAGTACGACCGGAAACCAA 900
296 ArgLeuIleGlyIleThrArgArgProSerAaspAlaLysValLeuGlnAaspLeuArg 315
901 CGGCTTTATCGGCATTACCACTCGCCCTCATCAGCGCAAGGTGTGCAAGACCTACGC 960
316 TyrGlnTyrAaspProValGlyAasnValIleAasnIleArgAasnAaspAlaGluAlaThrArg 335
961 TATCAATATGACCCAGTAGCAATGTCATGATGATGATGATGATGATGATGATGATGATG 1020
336 PheTrpArgAasnGlnLysValAlaProGluAasnSerTyrThrTyrAaspSerLeuTyrGln 355
1021 TTTTGGCGCAATCAGAAAGTAGCCCGGAGATAGCTATACCTACCTACCTACCTACCT 1080
356 LeuIleSerAlaThrGlyArgGluMetAlaAasnIleGlyGlnAasnAasnGlnLeuPro 375
1081 CTTTATCAGCGCCACCGCGGCGAGATGGCCAAATATCGGTGAGCAAGCAACCAACTTCC 1140
376 SerProAlaLeuProSerAaspAenAenThrTyrThrAasnTyrThrArgSerTyrSerTyr 395
1141 TCTCCCGCGCTACTCTTGATAACAATACCTACCAACATATACTCGCATTTACTTAT 1200
396 AspHisSerGlyAasnLeuThrGlnIleArgHisSerSerProAlaThrGlnAasnAenTyr 415
1201 GACCGTGGCGCAATTTGACGAAATTCAGCATAGTTTACCACCGCGCAAAATACTAC 1260
416 ThrValAlaIleThrLeuSerAenArgSerAasnArgGlyValLeuSerThrLeuThrThr 435
1261 ACAGCATATATAACGGTTTCAAATCGCAACACCGCGGTACTCAGCATTTGACCGCA 1320
436 AspProAasnGlnValAaspThrLeuPheAaspAlaGlyHisGlnThrSerLeuLeuPro 455
1321 GATCCAACTCAAGTCGATGCTTATTGATGCGGAGGCCATCAACACGCTGTTATCC 1380
456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAasnAasnGlyProGly 475
1381 GGCCAAAGTTCTAAGTGGACCGCGCGGCGAATTGAAACCAACCAATAGCGCAGGA 1440
476 AsnGluTrpTyrArgTyrAaspSerAasnGlyMetArgGlnLeuLysValSerGluGlnPro 495
1441 AATGAGTGGTATCGCTACGATACGACGCGCATACCGCAGCTAAAGAGTGAATGAACAA 1500
496 ThrGlnAasnThrThrGlnGlnArgValIleTyrLeuProGlyLeuLeuAaspThr 515
1501 ACTCAGATATATCCCGCAACCAAGGGTAACTTATCTACCGGGCTTGGAAATACGTACA 1560
516 ThrGlnSerAasnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
1561 ACCAGAACACCGCCCAACAACAGAGAGTTACAGCTTATCAGCTCGTAAAGCGCGC 1620
536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAaspValAasnAasn 555
1621 CGCGCGCAAGTCGAGTATTGCTATTTGGAGAGCGGTAACAGAGATATTATAAACAAT 1680
556 GlnLeuArgTyrSerTyrAaspAenLeuIleGlySerSerGlnLeuGluAaspAasnGln 575
1681 CAGCTTCTGTTACAGCTACGATTAATCTATTGGCTTCAGGCCAATCTCATATTAGTAGGCAC 1740
576 GlyGlnIleSerGluGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595

```



```
Qy 1 MetSerSerTyrAenSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 ATGGAACAATTGACCCAAACTTTATACCATACGCTACCGTCAGTGTTCAGATAAC 60

Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp 40
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 61 CGTGGACTAGCTATCCGTAATATTAGTTTTCACCGCACTACCGCGAGAAGCAATACCGAT 120

Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 121 ACCGGTATTACCGCCCATCAATATAATGCCGGCGATATTGTAACCAAGCAATGTATCCT 180

Qy 61 Arg-----LysAenLysAenGlnSerGlyProAenPheIleArgValPhe 75
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 181 CGCTGTATGCGCAACCAAGCACTAAACACGCTGTACACCGCAATTTTATCTGCGGACAT 240

Qy 76 AsnLeuAlaGlyGlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeu 95
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 241 AATTTGACCGGCAATATCTTGGCAACAGAGAGCGTCGATGCCGTCGGACGATTACCCCTC 300

Qy 96 AsnAspIleGluSerArgProValLeuIleIleAenAlaThrGlyValArgGlnAenHis 115
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 301 AACGATATTGAAGCCCGCGGTGTGACCATCAATGACGCGCGTGTCCGCGCAAAACCAT 360

Qy 116 ArgTyrGluAenAenThrLeuProGlyArgGluLeuAlaIleThrGluGlnValGlnAla 135
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 361 CGCTACGAAGATAACACCTGCGCGCGTCTGCTGCTATCAGCGAACAGGACAGGCA 420

Qy 136 GlyGluLysThrThrGluArgLeuIleTrpAlaGlyAenThrProGlnGluLysAspTyr 155
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 421 GAAGAGAANAACGACGAGCGCTTATCTGGCGCGCAATACGCCGCAAGAAAAGACCAC 480

Qy 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAenSer 175
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 481 AACCTTGGCGTCACTAGTCGCTCGGCATTACGATACCGCAGGACTCACTCAACTCAACAGC 540

Qy 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAenGlnAsp 195
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 541 CTTCCCTTGACCGCGCGCTTCTATCAAACTCTCAACAACTGCTTACCGATAACACGAGAT 600

Qy 196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 601 GCCACTGGACAGTGAAGACCAAGCTCTGGCAACAAAACTGAGTAGTGTCTAT 660

Qy 216 IleThrGlnSerAenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 661 ATCAACCAAGTAACACTGATGCCACCGGGCTTTACTGACCCAGACCGATGCCAAAGGC 720

Qy 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 721 AACATTACGGCGCTGGCCCTATGATGTGGCCGGGCGAGCTTAAAGGGAGTTGGTTAACTC 780

Qy 256 LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 781 AAAGCTCAGCGCGAACAGGTGATTTATCAATCGCTAACCTACTCCGCGCGCGGCAAAAA 840

Qy 276 LeuArgGluGluHisGlyAenGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 841 TTACGTGAAGAGCACGGTAACGGATTGTCTACTGAATACAGTACGAAACCGGAACCCAA 900

Qy 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 901 CGGCTTATCGGCATTTACCACTCGCGCTCCATCAGACGCCAAGGTTGTGCAAGACCTACGC 960

Qy 316 TyrGlnTyrAspProValGlyAenValIleAenIleArgAenAspAlaGluAlaThrArg 335
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 961 TATCAATATGACCCAGTAGGCAATGTCTATTAGTATCCGTATGATGCCGAAGCCACTCGC 1020

Qy 336 PheTrpArgAenGlnLysValAlaProGluAenSerTyrThrTyrAspSerLeuTyrGln 355
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1021 TTTTGGCGCAATCAGAAAGTAGCCCGCGAGAAATAGTATACCTACGATTCCCTGTATCAG 1080
```

```
Qy 356 LeuIleSerAlaThrGlyArgGluMetAlaAenIleGlyGlnGlnAenAenGlnLeuPro 375
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1081 CTTATCAGCGCCACCGCGCGAGATGGCCAATATCGGTACGAAAGCAACCAACTTCCC 1140

Qy 376 SerProAlaLeuProSerAspAenAenThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1141 TCTCCGCGCTACCTTCTGATAACAATACCTACACCAACTATATCTCGCACTTACTAT 1200

Qy 396 AspHisSerGlyAenLeuThrGlnIleArgHisSerSerProAlaThrGlnAenAenTyr 415
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1201 GACCGTGGCGGCAATTTGACGAAATTCACGATAGTTCACCGCCGCGCAAAATAACTAC 1260

Qy 416 ThrValAlaIleThrLeuSerAenArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1261 ACACCGATATAACGGTTTCAATCCGACGCAACCGCGGTACTCAGCACATTTGACCGCA 1320

Qy 436 AspProAenGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1321 GATCCAACTCAAGTCGATGCTTATTTGATCGGGAGGCCATCAAAACCACTTGTATCC 1380

Qy 456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAenAenGlyProGly 475
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1381 GGCCAACTTCTAACTTGGACACCGCGAGCGCAATTGAAACCAACCCACATAGCGCAGGA 1440

Qy 476 AsnGluTrpTyrArgTyrAspSerAenGlyMetArgGlnLeuLysValSerGluGlnPro 495
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1441 AATGAGTGGTATCGCTACGATACGACCGCATACGCCAGCTAAAGTGAATGAACAACAA 1500

Qy 496 ThrGlnAenThrThrGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1501 ACTCAGATATCCCGCAACAACAAGGGTAACTTATCTACCGGGGTGGAAATACGTACA 1560

Qy 516 ThrGlnSerAenAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1561 ACCCAACAACACCCCAACAACAAGAGAGTTACAGTTATCACCTCGGTAAAGCCGGC 1620

Qy 536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAenAenAsn 555
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1621 CGCGCGCAAGTCCGAGTATGTGCTTGGAGAGCGGTAAACACGAGAATATTATNACAAT 1680

Qy 556 GlnLeuArgTyrSerTyrAspAenLeuIleGlySerSerGlnLeuLeuAspAenGln 575
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1681 CAGCTCGTTACAGTACGATAATCTTATTTGGTCCAGCCAACTTCAATTAGATAGCGAC 1740

Qy 576 GlyGlnIleIleSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrpAlaAla 595
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1741 GSCAAATATCATGTGAAGAAGAAATATTATCCATTTGGTGGTACAGCGCTGTGGCGCGCA 1800

Qy 596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla 615
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1801 AGAATCAACCCAGACGAGTATAAACCATTTCTGTTATCTGGTAAAGAGCGGATGTT 1860

Qy 616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1861 ACCGGCTGTATTATTATGCTACCGTTATTACCAACCGTGGCGGCGCAGATGGTTAGGT 1920

Qy 636 AlaAspProIleGlyThrIleAspGlyLeuAenLeuTyrArgMetValArgAenAspPro 655
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1921 GCAGACCCGCGCAAAACCATTTGATGACTGAATTTATTCGATGGTGGTGAATAAACCCG 1980

Qy 656 ValSerLeuGlnAspGluAenGlyLeuAlaPro----- 666
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1981 GTACGCAATTTGATGTTTACGGGATTTATCACCGGCCCAACAGACAGAAAGACGATATA 2040

Qy 667 GluLysGlyLysTyrThrLysGluValAenPhePheAspGluLeuLysPheLysLeuAla 686
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 2041 AAACAGGGTTCCTTTACGGCA-----ATGGAAGAAGCTGTTTATAAAAAAATG 2088

Qy 687 AlaLys-----SerSerHisValLysTrpAenGluLysGluSer 700
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 2089 GCTAAACCTCAAACTTTCAACGCCCAAGAGCTATCGCTGCCCAACACAGACGAAGAGCC 2148

Qy 701 -----SerTyrThrLysAenLysSerLeuLysValValArgValGlyAspSerAspPro 718
```

```
Db 2149 CATGAATCATGACCAACACCTAGTGTAGATATT-----ACCCCAATT 2193
Qy 719 SerGlyTyrLeuLeuSerHisGluGluLeuLeuGlyLeuGlySerGlnIle 738
Db 2194 AAAAACTACACACAGATACCTCACAAATTAATGCCGCGATAGGAAATCGTATTACG 2253
Qy 739 TyrSerArgLeuGluGluAenSerSerLeuSerGluLeuSerLysThrAenLeuSerLeu 758
Db 2254 CCAGCAGTGGAAAGTTTAGACGCCACATATTATTCCTCAAGATAGACAAATGAGGGTA 2313
Qy 759 GlySerGluIleSerGlyTyrMetAlaArgThr----- 769
Db 2314 ACTATCGGGTGATGACCTATGATAGATAATTCACGCCATCGCCTGGCACTGCCACAG 2373
Qy 770 -----lleGlnAspThrIleSerGluTyrAla-----Glu 779
Db 2374 GAAGGAAATAGTATTAATGTTGGTGATATCGTTTCGATACACGCTTATTATCAACATCG 2433
Qy 780 GluHisLysTyrArgSerAen-----HisProAspPheTyrSerGluThrAspPhe--- 796
Db 2434 GCCCATCGTGTGTTTCTGAAATTTGTTTCAAAAAAGAAACCAAGTGAATCGATACGTC 2493
Qy 797 ---PheAlaLeuMetAspLysSerGluLysAen-----AspTyr 808
Db 2494 AAGATGGCATTTTAAACGAATGCGGGTGTCAATGTCCAGCAGCATCTATGTATAATAAT 2553
Qy 809 SerGlyGluArgLysIleTyrAlaAlaMetGluValLysValTyrHisAspLeuLysAen 828
Db 2554 GCTGGCGAGGAGCAAGTATTAAATG-----GATTTAAGCAT 2592
Qy 829 LysGlnSerGluLeuHisValAenTyrAlaLeuAlaHisProTyrThrGlnLeuSerAen 848
Db 2593 TCAAGAAAAGCCTTCTGTAATAATAAATAAGAGTCAGTGCAGCAACAATCGGACAA 2652
Qy 849 GluGluArgAlaLeuGlnGluThrGluProAlaIleAlaIleAspArgGluTyrAen 868
Db 2653 GCGGAATATTACTACTAGGGAACACAGTTCGAAGTTGTT-----TCAATGAA 2703
Qy 869 PheLysGlyValGlyLysPheLeuThrMetLysAlaIleLysLysSerLeuLysGlyHis 888
Db 2704 CATCAGGCGAGATACCTATGTATTATTGCAAGATATTAAACCAATCCGAGCCACTCAT 2763
Qy 889 LysIleAsnArgIleSerThrGluAlaIleAsnIleArgSerAlaIa 904
Db 2764 AGA---AATGTACGTAACACTTACACCGGTAATTTCAAATCATCCAGT 2808

RESULT 10
ACF69434
ID ACF69434 standard; DNA; 2817 BP.
XX
AC ACF69434;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens nucleotide sequence #7901.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
PN W0200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-18003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP ) INST PASTEUR.
```

```
PA
XX (CNRS ) CNRS CENT NAT RECH SCI.
PI Duchaud E, Taourit S, Glaeser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 7901; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 2817 BP; 922 A; 682 C; 588 G; 625 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,46e-200 Length: 2817
Score: 2845.50 Matches: 578
Percent Similarity: 71.01% Conservative: 71
Best Local Similarity: 63.24% Mismatches: 150
Query Match: 60.03% Indels: 115
DB: 10 Gaps: 11

US-10-647-956A-6 (1-915) x ACF69434 (1-2817)
Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAen 20
Db 1 ATGAAAAACATTGACCCCTAAACTTTATCACCATACCGCCGCTCAGTGTTCACGATAAC 60
Qy 21 ArgLysLeuAenValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAenSerAsp 40
Db 61 CGTGGACTCGCTATCGGTAAATATTAGTTTACCGCGCTACCGCAGAACCAATACCGAT 120
Qy 41 GluLeuIleThrPheTyrGluPheAenIleProGlyPheGlnValLysSerThrAspPro 60
Db 121 CCGCGTATTACTCGCCATCAATATAATCGCGGATATTGAACCAAGCATTGATCTCT 180
Qy 61 Arg-----LysAsnLysAenGlnSerGlyProAsnPheIleArgValPhe 75
Db 181 CCCTGTATGATGCTAAGCAGACTAACAAACCGCTCAACCCGAATTTTATCTGGCAGCAT 240
Qy 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 241 AATTGACCGCAATATCTCTGACAGAGAGCGGTGATGCTGGCCGACACATATTACCTTC 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAenHis 115
Db 301 AACGATATTGAAGTGCCTCGCGGTATTGACCATCAGCGCAACCGGTCTCCGCCAAATCAC 360
Qy 116 ArgTyrGluAspAenThrLeuProGlyArgLeuAlaIleThrGluGlnValGlnAla 135
Db 361 CTTTATGAAGATAACACCTTACCCGTCGCTACTCGCAATCACCCGAAACAGCACACA 420
```

136 GlyGluLysThrThrGluArgLeuIleThrAlaGlyAenThrProGlnGlnLysAspTyr 155
155
421 GAAGAGAAACACCGAGCGTCTTATCTGGCCGGCAATACGCCGAGGAAAGAGTAC 480
156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
175
481 AACCTTGCTGAGTACCGCGTCATTACGATACCGCGGAGCTCGCTCAACTCAACAGC 540
176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAsp 195
195
541 CTTCGCCGTCACCGCGCGCTTTATCAATCTCAACACCGCTCGTCGATAACCAAGAT 600
196 AlaAspTrpThrGlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyr 215
215
601 GCCGACTGGACAGGTGAAGACAGAGCTCTGGCGGCAAAAACTGAGTAGTGTAT 660
216 IleThrGlnSerAenThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
235
661 ACCACCAAAATAAAACCGATGCCCGGCTTTTACTTACCACAGCCGATGCTAAAGGC 720
236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLysGlySerTrpLeuThrLeu 255
255
721 AACATTACGGCGAAGCTATGATGTGGCGGTCAGCTAAAGGGAGCTGCTAAACATTA 780
256 LysGlyGlnAlaGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
275
781 AAAGTCAGACCGAACAGTGATTTCAATTCGCTGACCTACTCCGCGCGGCAAAAA 840
276 LeuArgGluGlnHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
295
841 TTACGCGAAGACGACGCTAACCGCATTTATACCGAATACAGCTATGAACCGGAACCTCAG 900
296 ArgLeuIleGlyIleThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
315
901 CGGCTTATCGGCATTACCACTCGCGCTCCATCAGACGCCAAGGTGTTCAGACCTACGC 960
316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
335
961 TATCAATATGACCGGTAGGCAATGTGATCAATATCCGTAAACGATGGGAGCCACCGC 1020
336 PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
355
1021 TTTTGGCGCAATCAAAAGTCATCCGAGAAATAGCTATACCTACGATTTCTCTATCAG 1080
356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGlnLeuPro 375
375
1081 CTTATCAGTCCACCGGACGCGTAAATGGCCAATATAGGTCAAGCCAAATAACCCACTCCCC 1140
376 SerProAlaLeuProSerAspAsnAsnThrTyrThrAenTyrThrArgSerTyrSerTyr 395
395
1141 TCCCTCGGCTACTCGTGAATACACACCTTACTACTACCCGACCGCACCCTATAGTTAT 1200
396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
415
1201 GACCGTGGCGCAATTTGATGAAATTCAGCATAGTTCCACCTGCGCACGCAAAATAACTAC 1260
416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
435
1261 ACAGCAATATAACGGTTTCTTAATTACAGCAACCGTGGCGTATTAAGTACACTGACCGAA 1320
436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
455
1321 GATCAACCCCAAGTTGATCGCTTTATTTGATTCGGGAGGCCATCAACCACTTATATCC 1380
456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly 475
475
1381 GGTCAAGTTCTAATATGACACCGCGAGCGCAATTTGAAACAAGTCAACAGTAGCGCAGGA 1440
476 AsnGluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro 495
495
1441 AATGAGTGGTATCACTACGATAGCAACCGCACACGACGCTAAAGTGAATGAACAA 1500

496 ThrGlnAsnThrThrGlnGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
515
1501 ACTCAAAATATCGCGCAACAGCAAGAGTCACTTATCTCGCGGGCTAGAACTACGCACA 1560
516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
535
1561 ACCCAACATGGCAGTACTACCAACGGAATATTTGCAAGTTATCACCTCGGTAAGCTGGT 1620
536 ArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsnAsn 555
555
1621 CGTGCAGAGTCGGGTATTAATTTGGGAGAGCGGAAACCCGGAAGATATCAACAAT 1680
1681 CAACTTCGTTACAGTACGATTAATCTTATCGGTTCCAGCAACTTGAATTAGATAGCGAA 1740
556 GlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAspAsnGln 575
575
1741 GGCACAAATATCAGTCAGGAAGAATATTTATCCATTTGGCGGTACAGCTCTGTGGCGACA 1800
596 AsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArgAspAla 615
615
1801 AGGAATCAAAACCGACAGCTATAAAACCATTCGTTATTCAGTAAAGACCGGATGCT 1860
616 ThrGlyLeuTyrTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrpLeuSer 635
635
1861 ACCGGCTGTATTTATTTACGCTACCGTATTTACCAACCGTGGTGGCAGATGTTAAGT 1920
636 AlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsnAsnPro 655
655
1921 GCGGACCCGCGCGAACCATTGATGGCTGAATTTATATCGCATGTGGAGAAATAATCCG 1980
656 ValSerLeuGlnAspGluAsnGlyLeuAlaPro----- 666
1981 GTGACCAATTTGATGTTTCAGGGAATTTCTCGGCTAACAGAACAGNAGCGATAATA 2040
667 GluLysGlyLysTyrThrLysGluValAsnPhePheAspGluLeuLysPheLysLeuAla 686
686
2041 AAACAGGTTCTTTTACAGCA-----ATGGAAGAAGCCGTTTATAAAAAAATG 2088
687 AlaLysSer----- 689
2089 GCGAAACCTCAAACTTTCAAAACGCAAGAGCTATCGCTACCCAAACAGAGCAAGAGCC 2148
689 ----- 689
2149 CATCAATTTGACCAACAATCCGGTGTAGATACTAGCCCAATTAAAGATTACACCAG 2208
690 -----SerHisValLysTyr 695
2209 GATAGCTCGCAATTAATCTGCAATAAGAGAAAAACCGTATTACATCGATAGTGAAGAT 2268
696 AsnGluLysGluSerSerTyrThrLysAsnLysSerLeuLysVal----- 710
710
2269 TTAGATTCTCTCATTTCTGCCCTGCAAGATAGACAAATACGGGTAACCTTATCGAGTGAT 2328
711 -----Val 711
2329 ACCTATATAGATTAATTCGAAGCCCTCCCTCGCACTCTCCACAGGAGGAAATAGCATC 2388
712 ArgValGlyAsp-----SerAspProSerGlyTyrLeu-----LeuSerHisGluGlu 727
727
2389 AACGTTGGTGATATCGTTTCAGAT---AATGCTATTATTAACAATCGGCCCATCGTGGT 2445
728 LeuLeuLysGlyLeuGluLysSerGlnIleIleTyrSerArgLeuGluGluAsnSerSer 747
747
2446 TTTCTGAATTTTGTGCAATAAAAAAGAAACCACTCGATATGTCNAATGGCAATTT 2505
748 LeuSerGlu-----LysSerLysThrAsnLeuSerLeuLys 760
760
2506 TTACCAATACAGGTGCAATGTGGCGACCAAAATCTAAGTATTAATAACGAAATGCGGAG 2565
761 GluIleSerGlyTyrMetAlaArgThrIleGlnAspThrIleSerGluTyrAlaGluGlu 780

```
Db 2566 AAAATA-----TTTAAGATGGATTAGATGATTCGGTGAAGAAAGCTTTGTTGAAAAA 2616
QY 781 HIGLYSTYrArgSerAsnHisProAsp-----PheTyrSerGlu 793
Db 2617 TTGAAATAAGACCAATGACCAAGAGCGGGGCAACGACAAATACTATTCGCCAGAGAA 2676
QY 794 ThrAspPhePheAlaLeuMetAspLysSerGluLysAsnAsp 807
Db 2677 ACACCGTTCAAGTTGTTTCAATGACACATCAAGGTAGAGAT 2718
```

RESULT 11

ACF65386_5/c
Continuation (6 of 7) of ACF65386 from base 500001 (Photorhabdus luminescens nucleotide
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386

Fragment Name	Begin	End
WP ACF65386_0	1	110000
WP ACF65386_1	100001	210000
WP ACF65386_2	200001	310000
WP ACF65386_3	300001	410000
WP ACF65386_4	400001	510000
WP ACF65386_5	500001	610000
WP ACF65386_6	600001	700779

Alignment Scores:

Pred. No.:	1,22e-198	Length:	110000
Score:	2845.50	Matches:	578
Percent Similarity:	71.01%	Conservative:	71
Best Local Similarity:	63.24%	Mismatches:	150
Query Match:	60.03%	Indels:	115
DB:	10	Gaps:	11

US-10-647-956A-6 (1-915) x ACF65386_5 (1-110000)

```
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
Db 15073 ATGAAATAACATTACCCCTAACTTTATACCATACCGCGCCAGCTAGTTTCACGATAAC 15014
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
Db 15013 CGTGGACTCGCTATCGCTAATATAGTTTCACCGCGCTACCGCAGAGCAAAATACCGAT 14954
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
Db 14953 CCGCGTATTACTCGCATCAATATAATCGCGCGGATATTGAACCAACGATTCATCCT 14894
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPhelleArgValPhe 75
Db 14893 CGCCTGTATGATGCTAAGCAGACTAAACACCGCGTACACCGGAATTTTATCTGGCAGCAT 14834
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
Db 14833 AATTTGACCGGCAATATCTTCGACAGAGAGGCTGATGCTGCGCGAACAATATACCTC 14774
QY 96 AsnAspIleGluSerArgProValLeuIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 14773 AACGATATTGAAGTCCCGCGTATTGACCATCAGCGCAACCGGTGTCCGCCAAATCAC 14714
QY 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAla 135
Db 14713 CTTTATGAAGATAAACCCCTACCCGTCGCTACTCGCATACCCGAAACAGACAGACA 14654
QY 136 GlyGluLysThrThrGluArgLeuIleTTPAlaGlyAsnThrProGlnGluLysAspTyr 155
Db 14653 GAAGAGAAAACAACCGGCGCTTTATCTGGCGCGGCAATACGCGCGAGGAAAAGAGTAC 14594
QY 156 AsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSer 175
Db 14593 AACCTTGTGTCAGTACCCGTCATTACGATACCGCGGACTCGCTCAACTCAACAGC 14534
QY 176 LeuSerLeuAlaGlyValValLeuSerGlnSerGlnLeuLeuThrAspAsnGlnAsp 195
Db 14533 CTTGCGCTGACCGCGCGCGTTTATCACAATCTCAACACCGCTCGTCGATACCAAGAT 14474
```

```
QY 196 AlaAspTTrpThrGlyGluAspGlnSerLeuTrpGlnLysLeuSerSerAspValTyr 215
Db 14473 GCGGACTGCACAGGTGAAGACCAGAGCCTCTGGCAGCAAAAACCTAGTAGTGTCTAT 14414
QY 216 IleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGly 235
Db 14413 ACCACCCAAAATAAAACCCATGCCCGGGTTTACTTACCAGACCCGATGCTAAAGGC 14354
QY 236 AsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeu 255
Db 14353 AACATTCAGGGCAAGCCTATGATGTGGCGGTGAGTAAAGGGAGCTGGCTAAACATTA 14294
QY 256 LysGlyGlnAlaGluGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLys 275
Db 14293 AAAGGTTCAGACCGCAACAGTGATTAACAATCGCTACCTACTCCGCGCGGACAAAAA 14234
QY 276 LeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGln 295
Db 14233 TTACGCGAAGAGCAGCGTAAACGCGCATTTATCCGAATACAGCTATGAACCGGAATCTAG 14174
QY 296 ArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAspLeuArg 315
Db 14173 CGGCTTATCGGCATTTACCACTCGCGTCCATCAGACGCCAGGTGTTCAGACCTACGC 14114
QY 316 TyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArg 335
Db 14113 TATCAATATGATCCCGGTAGGCAATGTGATCAATATCCGTAAACGATCGGGAAGCCACCGC 14054
QY 336 PheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGln 355
Db 14053 TTTTGGCGCAATCAAAAAGTCATCCCGAGAAATAGCTATACCTACGATTTCTCTGTATCAG 13994
QY 356 LeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuPro 375
Db 13993 CTTTACGTGCCACCGAGCTGAATGGCAATATAGGTTCAGCCAAATTAACCCACTCCCC 13934
QY 376 SerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyr 395
Db 13933 TCCCTTGCCTACCTGCTGATTAACAACACTACACTTAACACCGCACCTATAGTTAT 13874
QY 396 AspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyr 415
Db 13873 GACCGTGGCGGCAATTTGATGAAATTCAGCATAGTTCACTGCCACGCAAAATAACTAC 13814
QY 416 ThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThr 435
Db 13813 AGACGAATATACCGTTTCTAATTAACAACCGTCCGTATTAAGTACACTGACCGGAA 13754
QY 436 AspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuPro 455
Db 13753 GATCCAACCCAAAGTTGATGCTTATTTGATTCGGGAGGCCATCAAAACCACTTATTATCC 13694
QY 456 GlyGlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGly 475
Db 13693 GGTCAAGTTCTAATATGGACACCGCGAGCGCAATTCGAAACAGTCAACACTAGCGCAGGA 13634
QY 476 AsnGluTTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGluGlnPro 495
Db 13633 AATGAGTGTATCATCTACCATAGCAACGCGCACACGACAGCTAAGTGAATGAACAAACAA 13574
QY 496 ThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeuArgThr 515
Db 13573 ACTCAGATATTCGCGCAACAGCAAGAGTCACTTATCTCGCGGGGCTAGAACTACGCACA 13514
QY 516 ThrGlnSerAsnAlaThrThrThrGluGluLeuHisValIleThrLeuGlyGluAlaGly 535
Db 13513 ACCCAACATGGCAGTACTACCGCAATATTTGCAAGTTATCACACTCGGTAAAGTGT 13454
QY 536 ArgAlaGlnValArgValLeuHisTTrpGluSerGlyLysProGluAspValAsnAsn 555
Db 13453 CGTGCACCAAGTCCGGGTATTACATTTGGGAGAGCGGAAAACCCGGAAGATATCAACAACAT 13394
```


Db 1 ATGATTGGTTACAATTCTGCAATTAACCGAATAATACCCCATCTCTGTACGGTACGAGATAAT 60
Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGlu---AsnSer 39
Db 61 CGAGGGTTAAATATACATACGCTGGAATATCTCGGGACTCAAGCTGATGAACCAATAGC 120
Qy 40 AspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAsp 59
Db 121 AACCAATTGATCATCTCGCTATCAATTTAATATCTACCGGACTTCAAGTATAAAAGCACAGAC 180
Qy 60 ProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGly 79
Db 181 CCACGGTAGATATAAAACACAGAGTGGTTCAAACTTCACTCGTATCTTTAGTCTCGCTGGG 240
Qy 80 GlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
Db 241 AATACACTGGTCAAGAAAGTATCGATGCTGCGGCAACGATTACCTTGAACGATATCGAA 300
Qy 100 SerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAsp 119
Db 301 GGACGCCAGTACTGATATCAATGCAATCGCGGCTCGTCAGACCCCATCACTATGAAGGT 360
Qy 120 AsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 139
Db 361 AATACCTTGGCCGCGCGCTTGCCTGGCTGTCCAGGTAAATACAAAGAACGAGAAACC 420
Qy 140 ThrGluArgLeuIleThrAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
Db 421 ACGAGCGCCTTATTTGGGCAACATACAGATGCGAGGAAACACAGAACTCTCGCGGG 480
Qy 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
Db 481 CAATGTATACGCCATTATGATCTCGCGGGCTGTCAACCTGGAAAGTTTGTCTTAAACA 540
Qy 180 GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspThrThr 199
Db 541 GGATCGGTTTTATCACAGTCTCGTCAATTAATAGCCGACGATCAGGAAGCTGATGGCGC 600
Qy 200 GlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSer 219
Db 601 GGTGATGATGAATAAGTAGCTGGCTACAAATGAAATGGAACATATTCAGACTCAACAT 660
Qy 220 AsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArg 239
Db 661 AAAACTGATGCCATTGGTCTCTGCTAACTCAATCGACGCCAAGGGAATAATGCAACGG 720
Qy 240 LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAla 259
Db 721 CTGGCCTATGATGTGCGGGCCCAACTGAAAGGTAGCTGGTTAAACACTAAAGGCCAAGCC 780
Qy 260 GlnGlnValIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
Db 781 GAAAAGTTATTGTACAGTCTATTACTGGTCAAGCCGCAACAAAATTCAGAGAAGAG 840
Qy 280 HisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGly 299
Db 841 CACGGTAATGGCGTTATTACGAATATACCTATGAAACCAAGACCCCAACGATTAAATAAC 900
Qy 300 IleThrThrArgArgProSerAspAla---LysValLeuGlnAspLeuArgTyrGlnTyr 318
Db 901 ATTACAAACCCGCGAACTAGAGATAGTACAAAACCACTACAAAGATTTCGTTATGAATAT 960
Qy 319 AspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArg 338
Db 961 GATCCCGTTGGCAATGTGATCAATATTCGTAATGATGCAGAGCAACCCGATTCGGCGT 1020
Qy 339 AsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSer 358
Db 1021 AATCAGAAAAATAGTACGGAAAAATGCATATTCCTATGATCTCTGTACCAACTCATCCAA 1080
Qy 359 AlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSer----- 376
Db 1081 GCAACCGCGCGGAAATGGCTAACTTGGTTCAGCAAGGAAGCCAGCTCCCTCTTTAATT 1140

Qy 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAsp 396
Db 1141 ACCCTCTTCTTACCGATGACAATACTTATCTAATACTATATTCGTATCTATACCTACGAC 1200
Qy 397 HisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThr 416
Db 1201 GATAGCGGCAACCTGACAAAATCCAGCACAGTGTCTCCGGCAAGTAACATAACTACACC 1260
Qy 417 ValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAsp 436
Db 1261 ACNATATCACCAATTCNAAACCGTAATACCGGGGTCTCTCAGTACCTCACCACGAC 1320
Qy 437 ProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGly 456
Db 1321 CCNATCTCGTTGATACATCTTTGATCGAGTGGTGCATCAACACAGTCTGTCTCAGGG 1380
Qy 457 GlnThrLeuIleThrProArgGlyGluLeuLysGlnValAsnAsnGlnYProGlyAsn 476
Db 1381 CAATCTTAACTGGACACCGCGGAGAACTACAACTAGTGAACCAAGT---GGTAAT 1437
Qy 477 -----GluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGlu 493
Db 1438 ACGCGCGTGAGTGTACCACTATGACAGTACGGCATGCGGTACTGAAATAAAGCAA 1497
Qy 494 GlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeu 513
Db 1498 CAGCAAACTCAATACCAACGACGAGCAACAGTCACTTATCTCGCAGGGTTGAATTA 1557
Qy 514 ArgThrThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGlu 533
Db 1558 CACACACACAAAGCGGCACCAATATCACCGAAGACTTCAAGTTATTACTGTGACGCAA 1617
Qy 534 AlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsn 553
Db 1618 GCMGAAAAGCACAGTACGCGTACTACACTGGGAAAAGGCCCAACCCACCGCATAAAT 1677
Qy 554 AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp 573
Db 1678 AAGCATCAAGTCAGATATAGTACGATAATCTTACACACAGCAGCGAATTAGAACTGGAT 1737
Qy 574 AsnGlnGlyGlnIleSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrp 593
Db 1738 ATGCACGGAGAATGATGATTTGGGAAGAGTATATCCCTATGTGGCGCACCGCAGTAGG 1797
Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg 613
Db 1798 GCAGCAAGAATCAGATTGAGCTGGTTACAAAACCATTCGTTATTTCAGGTAAAGAACGT 1857
Qy 614 AspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTrp 633
Db 1858 GATGCAACGGAGCTGTACTATTACGGCTACCGCTATTATCAACCGTGGCGCGGTAGATGG 1917
Qy 634 LeuSerAlaAspProAlaGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
Db 1918 TTAAGCGCTGACCGCGCTGGAACCGTAGATGGTCTGAATTTGTACCGTATGGTAAGAAAT 1977
Qy 654 AsnProValSerLeuGlnAspGluAsn----- 662
Db 1978 AATCCAATGACCGGCATAGATGAAGATGGCGGTATGTTTAAAACCGTAGCACACAGGTGCA 2037
Qy 663 -----GlyLeuAlaProGluLysGlyLysTyrThrLysGlu----- 674
Db 2038 TTAGGCATTGGCGGTATGCATACGAGCTTTACAAATATATAAAATCAACAGTTGAAAAG 2097
Qy 675 -----ValAsnPheAspGluLeuLysPheLysLeuAla 686
Db 2098 CCTCAGATGCCATCTCTCTCTGTAATCCTACGGTGATCAACCAAGTCAGCAAAATCACC 2157
Qy 687 AlaLysSerSer----- 690
Db 2158 CAAAAGCGAGTGTCTTTAAAGCAAACTATGACCCGATGACGAGATGGCCCATTAACATA 2217

Qy	691	-----HisValVallyserTrpAsnGluLysGluSerSerTyr	702
Db	2218	ACGGGGCGTAAGAGCCGAGACATCTGCACAGGGTCAAGTCCCTGGCGTCAAGCA	2277
Qy	703	ThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyrLeu	722
Db	2278	ATAAAGAAGGGCAAGCTAGTGGCGGTGCGGAGAAATTTGCTGGCGGTGGCAATGTC	2337
Qy	723	-----LeuSerHisGluGluLeuLeuLys-----	730
Db	2338	GGTGAACATAACAAACACCGCTAACAAAGACCGCGGACCGACGCAATTAATAATTTT	2397
Qy	731	-----GlyIleGluLys-----SerGlnIle	737
Db	2398	AGTCTACCTTGGACGGTATAAAGATTTTAAGCAGCGCGGCTAGTGTACCGTC	2457
Qy	738	IleTyrSerArgLeuGluGlu-----AsnSerSerLeuSerGluLysSerLys	753
Db	2458	AGCCACGAAATTTGAAGAGCTGCAAAAGCACTGATGATTTTAAAGAGGTGCGCAACA	2517
Qy	754	ThrAsnLeuSerLeuGlySerGluLysSerGlyTyrMetAlaArgThrIleGln-----	771
Db	2518	GATACGCTAATTACCGGGGATCGCTAGTGGCAGACGTGGAGCCACACTGGATACCGCC	2577
Qy	771	-----	771
Db	2578	GCGCGGTGTCGCACACCGGTAGCCAAAGTGCGCACTCAAGGTCTGTCTATGGCATGG	2637
Qy	772	-----AspThrIleSerGluTyrAlaGluGluHisLys	782
Db	2638	AAAGTTACCGCATTTGTTTCACACCGCAGAGAAATTAAGCGAGCTCGCAGAAAAACATAAG	2697

RESULT 13

ACF67367_39/c

Continuation (40 of 57) of ACF67367 from base 3900001 (Phototaxibodus luminescens nucleoti

WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000
WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000

WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Alignment Scores:

Pred. No.:	1.6e-182	Length:	110000
Score:	2627.50	Matches:	528
Percent Similarity:	69.78%	Conservative:	100
Best Local Similarity:	58.67%	Mismatches:	153
Query Match:	55.43%	Indels:	119
DB:	10	Gaps:	13

US-10-647-956A-6 (1-915) x ACF67367_39 (1-110000)

Qy	1	MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn	20
Db	49602	ATGATTCGTACAAATTCGCAATTAACCCCAATATCCCTCTGTACGCGTACGAGATAAT	49543
Qy	21	ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGlu---AsnSer	39
Db	49542	CGAGGGTTAAATATACATACGCTGGAAATATCTGGGACTCAAGCTGATGAACCAATAGC	49483
Qy	40	AspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAsp	59
Db	49482	AACGAATTGATCACTCGCTATCAATTAATTAATCACTCACGGACTTCAAGTAAAGACACAGC	49423
Qy	60	ProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGly	79
Db	49422	CCACGTAGATATAAAACCAGAGTGGTCAAACTTCACGTAATCTTTAGTCTCGCTGGG	49363
Qy	80	GlnValLeuArgGluGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu	99
Db	49362	AATACACTGGGTGAGAGAAAGATATCGATGCTGGCCGAAACGATTACCTTGAACGATATCGAA	49303
Qy	100	SerArgProValLeuIleleAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAsp	119
Db	49302	GGACGGCCAGTACTGACTATCAATGCAATCGCGGCTCGTCAGACCCATCATATGAAGGT	49243
Qy	120	AsnThrLeuProGlyArgLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr	139
Db	49242	AATACCTTGCCCGCGCTTGTGGGTGTCCACAGTAAATAAAAGAACGAGAAACCC	49183
Qy	140	ThrGluArgLeuIleTrpAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly	159
Db	49182	ACGGAGCGCTTATTTGGGGCAACATACAGATGCAGAGAAAAACAGAGATCTCGCGGG	49123
Qy	160	GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla	179
Db	49122	CAATGTATACGCCATTATGATCTCTGGGGCTGGTCACTGGAAGTTTGTCTCTTAACA	49063
Qy	180	GlyValValLeuSerGlnSerGlnGlnLeuThrAspAsnGlnAspAlaAspTrpThr	199
Db	49062	GGATCGGTTTTATCACAGTCTCGTCAATTAATAGCCGACGATCAGGAAGCTGATTCGCGC	49003
Qy	200	GlyGluAspGlnSerLeuTrpGlnGlnLysLeuSerSerAspValTyrIleThrGlnSer	219

Wp ACF65388_02 200001 310000
 Wp ACF65388_03 300001 410000
 Wp ACF65388_04 400001 510000
 Wp ACF65388_05 500001 610000
 Wp ACF65388_06 600001 710000
 Wp ACF65388_07 700001 810000
 Wp ACF65388_08 800001 910000
 Wp ACF65388_09 900001 1010000
 Wp ACF65388_10 1000001 1110000
 Wp ACF65388_11 1100001 1210000
 Wp ACF65388_12 1200001 1225559
 Alignment Scores:
 Pred. No.: 1.6e-182 Length: 110000
 Score: 2627.50 Matches: 528
 Percent Similarity: 69.78% Conservative: 100
 Best Local Similarity: 58.67% Mismatches: 153
 Query Match: 55.43% Indels: 119
 DB: 10 Gaps: 13
 US-10-647-956A-6 (1-915) x ACF65388_08 (1-110000)
 Qy 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAsn 20
 Db 75335 ATGATTCGTTACAATTCGCAATTAACCGAATAACCCCATCTGTGAGCGTACGAGATAAT 75394
 Qy 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGlu---AsnSer 39
 Db 75395 CGAGGGTTAAATATACATACGCTGGAATATCTGCGGACTCAAGCTGATGAACCAATAGC 75454
 Qy 40 AspGluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAsp 59
 Db 75455 AACGAAATGATCATCTCGCTATCAATTTAATACTCAGCGACTTCAAGTAAAGAAGCACAGAC 75514
 Qy 60 ProArgLysAsnLysAsnGlnSerGlyProAsnPheIleArgValPheAsnLeuAlaGly 79
 Db 75515 CCACGTAGATATAAAACCAGAGTGGTTCAAACTTCACTCGTATCTTTAGTCTCGCTGGG 75574
 Qy 80 GlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeuAsnAspIleGlu 99
 Db 75575 AATACACTGCGTGGAAGAAAGTATCGATGCTGCGCGAAGCATTTACTTGAACGATATCGAA 75634
 Qy 100 SerArgProValLeuIleAlaAsnAlaThrGlyValArgGlnAsnHisArgTyrGluAsp 119
 Db 75635 GGACGCCCGACTACTGACTATCAATGCAATCCGCGCTCGTCAGACCCATCATATGAAGGT 75694
 Qy 120 AsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnValGlnAlaGlyGluLysThr 139
 Db 75695 AATACCTTGGCCGCGCTTCTGCTGCTGTCACCGAGTTAATACAAAAGAACGAGAAAACC 75754
 Qy 140 ThrGluArgLeuIleTropAlaGlyAsnThrProGlnGluLysAspTyrAsnLeuAlaGly 159
 Db 75755 ACGGAGCGCCTTATTTGGGGCAACAATACAGATCGCAGAGAAAACCCAGAAATCTCGCCGGG 75814
 Qy 160 GlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeuAsnSerLeuSerLeuAla 179
 Db 75815 CAATGTATACCCATATGATCCTCGCGGGCTGGTACACTGGAAAGTTTGCTCTTAACA 75874
 Qy 180 GlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsnGlnAspAlaAspTyrThr 199
 Db 75875 GGATCGGTTTTATCACAGTCTCGTCAATTAATAGCCGACGATCAGGAAGCTGATTGGCGC 75934
 Qy 200 GlyGluAspGlnSerLeuTyrGlnLysLeuSerSerAspValTyrIleThrGlnSer 219
 Db 75935 GGTGATGATGAATAATAGCTGCGGTACAAAACCTGAATGGCAACATATTACACACTCAACAT 75994
 Qy 220 AsnThrAspAlaThrGlyAlaLeuLeuThrGlnThrAspAlaLysGlyAsnIleGlnArg 239
 Db 75995 AAAACTGATGCATTTGGTGTCTGCTAACTCAATATCGACGCGCAAGGGAATATGCAACGG 76054
 Qy 240 LeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeuThrLeuLysGlyGlnAla 259
 Db 76055 CTGGCCTATGATGTGCGGGCCAACTGAAGAGTAGTCTGTTAAACACTAAAAAGGCCAAGCC 76114

Qy 260 GluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGlyGlnLysLeuArgGluGlu 279
 Db 76115 GAAAAGTTATTGTACAGTCTATTACCTGTCAGCAGCCGGACAAAATATACGAGAAGAG 76174
 Qy 280 HisGlyAsnGlyIleValThrGluTyrSerTyrGluProGluThrGlnArgLeuIleGly 299
 Db 76175 CACGGTAATGGCGTTATTACGGAATATACCTATGAACACGAGACCCCAACGATTAATTAAC 76234
 Qy 300 IleThrThrArgArgProSerAspAla---LysValLeuGlnAspLeuArgTyrGlnTyr 318
 Db 76235 ATTACAAACCGCCGAACTAGATACAAACCACTCAAGATTACGTTATGAATAT 76294
 Qy 319 AspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAlaThrArgPheTrpArg 338
 Db 76295 GATCCCGTTGGCAATGTGATCAATATTCGTATATGATGACAGAACACCGATTCGGCGT 76354
 Qy 339 AsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeuTyrGlnLeuIleSer 358
 Db 76355 AATCAGAAAATAGTACCGGAAAATGCATATTCCTATGATTTCTCTGTACCAACTCATCAA 76414
 Qy 359 AlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnGlnLeuProSer----- 376
 Db 76415 GCAACCGCGCGCAAAATGGCTAACTTGGTCAGCAAGGAAGCCAGCTTCCCTCTTAATT 76474
 Qy 377 ProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyrSerTyrAsp 396
 Db 76475 ACCCTCTTCTCCTACCGATGCATATCTTACTACTATATTCGTACTTATCTACTAGC 76534
 Qy 397 HisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsnAsnTyrThr 416
 Db 76535 GATAGCGGCAACCTGCACACAAATCCAGCACAGTGTCTCCGCAAGTAAACAATAACTACCC 76594
 Qy 417 ValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeuThrThrAsp 436
 Db 76595 ACAAAATATCAACATTTCAAACCGTAATACCGCGGTGCTCTAGTACCTCCACCAACGAC 76654
 Qy 437 ProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeuLeuProGly 456
 Db 76655 CCCAATCTCGTTGATACATCTTTGATGAGGTGGTCACTCAACACAGTCTGTTCTCAGG 76714
 Qy 457 GlnThrLeuIleTrpThrProArgGlyGluLeuLysGlnValAsnAsnGlyProGlyAsn 476
 Db 76715 CAATCTCTAACTGGACACACCGCGGAGAACTACAACAGTGAACCAAAAGT---GGTAAT 76771
 Qy 477 -----GluTrpTyrArgTyrAspSerAsnGlyMetArgGlnLeuLysValSerGlu 493
 Db 76772 ACCGCGGTGAGTGGTACCACTATGACAGTACGCGCATGCGGCTACTGAAAAATAACGAA 76831
 Qy 494 GlnProThrGlnAsnThrThrGlnGlnArgValIleTyrLeuProGlyLeuGluLeu 513
 Db 76832 CAGCAAACTCCATACCGACGACGACCAAGTCACTATCTGCCAGGTTGGAATTA 76891
 Qy 514 ArgThrThrGlnSerAsnAlaThrThrGluGluLeuHisValIleThrLeuGlyGlu 533
 Db 76892 CACACACACAAAAGCGCACCAATATCACCGAAGACTTACAAGTATTACTGTGAGCAA 76951
 Qy 534 AlaGlyArgAlaGlnValArgValLeuHisTrpGluSerGlyLysProGluAspValAsn 553
 Db 76952 GCAGGAAAAGCACAAAGTACGCTACACTGGGNAAGGCGCAACCCCGCATAAAT 77011
 Qy 554 AsnAsnGlnLeuArgTyrSerTyrAspAsnLeuIleGlySerSerGlnLeuGluLeuAsp 573
 Db 77012 AACGATCACTGATATAGTACGATATCTTACACAGACGACGAAATTAGAATCGAT 77071
 Qy 574 AsnGlnGlyGlnIleLeuSerGluGluTyrTyrProPheGlyGlyThrAlaLeuTrp 593
 Db 77072 ATGCACGAGAAATGATCAGTTCGGGAAGAGTATTACCCCTTATGTTGGCAGCAGTATGG 77131
 Qy 594 AlaAlaAsnSerGlnThrGluAlaSerTyrLysThrIleArgTyrSerGlyLysGluArg 613
 Db 77132 GCAGCAAGAAATCAGATTGAAGCTGGTTACAAAACCAATTCGTTATTTCAGGTAAAGAACGT 77191

```
QY 614 AspAlaThrGlyLeuTyrTyrGlyTyrArgTyrTyrGlnProTrpAlaGlyArgTyr 633
DB 77192 GATGCAACGGGACTGTACTATTACGGCTACCGCTATTATCAACCGTGGCGGTAGATGG 77251
QY 634 LeuSerAlaAspProIleGlyThrIleAspGlyLeuAsnLeuTyrArgMetValArgAsn 653
DB 77252 TTAAGCGCTGACCGCTGGAACCGTAGATGGTCTGAATTGTGTACCGTATGGTAAGAAAT 77311
QY 654 AsnProValSerLeuGlnAspGluAsn----- 662
DB 77312 AATCCAAATGACCGGCTAGATGAAGATGGCGTATGTTTAAACCGTAGCAACAGGTGCA 77371
QY 663 -----GlyLeuAlaProGluLeuGlyGlyTyrThrLysGlu----- 674
DB 77372 TTAGGCATTGGCGGTATGGCATACGAGCTTTACAAATATATAAAATCAACAAGTTGAAG 77431
QY 675 -----ValAsnPheAspGluLeuLysPheLysLeuAla 686
DB 77432 CCTCAGATGCCATCTCTGTCTGAATCTCAGGTGATCAACAAGTCAAGCAAAATCACC 77491
QY 687 AlaLysSerSer----- 690
DB 77492 CAAAAGCGAGTCTTTAAAGCAAACTATGACCCGATGAGCAGATGGCCCATACATA 77551
QY 691 -----HisValValLysTyrAsnGluLysGluSerSerTyr 702
DB 77552 ACGGGCGTAAGAACCGCAGAACATCTCGCACAGGCTCAAGTCCCTCGCGCTCAAGCA 77611
QY 703 ThrLysAsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyrLeu 722
DB 77612 ATAAAGAAGGGCAAGCTTAGTTCGGGCTCGCGAGATTTTCTCGCGGTGCGCAATGTC 77671
QY 723 -----LeuSerHisGluLeuLeuLys----- 730
DB 77672 GGTGAATAAAACCAACCGCTTAACAAAGCCCGCCGACCGACCGCAATTAATAATTT 77731
QY 731 -----GlyIleGluLys-----SerGlnIle 737
DB 77732 AGTCTCACCTTGGACGGTATATAAAGGTATTTAAGCAGCGCGGCTAGTCTACCGTC 77791
QY 738 IleTyrSerArgLeuGluGlu-----AsnSerSerLeuSerGluLysSerLys 753
DB 77792 AGCCAGAAAAATTTGAAGAGCTGCAAAAACCACTGATGATTTAAAGAGAGTTCGCAACA 77851
QY 754 ThrAsnLeuSerLeuGlySerGluIleSerGlyTyrMetAlaArgThrIleGln----- 771
DB 77852 GATACGCTAATTACCGGGGCTACGCTAGTGGCAGACAGTGGAGCCACACTGGATACCGCC 77911
QY 771 ----- 771
DB 77912 GCGCGGTCTGTCACACCGCGTAGCCAAAGTGGCACTCAAGGTCTGTCTATTGGCATGG 77971
QY 772 -----AspThrIleSerGluTyrAlaGluGluHisLys 782
DB 77972 AAAGTTACCGGCATTGTTTCACCGCAGAGAAGATTAAGCGAGCTCGCAGAAAAACATAAG 78031
RESULT 15
ID ACF71155 standard; DNA; 2898 BP.
AC
AC ACF71155;
XX
XX 20-NOV-2003 (first entry)
XX
XX Photorhabdus luminescens nucleotide sequence #9622.
XX
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
XX detection; food; gene expression; plant; animal; microorganism; toxin;
XX antibiotic; biopesticide; virulence factor; disease model; plague;
XX whooping cough; gene; ds.
XX
XX Photorhabdus luminescens.
XX
```

```
PN WO200294867-A2.
PD 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001PR-00001659.
XX
XX (INSP ) INST PASTEUR.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
XX Buchrieser C;
XX
XX WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 9622; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
XX proteins from Photorhabdus luminescens. The isolated sequences are
XX sources of probes and primers for detecting the genome of P. luminescens
XX and related species; to study polymorphisms; for gene analysis and for
XX detection/amplification of the genes. Antibodies (Ab) raised against the
XX polypeptides encoded by the genes are used for detection/identification
XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX carry a gene-containing vector are used to select compounds that
XX modulate, regulate, induce or inhibit expression of the genes in plants,
XX animals or microorganisms other than P. luminescens and are able to alter
XX response or sensitivity to toxins and antibiotics produced by P.
XX luminescens. Cells transformed to express the genes are useful for
XX recombinant production of the proteins, particularly toxins and
XX antibacterials useful as insecticides, bactericides and fungicides. The
XX genes, proteins, vectors containing the genes and Ab are also useful
XX therapeutically (to treat microbial infection by bacteria or fungi that
XX are sensitive to P. luminescens-encoded toxins or antibiotics) and as
XX biopesticides. Other uses of the genes and the proteins are as virulence
XX factors and for identifying targets of human diseases for which P.
XX luminescens is a model (particularly plague and whooping cough). This
XX sequence represents one of the isolated P. luminescens genes
XX
XX Sequence 2898 BP; 978 A; 640 C; 632 G; 648 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8,29e-181 Length: 2898
Score: 2578.50 Matches: 532
Percent Similarity: 68.82% Conservative: 97
Best Local Similarity: 58.21% Mismatches: 184
Query Match: 54.40% Indels: 101
DB: 16 Gaps: 16
US-10-647-956A-6 (1-915) x ACF71155 (1-2898)
QY 1 MetSerSerTyrAsnSerAlaIleAspGlnLysThrProSerIleLysValLeuAspAen 20
DB 1 ATGAACAATTGACCCCAAAATTTACCAACACACTCCCACTATCTGTTCCAGATAAC 60
QY 21 ArgLysLeuAsnValArgThrLeuGluTyrLeuArgThrGlnAlaAspGluAsnSerAsp 40
DB 61 CGTGGGCTGGATGTCGGTGAATCCATTATCACCAGACTACCCGACAGAAAAATAGTGAT 120
QY 41 GluLeuIleThrPheTyrGluPheAsnIleProGlyPheGlnValLysSerThrAspPro 60
DB 121 ATCCGTATCACCCTCATCAGTATGATGTTCTCGACACCTGACCAAGATTTGACCCA 180
QY 61 Arg-----LysAsnLysAsnGlnSerGlyProAsnPheIleArgValPhe 75
DB 181 CGCTGTATGACCGCTGGCAGAAAGATAGTCCGTAACCAATTTCTCTGCAGTAT 240
QY 76 AsnLeuAlaGlyGlnValLeuArgGluSerValAspAlaGlyArgThrIleThrLeu 95
XX
```


Db 241 GATTAAAGCGGACGGCTCTACGTACAGAGAGTGCCGATGCGGTAACTACTGTCACTCTT 300
Qy 96 AsnAspIleGluSerArgProValLeuIleIleAsnAlaThrGlyValArgGlnAsnHis 115
Db 301 CATGATATTGAAACCGCTGGTCTGCTGACTGTATAACGGCAACGGGTGTCAAGCAGACCCGG 360
Qy 116 ArgTyrGluAspAsnThrLeuProGlyArgLeuLeuAlaIleThrGluGlnVal----- 133
Db 361 CAATATGAGATATTTCTTGCCTGGTCTGCTGCTATCCGTAAACGGAACAGACCCAGAC 420
Qy 134 GlnAlaGlyGluIleThrThrGluArgLeuIleIleIleIleIleIleIleIleIleIleIle 153
Db 421 GAAAGGGCATCCCATATACACCGAACGCTCATCTGGCTGGAAACACCGCGCAGAAAAA 480
Qy 154 AspTyrAsnLeuAlaGlyGlnCysValArgHisTyrAspThrAlaGlyLeuThrGlnLeu 173
Db 481 GAGCAAAATCTTGCTGCTGATGTATGATCATCACTACGATACAGCAGGAGCCACCACTG 540
Qy 174 AsnSerLeuSerLeuAlaGlyValValLeuSerGlnSerGlnGlnLeuLeuThrAspAsn 193
Db 541 AATCACCTTTCCCTAACCGGAGCGGCTTTATCACAATCCCGTCAGCTACTGGTTGATGGC 600
Qy 194 GlnAspAlaAspTTPThrGlyGluAspGlnSerLeuIleIleIleIleIleIleIleIleIle 213
Db 601 CAAGAAGCGGATTGGTTCGGCGGATGATAAAAGATCTGGGATAAGAAATTAAGTAACGAT 660
Qy 214 ValTyrIleThrGlnSerAsnThrAspAlaThrGlyAlaLeuLeuLeuThrGlnThrAspAla 233
Db 661 GTATACACCAACCGAAAAACAGACGGATGCTACCGGCATCTGTGTGACACAAACCGATGCC 720
Qy 234 LysGlyAsnIleGlnArgLeuAlaTyrAspValAlaGlyGlnLeuLysGlySerTrpLeu 253
Db 721 AAAGAAACATCCAGCATCTGGCCCTAATGTAGCCGCAANTTGAAGGAAGCTGGCTA 780
Qy 254 ThrLeuLysGlyGlnAlaGluGlnValIleIleLysSerLeuThrTyrSerAlaAlaGly 273
Db 781 ACGGTAAAGGCCAAAAAGAGCAGATATATCAATTAATCCCTAACCTATTACGCCGCGAGA 840
Qy 274 GlnLysLeuArgGluGluHisGlyAsnGlyIleValThrGluTyrSerTyrGluProGlu 293
Db 841 CAAAAATACGCGAAGACGCGTAACGGTATCATCACCGAATATACTTACGAGCCGGAA 900
Qy 294 ThrGlnArgLeuIleGlyIleThrThrArgArgProSerAspAlaLysValLeuGlnAsp 313
Db 901 ACCCAGGCACTAATGGGCATCACAAACCGTCGTTCACTGATGACAAAGGCTTTACAAGAC 960
Qy 314 LeuArgTyrGlnTyrAspProValGlyAsnValIleAsnIleArgAsnAspAlaGluAla 333
Db 961 TTACGTTATGAATATGATCCGGTTGGCAACATAATCAGTCTCCGTAAACGATGCAGAAGCG 1020
Qy 334 ThrArgPheTrpArgAsnGlnLysValAlaProGluAsnSerTyrThrTyrAspSerLeu 353
Db 1021 ACCCGCTTCTGGCGCAATCAGAAATGGTGCAGAGAATATCTATACCTACGATTCCTCTG 1080
Qy 354 TyrGlnLeuIleSerAlaThrGlyArgGluMetAlaAsnIleGlyGlnGlnAsnAsnGln 373
Db 1081 TATCAGCTTATACGCCAACAGGCGCGAAATGGCGAATATCGGCCAGCAGAAATCAGAAT 1140
Qy 374 LeuProSerProAlaLeuProSerAspAsnAsnThrTyrThrAsnTyrThrArgSerTyr 393
Db 1141 CTCCCTCTACAGCACTCCCTTCGATAACCAACACTTATACCAATTAACCCGCACTTAT 1200
Qy 394 SerTyrAspHisSerGlyAsnLeuThrGlnIleArgHisSerSerProAlaThrGlnAsn 413
Db 1201 GCCTATACCGTGTGGCAACTCAGCCCAATCGGCATAGCTCACCCTGGAGCCAAAAAC 1260
Qy 414 AsnTyrThrValAlaIleThrLeuSerAsnArgSerAsnArgGlyValLeuSerThrLeu 433
Db 1261 AACTACACCAACAGACATACCGTCTCGAACCGCAGCAACCGCGGTACTGATGATCTTG 1320
Qy 434 ThrThrAspProAsnGlnValAspThrLeuPheAspAlaGlyGlyHisGlnThrSerLeu 453
Db 1321 ACCACTACCGCAAAAGTGGATGCAATTGTTTTCAGCGCAGGTGCTCATCAGGACACATTA 1380

Qy 454 LeuProGlyGlnThrLeuIleTTPThrProArgGlyGluLeuLysGlnVal----- 470
Db 1381 CTACCGGGCAAAACCTAAACTGGAATGACAGGGTGAACACTACACAGATGACACCCGTA 1440
Qy 471 -----AsnAsnGlyProGlyAsnGluTrpTyrArgTyrAspSerAsn 484
Db 1441 AAACGGGATAACCTCACTGACCGGTGACCGCATAGAGTGGTATCGCTATGCAACGAC 1500
Qy 485 GlyMetArgGlnLeuLysValSerGluGlnProThrGlnAsnThrThrGlnGlnArg 504
Db 1501 GGAATCGCGTGTAAAGTCACTGAACAGCAAAATGCAGAAATATCTCTCCAGCAACGACGA 1560
Qy 505 ValIleTyrLeuProGlyLeuGluLeuArgThrThrGlnSerAsnAlaThrThrGlu 524
Db 1561 GTCGTTTACCTGTTCAGGATTTAGAACCTACGTACAAACCAAAACCGGTGATATCAGAAGAA 1620
Qy 525 GluLeuHisValIleThrLeuGlyGluAlaGlyArgAlaGlnValArgValLeuHisTrp 544
Db 1621 GAGTTGCAGATTAATACCGTGGGTGAAGCGGTCTGTCGCAAGTGGGAGTTCTACATTGG 1680
Qy 545 GluSerGlyLysProGluAspValAsnAsnGlnLeuArgTyrSerTyrAspAsnLeu 564
Db 1681 GAAAGCGCAAAACCGAAAAACATCAACAATAATCAGGTACGTTACAGTTATGCGCAATCTC 1740
Qy 565 IleGlySerSerGlnLeuGluLeuAspAsnGlnGlyGlnIleIleSerGluGluGluTyr 584
Db 1741 ATTGGCTCCAGCAGCTTGAGCTAGATAGTGGGCAAAATATCAGTCAAGAAGAGTAC 1800
Qy 585 TyrProPheGlyThrAlaLeuTrpAlaAsnSerGlnThrGluAlaSerTyrLys 604
Db 1801 TATCCATTTGGCGGTACAGCGCTCTGGCGCGCAAGAAACAGACAGAGCCAGCTTACAAA 1860
Qy 605 ThrIleArgTyrSerGlyLysGluArgAspAlaThrGlyLeuTyrTyrGlyTyrArg 624
Db 1861 ACGATCGGTATTCTGGTAAAGAGCGGATGCCACCGGACTGTTATTATTACGGCTATCGG 1920
Qy 625 TyrTyrGluProTrpAlaGlyArgTrpLeuSerAlaAspProAlaGlyThrIleAspGly 644
Db 1921 TATTATCAGCGGTGGTGGAGAGTGGCTAAGTGCCTGATCCACAGAGAACAGATAGATGGG 1980
Qy 645 LeuAsnLeuTyrArgMetValArgAsnAsnProValSerLeuGlnAspGluAsnGlyLeu 664
Db 1981 CTAAATTTATTCGGATGGTCAGGAATATCCATTTCTCTATCAGTAAATACGATTA 2040
Qy 665 AlaProGluLysGlyLysTyrThrLysGluValAsn----- 676
Db 2041 CATCCAAATAGTAAATAACAATAGCACTAGAACGAAATCATCCACTTTACTATCTGGATTA 2100
Qy 677 -----PhePheAspGluLeuLysPheLys 684
Db 2101 GCTGGAGTTTATTAATGTCAACGATAAAGAACTTTTCTACACTTAAAGAGT 2160
Qy 685 LeuAlaAlaLysSerSerHisValValLysTrpAsnGluLysGluSerSerTyrThrLys 704
Db 2161 TTTGGCGCACTTCT-----TGGGGAACAAAGCTCAGTATAAACACAA 2205
Qy 705 AsnLysSerLeuLysValValArgValGlyAspSerAspProSerGlyTyrLeuLeuSer 724
Db 2206 ACAATACTTTCCGCTCAGCAGAAATATGGAAT-----TAAAAA 2244
Qy 725 HisGluGluLeuLeuLysGlyIleGluLysSerGlnIleIleTyrSerArgLeuGluGlu 744
Db 2245 CAC-----AAAAACAAATGGAATATAAT----- 2268
Qy 745 AsnSerSerLeuSerGluLysSer-----LysThrAsnLeu 756
Db 2269 AACAAAAAGTTAATGAGACATCTCTCGATGGTAAATTCAAATATGCGAAAAACAAATTA 2328
Qy 757 SerLeuGlySerGluIleSerGly-----TyrMetAlaArgThrIleGlnAspThrIle 774
Db 2329 CAAGATCAAGCGGCACATGCGCGGATCGCATTTTAAACCTGCACCCCGCATATCCGATAAC--- 2385

```
QY 775 SerGluTyrAlaGluGluHisLysTyrArgSerAsnHisProAspPheTyrSerGluThr 794
Db 2386 -----GAGAAAGAGGATGGACATTTAATTATAAGAT----- 2418
QY 795 AspPhePheAlaLeuMetAspLysSerGluLysAsnAspTyrSerGlyGluArgLysIle 814
Db 2419 GAATTGTTAACTTAAAGATAAA--GAAAAATCC-----TTAGGAAAAGGAAAATTA 2469
QY 815 TyrAlaAlaMetGluVal-----LysValTyr 823
Db 2470 TTCCTGGTGTGGAACCTCTGCCGGAATAATCCAGAGCACTATAAAGTTCAGAATGTTAGC 2529
QY 824 HisAspLeuLysAsnLysGlnSerGluLeuHisValAsnTyrAlaLeuAlaHisProTyr 843
Db 2530 GAATTTATTCTGGGATTGAATCCGCTACAAAAATAAATGAGTAGAGTTACATCCATT 2589
QY 844 ThrGln-----LeuSerAsnGluGlu 850
Db 2590 ACATCATCATTAATTAATAAAACACATCTTAAAAAATGNAGAG 2631
```

Search completed: December 14, 2005, 10:29:56
Job time : 1738 secs

This Page Blank (uspo)

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspio)